

- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17523
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17524
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17525
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17526
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17527
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17528
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17529
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17530
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17531
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17532
- gi No. 170354

- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17533
- gi No. 1762374
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 1 to 44

- Alignment No. 17534
- gi No. 1762935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17535
- gi No. 1763015
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17536
- gi No. 1771780
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17537
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17538
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17539
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17540
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17541
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17542
- gi No. 1800281
- % Identity 81.1

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17543
- gi No. 1800281
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17544
- gi No. 1800281
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17545
- gi No. 1800281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17546
- gi No. 1800281
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17547
- gi No. 1805696
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 1 to 38

- Alignment No. 17548
- gi No. 1805696
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17549
- gi No. 1841849
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49

- Alignment No. 17550
- gi No. 208558
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17551
- gi No. 208560
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17552
- gi No. 208562
- % Identity 79.2
- Alignment Length 53

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- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17553
- gi No. 208564
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17554
- gi No. 208566
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17555
- gi No. 208568
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17556
- gi No. 208891
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17557
- gi No. 209603
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17558
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17559
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17560
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17561
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17562
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17563
- gi No. 2118959
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17564
- gi No. 2118960
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17565
- gi No. 2118960
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17566
- gi No. 2118961
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17567
- gi No. 2118961
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17568
- gi No. 2118962
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17569
- gi No. 2118962
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17570
- gi No. 2118963
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49

- Alignment No. 17571
- gi No. 2118963
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48

- Alignment No. 17572
- gi No. 2118964
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2728: from 9 to 49

- Alignment No. 17573
- gi No. 2118964
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17574
- gi No. 2118964
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17575
- gi No. 2118964
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17576
- gi No. 2118965
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17577
- gi No. 2118965
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17578
- gi No. 2118965
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17579
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17580
- gi No. 2129452
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17581
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17582
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17583

- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17584
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17585
- gi No. 2133278
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17586
- gi No. 2133549
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2728: from 1 to 20
- Alignment No. 17587
- gi No. 2133549
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2728: from 16 to 49
- Alignment No. 17588
- gi No. 2133549
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17589
- gi No. 2144011
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17590
- gi No. 2144275
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17591
- gi No. 2144734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17592
- gi No. 2144734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17593
- gi No. 2144734

- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17594
- gi No. 2144734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17595
- gi No. 2149467
- % Identity 75
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17596
- gi No. 2209091
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17597
- gi No. 2209091
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17598
- gi No. 223061
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48

- Alignment No. 17599
- gi No. 224321
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2728: from 11 to 49

- Alignment No. 17600
- gi No. 224321
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17601
- gi No. 224321
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17602
- gi No. 225317
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17603
- gi No. 225319
- % Identity 78.3

- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17604
- gi No. 225320
- % Identity 76.1
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17605
- gi No. 2281952
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17606
- gi No. 2281954
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17607
- gi No. 2281955
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2728: from 1 to 24

- Alignment No. 17608
- gi No. 2281959
- % Identity 72.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 1 to 44

- Alignment No. 17609
- gi No. 2330875
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17610
- gi No. 2408009
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17611
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17612
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17613
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17614
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17615
- gi No. 2558539
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17616
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17617
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17618
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17619
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17620
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17621
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17622
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17623
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

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- Alignment No. 17624
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17625
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17626
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17627
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17628
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17629
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17630
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17631
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17632
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17633
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17634
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17635
- gi No. 2627133
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17636
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17637
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17638
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17639
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17640
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17641
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17642
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17643
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17644

- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17645
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17646
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17647
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17648
- gi No. 2641213
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 1 to 36

- Alignment No. 17649
- gi No. 2641213
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17650
- gi No. 2654141
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17651
- gi No. 2654141
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17652
- gi No. 2654141
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17653
- gi No. 2654141
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17654
- gi No. 2654141

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- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17655
- gi No. 2707837
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17656
- gi No. 2707837
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17657
- gi No. 2707837
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17658
- gi No. 2707837
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17659
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17660
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17661
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17662
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17663
- gi No. 2760345
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17664
- gi No. 2760345
- % Identity 81.1

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17665
- gi No. 2760345
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17666
- gi No. 2760345
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17667
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17668
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17669
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17670
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17671
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17672
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17673
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17674
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53

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- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17675
- gi No. 2760349
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17676
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17677
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17678
- gi No. 279635
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17679
- gi No. 279636
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17680
- gi No. 280386
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17681
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17682
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17683
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17684
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

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- Alignment No. 17685
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17686
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17687
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17688
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17689
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17690
- gi No. 2894306
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17691
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17692
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17693
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17694
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17695
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17696
- gi No. 2995277
- % Identity 83.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2728: from 20 to 49

- Alignment No. 17697
- gi No. 2995949
- % Identity 82.9
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2728: from 15 to 49

- Alignment No. 17698
- gi No. 2995949
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17699
- gi No. 3047314
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17700
- gi No. 3047316
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17701
- gi No. 3047318
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17702
- gi No. 3047318
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17703
- gi No. 3047318
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17704
- gi No. 3047318
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17705

- gi No. 3047318
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17706
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17707
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17708
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17709
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17710
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17711
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17712
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17713
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17714
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17715
- gi No. 3126967

- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17716
- gi No. 3152950
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17717
- gi No. 3158372
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2728: from 24 to 49

- Alignment No. 17718
- gi No. 3158372
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17719
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17720
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17721
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17722
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17723
- gi No. 322750
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17724
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17725
- gi No. 323157
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17726
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17727
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17728
- gi No. 323157
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17729
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17730
- gi No. 323208
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2728: from 3 to 49

- Alignment No. 17731
- gi No. 323208
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17732
- gi No. 323230
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48

- Alignment No. 17733
- gi No. 3265058
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17734
- gi No. 3319208
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17735
- gi No. 3335355
- % Identity 86.4
- Alignment Length 22

- Location of Alignment in SEQ ID NO 2728: from 29 to 50
- Alignment No. 17736
- gi No. 3335355
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2728: from 1 to 23
- Alignment No. 17737
- gi No. 3335355
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17738
- gi No. 3335355
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17739
- gi No. 3335355
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17740
- gi No. 340062
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17741
- gi No. 3452083
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17742
- gi No. 348148
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2728: from 1 to 20
- Alignment No. 17743
- gi No. 348148
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2728: from 16 to 49
- Alignment No. 17744
- gi No. 348149
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17745
- gi No. 3603456
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2728: from 13 to 49

- Alignment No. 17746
- gi No. 3603456
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17747
- gi No. 3603456
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17748
- gi No. 3603456
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17749
- gi No. 3687425
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17750
- gi No. 3687425
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17751
- gi No. 3687425
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17752
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17753
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17754
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17755
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17756
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17757
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17758
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17759
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17760
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17761
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17762
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17763
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17764
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17765
- gi No. 3789940
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17766

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- gi No. 3789940
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17767
- gi No. 3789940
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17768
- gi No. 3789940
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17769
- gi No. 3789942
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17770
- gi No. 3789942
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17771
- gi No. 3789942
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17772
- gi No. 3789942
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17773
- gi No. 3789942
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17774
- gi No. 385076
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17775
- gi No. 3882081
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17776
- gi No. 3882081

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- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17777
- gi No. 3882081
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17778
- gi No. 3885463
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17779
- gi No. 3892189
- % Identity 78.8
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17780
- gi No. 402242
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17781
- gi No. 4049712
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17782
- gi No. 4102845
- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17783
- gi No. 4105408
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17784
- gi No. 4105408
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17785
- gi No. 4105408
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17786
- gi No. 4105408
- % Identity 79.2

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- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17787
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17788
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17789
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17790
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17791
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17792
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17793
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17794
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17795
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17796
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17797
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17798
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17799
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17800
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17801
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17802
- gi No. 4150914
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17803
- gi No. 4150914
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17804
- gi No. 4151082
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17805
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17806
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17807
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17808
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17809
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17810
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17811
- gi No. 421867
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17812
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17813
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17814
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17815
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17816
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17817
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17818
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17819
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17820
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17821
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17822
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17823
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17824
- gi No. 422269
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17825
- gi No. 422270
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17826
- gi No. 422271
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17827

- gi No. 433970
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49

- Alignment No. 17828
- gi No. 433970
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17829
- gi No. 433970
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17830
- gi No. 433970
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17831
- gi No. 433970
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17832
- gi No. 433970
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17833
- gi No. 444791
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17834
- gi No. 444791
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17835
- gi No. 444791
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17836
- gi No. 444791
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17837
- gi No. 4506713

- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17838
- gi No. 4507761
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17839
- gi No. 4510359
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49

- Alignment No. 17840
- gi No. 4586594
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17841
- gi No. 4587232
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17842
- gi No. 4587234
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17843
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17844
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17845
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17846
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17847
- gi No. 4587236
- % Identity 79.2

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- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17848
- gi No. 4587236
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17849
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17850
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17851
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17852
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17853
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17854
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17855
- gi No. 4589760
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17856
- gi No. 4589760
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17857
- gi No. 463363
- % Identity 73.6
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17858
- gi No. 463365
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17859
- gi No. 463367
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17860
- gi No. 463369
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17861
- gi No. 463371
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17862
- gi No. 463373
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17863
- gi No. 463375
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17864
- gi No. 464990
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17865
- gi No. 468272
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17866
- gi No. 4737
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2728: from 1 to 19
- Alignment No. 17867
- gi No. 477630
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

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- Alignment No. 17868
- gi No. 477630
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17869
- gi No. 477815
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17870
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17871
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17872
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17873
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17874
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17875
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17876
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17877
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17878
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17879
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17880
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17881
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17882
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17883
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17884
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17885
- gi No. 485427
- % Identity 76.1
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17886
- gi No. 485518
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17887
- gi No. 49586
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 1 to 44

- Alignment No. 17888

- gi No. 49586
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17889
- gi No. 49586
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17890
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17891
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17892
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17893
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17894
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17895
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17896
- gi No. 510473
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17897
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17898
- gi No. 510473

- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17899
- gi No. 510476
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17900
- gi No. 5107695
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17901
- gi No. 539404
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17902
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17903
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17904
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17905
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17906
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17907
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17908
- gi No. 541546
- % Identity 81.1

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- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17909
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17910
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17911
- gi No. 541953
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17912
- gi No. 541954
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17913
- gi No. 542395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17914
- gi No. 5441519
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17915
- gi No. 552237
- % Identity 78.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49

- Alignment No. 17916
- gi No. 5523967
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17917
- gi No. 5523969
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17918
- gi No. 5523969
- % Identity 77.4
- Alignment Length 53

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- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17919
- gi No. 5523971
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2728: from 31 to 49
- Alignment No. 17920
- gi No. 5523971
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17921
- gi No. 5523973
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17922
- gi No. 5523975
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17923
- gi No. 5523977
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17924
- gi No. 5523979
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17925
- gi No. 5523979
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17926
- gi No. 5523981
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17927
- gi No. 5523983
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17928
- gi No. 5523985
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 2 to 49

- Alignment No. 17929
- gi No. 5523985
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17930
- gi No. 5523987
- % Identity 79.2
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 2 to 49

- Alignment No. 17931
- gi No. 5523987
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17932
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17933
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17934
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17935
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17936
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17937
- gi No. 5531278
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17938
- gi No. 5531281
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17939
- gi No. 554564
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17940
- gi No. 567767
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17941
- gi No. 567767
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17942
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17943
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17944
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17945
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17946
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17947
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17948
- gi No. 576773
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17949

- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17950
- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17951
- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17952
- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17953
- gi No. 576775
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17954
- gi No. 578545
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48

- Alignment No. 17955
- gi No. 578545
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17956
- gi No. 578545
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17957
- gi No. 578545
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17958
- gi No. 578545
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17959
- gi No. 578546

- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48

- Alignment No. 17960
- gi No. 578546
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17961
- gi No. 578546
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17962
- gi No. 578549
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17963
- gi No. 578549
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17964
- gi No. 578551
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17965
- gi No. 578551
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48

- Alignment No. 17966
- gi No. 578551
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17967
- gi No. 578551
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17968
- gi No. 578551
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17969
- gi No. 600539
- % Identity 76.4

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- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17970
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17971
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17972
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17973
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17974
- gi No. 625174
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17975
- gi No. 625174
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17976
- gi No. 625174
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17977
- gi No. 625509
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2728: from 30 to 49

- Alignment No. 17978
- gi No. 625509
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2728: from 1 to 23

- Alignment No. 17979
- gi No. 625509
- % Identity 81.1
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17980
- gi No. 625509
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17981
- gi No. 625509
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17982
- gi No. 630455
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17983
- gi No. 630479
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17984
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17985
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17986
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17987
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17988
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17989
- gi No. 70636
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17990
- gi No. 70636
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17991
- gi No. 70636
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17992
- gi No. 70637
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2728: from 1 to 47
- Alignment No. 17993
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17994
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17995
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17996
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17997
- gi No. 70640
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17998
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17999
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18000
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18001
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18002
- gi No. 70642
- % Identity 81.5
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 18003
- gi No. 70643
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18004
- gi No. 70644
- % Identity 83.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2728: from 20 to 49

- Alignment No. 18005
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18006
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18007
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18008
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18009
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18010

- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18011
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18012
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18013
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18014
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18015
- gi No. 70646
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18016
- gi No. 70647
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18017
- gi No. 70647
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18018
- gi No. 70647
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 18019
- gi No. 70648
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18020
- gi No. 70653

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- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18021
- gi No. 70654
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18022
- gi No. 70657
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18023
- gi No. 70658
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18024
- gi No. 70659
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18025
- gi No. 70660
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2728: from 1 to 53

- Alignment No. 18026
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18027
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18028
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18029
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18030
- gi No. 726391
- % Identity 79.2

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- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18031
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18032
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18033
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18034
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18035
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18036
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18037
- gi No. 82040
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49

- Alignment No. 18038
- gi No. 82040
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18039
- gi No. 82040
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18040
- gi No. 82040
- % Identity 81.1
- Alignment Length 53

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- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18041
- gi No. 82284
- % Identity 78.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2728: from 1 to 29
- Alignment No. 18042
- gi No. 82286
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2728: from 30 to 49
- Alignment No. 18043
- gi No. 82287
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2728: from 1 to 20
- Alignment No. 18044
- gi No. 82288
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2728: from 9 to 49
- Alignment No. 18045
- gi No. 82426
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2728: from 32 to 49
- Alignment No. 18046
- gi No. 82426
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18047
- gi No. 82426
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18048
- gi No. 82512
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2728: from 13 to 49
- Alignment No. 18049
- gi No. 82512
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18050
- gi No. 82512
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

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- Alignment No. 18051
- gi No. 825728
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2728: from 12 to 49

- Alignment No. 18052
- gi No. 82733
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18053
- gi No. 82734
- % Identity 81.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2728: from 7 to 49

- Alignment No. 18054
- gi No. 82734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18055
- gi No. 82734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18056
- gi No. 82734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18057
- gi No. 829173
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18058
- gi No. 83594
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18059
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18060
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18061
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18062
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18063
- gi No. 83596
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 18064
- gi No. 84151
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18065
- gi No. 84151
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18066
- gi No. 84151
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18067
- gi No. 84152
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18068
- gi No. 84152
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18069
- gi No. 84152
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18070
- gi No. 84152
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18071

- gi No. 84152
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 18072
- gi No. 84336
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18073
- gi No. 84337
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18074
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18075
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18076
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18077
- gi No. 84478
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18078
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18079
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18080
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18081
- gi No. 84478

- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18082
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18083
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18084
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18085
- gi No. 84834
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18086
- gi No. 84834
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 18087
- gi No. 85106
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18088
- gi No. 85106
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18089
- gi No. 85106
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18090
- gi No. 86473
- % Identity 76.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2728: from 17 to 50

- Alignment No. 18091
- gi No. 86474
- % Identity 87.5

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- Alignment Length 16
- Location of Alignment in SEQ ID NO 2728: from 34 to 49

- Alignment No. 18092
- gi No. 870794
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18093
- gi No. 870794
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18094
- gi No. 89311
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2728: from 24 to 49

- Alignment No. 18095
- gi No. 89311
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18096
- gi No. 89311
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18097
- gi No. 89311
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18098
- gi No. 899115
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18099
- gi No. 899608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18100
- gi No. 899608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18101
- gi No. 899608
- % Identity 81.1
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18102
- gi No. 899608
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18103
- gi No. 899608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18104
- gi No. 902525
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 18105
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18106
- gi No. 902584
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18107
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18108
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18109
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18110
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18111
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18112
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18113
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18114
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18115
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18116
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18117
- gi No. 91870
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18118
- gi No. 91871
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18119
- gi No. 9295
- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18120
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18121
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18122
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18123
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18124
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18125
- gi No. 940395
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18126
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18127
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18128
- gi No. 967985
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18129
- gi No. 99469
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 10 to 49

- Alignment No. 18130
- gi No. 99771
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18131
- gi No. 99772
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18132

- gi No. 99975
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

Maximum Length Sequence corresponding to clone ID 317675

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2729
- Ceres seq_id 1504393

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2730
- Ceres seq_id 1504394
- Location of start within SEQ ID NO 2729: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2731
- Ceres seq_id 1504395
- Location of start within SEQ ID NO 2729: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 18133
- gi No. 132962
- % Identity 88
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

- Alignment No. 18134
- gi No. 132963
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

- Alignment No. 18135
- gi No. 2500379
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

- Alignment No. 18136
- gi No. 3142154
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2731: from 22 to 38

- Alignment No. 18137
- gi No. 3142154
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2731: from 22 to 40

- Alignment No. 18138
- gi No. 3492819
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

- ```
- Alignment No. 18139
- gi No. 3914754
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2731: from 27 to 46

- Alignment No. 18140
- gi No. 4581465
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

- Alignment No. 18141
- gi No. 464638
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46
```

Maximum Length Sequence corresponding to clone ID 317687

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2732  
- Ceres seq id 1504400

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 2733
- Ceres seq_id 1504401
- Location of start within SEQ ID NO 2732: at 2 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 18142
- Mitochondrial carrier proteins
- Location within SEQ ID NO 2733: from 1 to 64 aa.

(D) Related Amino Acid Sequences

- ```
- Alignment No. 18143
- gi No. 2398829
- % Identity 85.5
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2733: from 1 to 69

- Alignment No. 18144
- gi No. 3115108
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2733: from 1 to 66

- Alignment No. 18145
- gi No. 3451392
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2733: from 1 to 66

- Alignment No. 18146
- gi No. 4063007
- % Identity 72.7
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2733: from 1 to 66
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2734

- Ceres seq\_id 1504402
- Location of start within SEQ ID NO 2732: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 18147
- Mitochondrial carrier proteins
- Location within SEQ ID NO 2734: from 1 to 56 aa.

(D) Related Amino Acid Sequences

- Alignment No. 18148
- gi No. 2398829
- % Identity 85.5
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2734: from 1 to 61
- Alignment No. 18149
- gi No. 3115108
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2734: from 1 to 58
- Alignment No. 18150
- gi No. 3451392
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2734: from 1 to 58
- Alignment No. 18151
- gi No. 4063007
- % Identity 72.7
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2734: from 1 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2735
- Ceres seq\_id 1504403
- Location of start within SEQ ID NO 2732: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 18152
- Mitochondrial carrier proteins
- Location within SEQ ID NO 2735: from 1 to 55 aa.

(D) Related Amino Acid Sequences

- Alignment No. 18153
- gi No. 2398829
- % Identity 85.5
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2735: from 1 to 60
- Alignment No. 18154
- gi No. 3115108
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2735: from 1 to 57
- Alignment No. 18155
- gi No. 3451392
- % Identity 83.3



(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..789
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atcatcaaca | aaaacaattc | tcaatacaca  | aaacacaaaa | cacaaagaag | tttaattctc | 60  |
| tgaagaaaga | tgagttctac | aagcaaagca  | tggacagtgg | cagtgagcat | cggagccgta | 120 |
| gaggcattaa | aagaccaact | aggtctttgt  | cggtggaact | acatactccg | gtcggttaat | 180 |
| caacatctcc | ggaacaacgt | tagatctgtt  | tctcaaggga | aaaggttctc | ttcgtcttct | 240 |
| gtctccgcag | ccgttacctc | ctctgggtgag | agcgagaaga | cgaagagaac | cttttccttt | 300 |
| gagaaacaat | tgatcagagc | tttaaagaaa  | aagatggaat | tcaccgcaga | gcagctaagc | 360 |
| caataacaag | gcaccgacga | atcaaagccg  | atctacgtcg | caatcaaagg | ccgtgtgttc | 420 |
| gaygtcacca | ccggaaaatc | cttctacggc  | tccggaggcg | attactcgat | gttcgccgga | 480 |
| aaagacgcga | gcagagcttt | gggtaagatg  | agtaagaacg | aagaagatgt | gtctccttct | 540 |
| cttgaaggtc | tactgagaaa | agagatcaat  | actcttaatg | attgggagac | caaatttgaa | 600 |
| gctaagtatc | ctgtcgttgg | ccgtgttgtc  | tcttaggtct | ctcttctgag | attgcactat | 660 |
| gttatgtaac | tattgtgtgt | gaggatcttt  | gtgttgtgtg | ttttctgatt | tcgtgtttgg | 720 |
| atctgatcgt | tttgatacaa | ttaccataag  | taccaaatta | tctatgaaat | aaatcgggga | 780 |
| tttcgtgtt  |            |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Ser | Thr | Ser | Lys | Ala | Trp | Thr | Val | Ala | Val | Ser | Ile | Gly | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Glu | Ala | Leu | Lys | Asp | Gln | Leu | Gly | Leu | Cys | Arg | Trp | Asn | Tyr | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Arg | Ser | Val | Asn | Gln | His | Leu | Arg | Asn | Asn | Val | Arg | Ser | Val | Ser |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gln | Gly | Lys | Arg | Phe | Ser | Ser | Ser | Ser | Val | Ser | Ala | Ala | Val | Thr | Ser |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Gly | Glu | Ser | Glu | Lys | Thr | Lys | Arg | Thr | Phe | Ser | Leu | Glu | Lys | Gln |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Leu | Ile | Arg | Ala | Leu | Lys | Lys | Lys | Met | Glu | Phe | Thr | Ala | Glu | Gln | Leu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser | Gln | Tyr | Asn | Gly | Thr | Asp | Glu | Ser | Lys | Pro | Ile | Tyr | Val | Ala | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Lys | Gly | Arg | Val | Phe | Xaa | Val | Thr | Thr | Gly | Lys | Ser | Phe | Tyr | Gly | Ser |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Gly | Asp | Tyr | Ser | Met | Phe | Ala | Gly | Lys | Asp | Ala | Ser | Arg | Ala | Leu |  |
|     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |     |  |
| Gly | Lys | Met | Ser | Lys | Asn | Glu | Glu | Asp | Val | Ser | Pro | Ser | Leu | Glu | Gly |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Leu | Thr | Glu | Lys | Glu | Ile | Asn | Thr | Leu | Asn | Asp | Trp | Glu | Thr | Lys | Phe |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Glu | Ala | Lys | Tyr | Pro | Val | Val | Gly | Arg | Val | Val | Ser |     |     |     |     |  |

180 185  
(2) INFORMATION FOR SEQ ID NO:3:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..100  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497853  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
Met Glu Phe Thr Ala Glu Gln Leu Ser Gln Tyr Asn Gly Thr Asp Glu  
1 5 10 15  
Ser Lys Pro Ile Tyr Val Ala Ile Lys Gly Arg Val Phe Xaa Val Thr  
20 25 30  
Thr Gly Lys Ser Phe Tyr Gly Ser Gly Gly Asp Tyr Ser Met Phe Ala  
35 40 45  
Gly Lys Asp Ala Ser Arg Ala Leu Gly Lys Met Ser Lys Asn Glu Glu  
50 55 60  
Asp Val Ser Pro Ser Leu Glu Gly Leu Thr Glu Lys Glu Ile Asn Thr  
65 70 75 80  
Leu Asn Asp Trp Glu Thr Lys Phe Glu Ala Lys Tyr Pro Val Val Gly  
85 90 95  
Arg Val Val Ser  
100

(2) INFORMATION FOR SEQ ID NO:4:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1005 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1005  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497854  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
aaaaacaaac aaaaaaatca gtgttcggct ctaacacgct cgacgaccat ggcgggtctcg 60  
tttaatacaaa cgcttcacca gccttctctg agtccagct gtagcatcaa gctttattct 120  
gggttaaagc ctcaatctgc aagctttttg gcaagtgggt atcagaattt gaataaggag 180  
ttctatggaa gagttcataa gagtctgcaa tctgggactg gcaaagcgag caggtcacgg 240  
gtaaagatga tgccaatagg aacaccgaga gtgccctaca gaaaccgtga agaaggcact 300  
tggcaakggg ttgatatatg gaatgccctt tatcgagagc gtgtaatctt cattggacaa 360  
aacattgatg aagagtttag caaccagata ttagcaacca tgttgtacct tgatactctt 420  
gatgactcga ggaggattta tatgtacctt aatgggtccg gtggtgatct tactccaagt 480  
ctagccatct atgatacaat gaagagcttg aaaagtcgg ttgggacaca ttgcgttggg 540  
cttgcttaca accttgacag ttttcttctt gcggctggag aaaaggggtca ccgatttgcg 600  
atgccattgt caagaatcgc cctccaatca ccagctgggt cagcccgtgg ccaggctgat 660  
gatatccaaa atgaagcaaa agagctttca aggataagag actacctctt caatgaacta 720  
gccaaagaata caggccagcc tgcggaaagg gtcttcaaag acttgagccg ggtgaaaagg 780  
ttcaatgcag aggaagcaat cgagtatgga cttattgata agattgttag accaccgcgc 840  
atcaaagaag acgtcctcgc ccaagacgaa agcgcagggc taggctagtc ttttttgttt 900  
gtttgttatg tcaaaaagttt taatctttat gttattgtga ttgtgattgt tacctaaaaa 960  
aatcactgat tattgttttt tcattccacc gattttctga tttct

(2) INFORMATION FOR SEQ ID NO:5:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 295 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..295  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Lys | Gln | Lys | Asn | Gln | Cys | Ser | Ala | Leu | Thr | Arg | Ser | Thr | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Ala | Val | Ser | Phe | Asn | Thr | Thr | Leu | His | Gln | Pro | Ser | Leu | Ser | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Cys | Ser | Ile | Lys | Leu | Tyr | Ser | Gly | Leu | Lys | Pro | Gln | Ser | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Ala | Ser | Gly | Tyr | Gln | Asn | Leu | Asn | Lys | Glu | Phe | Tyr | Gly | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | His | Lys | Ser | Leu | Gln | Ser | Gly | Thr | Gly | Lys | Ala | Ser | Arg | Ser | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Lys | Met | Met | Pro | Ile | Gly | Thr | Pro | Arg | Val | Pro | Tyr | Arg | Asn | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Glu | Glu | Gly | Thr | Trp | Gln | Xaa | Val | Asp | Ile | Trp | Asn | Ala | Leu | Tyr | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Arg | Val | Ile | Phe | Ile | Gly | Gln | Asn | Ile | Asp | Glu | Glu | Phe | Ser | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Ile | Leu | Ala | Thr | Met | Leu | Tyr | Leu | Asp | Thr | Leu | Asp | Asp | Ser | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Ile | Tyr | Met | Tyr | Leu | Asn | Gly | Pro | Gly | Gly | Asp | Leu | Thr | Pro | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Ala | Ile | Tyr | Asp | Thr | Met | Lys | Ser | Leu | Lys | Ser | Pro | Val | Gly | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Cys | Val | Gly | Leu | Ala | Tyr | Asn | Leu | Ala | Gly | Phe | Leu | Leu | Ala | Ala |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Glu | Lys | Gly | His | Arg | Phe | Ala | Met | Pro | Leu | Ser | Arg | Ile | Ala | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Ser | Pro | Ala | Gly | Ala | Ala | Arg | Gly | Gln | Ala | Asp | Asp | Ile | Gln | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Ala | Lys | Glu | Leu | Ser | Arg | Ile | Arg | Asp | Tyr | Leu | Phe | Asn | Glu | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ala | Lys | Asn | Thr | Gly | Gln | Pro | Ala | Glu | Arg | Val | Phe | Lys | Asp | Leu | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Arg | Val | Lys | Arg | Phe | Asn | Ala | Glu | Glu | Ala | Ile | Glu | Tyr | Gly | Leu | Ile |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Lys | Ile | Val | Arg | Pro | Pro | Arg | Ile | Lys | Glu | Asp | Ala | Pro | Arg | Gln |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Glu | Ser | Ala | Gly | Leu | Gly |     |     |     |     |     |     |     |     |     |
| 290 |     |     |     |     | 295 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 279 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..279  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Ser | Phe | Asn | Thr | Thr | Leu | His | Gln | Pro | Ser | Leu | Ser | Pro |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Ser | Cys | Ser | Ile | Lys | Leu | Tyr | Ser | Gly | Leu | Lys | Pro | Gln | Ser | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

```

Phe Leu Ala Ser Gly Tyr Gln Asn Leu Asn Lys Glu Phe Tyr Gly Arg
 35 40 45
Val His Lys Ser Leu Gln Ser Gly Thr Gly Lys Ala Ser Arg Ser Arg
 50 55 60
Val Lys Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg
 65 70 75 80
Glu Glu Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg
 85 90 95
Glu Arg Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn
 100 105 110
Gln Ile Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg
 115 120 125
Arg Ile Tyr Met Tyr Leu Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser
 130 135 140
Leu Ala Ile Tyr Asp Thr Met Lys Ser Leu Lys Ser Pro Val Gly Thr
 145 150 155 160
His Cys Val Gly Leu Ala Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala
 165 170 175
Gly Glu Lys Gly His Arg Phe Ala Met Pro Leu Ser Arg Ile Ala Leu
 180 185 190
Gln Ser Pro Ala Gly Ala Ala Arg Gly Gln Ala Asp Asp Ile Gln Asn
 195 200 205
Glu Ala Lys Glu Leu Ser Arg Ile Arg Asp Tyr Leu Phe Asn Glu Leu
 210 215 220
Ala Lys Asn Thr Gly Gln Pro Ala Glu Arg Val Phe Lys Asp Leu Ser
 225 230 235 240
Arg Val Lys Arg Phe Asn Ala Glu Glu Ala Ile Glu Tyr Gly Leu Ile
 245 250 255
Asp Lys Ile Val Arg Pro Pro Arg Ile Lys Glu Asp Ala Pro Arg Gln
 260 265 270
Asp Glu Ser Ala Gly Leu Gly
 275

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg Glu Glu
 1 5 10 15
Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg Glu Arg
 20 25 30
Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn Gln Ile
 35 40 45
Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg Arg Ile
 50 55 60
Tyr Met Tyr Leu Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser Leu Ala
 65 70 75 80
Ile Tyr Asp Thr Met Lys Ser Leu Lys Ser Pro Val Gly Thr His Cys
 85 90 95
Val Gly Leu Ala Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala Gly Glu
 100 105 110
Lys Gly His Arg Phe Ala Met Pro Leu Ser Arg Ile Ala Leu Gln Ser
 115 120 125
Pro Ala Gly Ala Ala Arg Gly Gln Ala Asp Asp Ile Gln Asn Glu Ala

```



130 135 140  
Lys Glu Leu Ser Arg Ile Arg Asp Tyr Leu Phe Asn Glu Leu Ala Lys  
145 150 155 160  
Asn Thr Gly Gln Pro Ala Glu Arg Val Phe Lys Asp Leu Ser Arg Val  
165 170 175  
Lys Arg Phe Asn Ala Glu Glu Ala Ile Glu Tyr Gly Leu Ile Asp Lys  
180 185 190  
Ile Val Arg Pro Pro Arg Ile Lys Glu Asp Ala Pro Arg Gln Asp Glu  
195 200 205  
Ser Ala Gly Leu Gly  
210

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..678
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

|          |        |         |        |         |        |         |        |         |        |        |       |     |
|----------|--------|---------|--------|---------|--------|---------|--------|---------|--------|--------|-------|-----|
| aatcgcat | tcgata | cgaa    | tagccg | acgg    | agaaat | gacc    | aagttc | cagga   | agctcg | gccg   | 60    |     |
| cccagc   | caggt  | caccgt  | atgt   | ccatgc  | tcag   | gactat  | gggt   | tctcaat | tgg    | tgcaac | acga  | 120 |
| gcgaatt  | gag    | accact  | gtta   | caaagg  | ctat   | agaagt  | tcgt   | cgtctt  | gctg   | ataat  | atgat | 180 |
| tcaact   | cgg    | aaagag  | gggt   | cactag  | ctgc   | agcaag  | aaga   | gctg    | ctgg   | ttgtt  | agagg | 240 |
| agatgat  | gta    | cttcac  | aaga   | ttttta  | caga   | attggc  | kcat   | cgatac  | aaag   | atagag | ctgg  | 300 |
| tggata   | caca   | agaatg  | cttc   | gtactc  | gcat   | tcgtgt  | tggg   | gatg    | ctgcc  | caatgg | ccta  | 360 |
| tatcgag  | ttt    | atcgat  | agag   | agaacg  | agct   | aaggca  | aatca  | aaacc   | agcta  | ctcct  | caacc | 420 |
| tccacct  | cga    | gtgcc   | acttg  | atccat  | gggc   | tagatc  | cccg   | ctcacc  | aggc   | agtat  | gctcc | 480 |
| accaaag  | gag    | gcaaaaa | act    | tctgat  | tctg   | acctata | aaat   | agaaga  | agat   | ctctct | cgt   | 540 |
| ctctcac  | acc    | agaagat | cat    | gtttttt | tttc   | cccttg  | ccca   | tgttgt  | ttct   | ccttca | accc  | 600 |
| atagctt  | tgt    | atgtct  | ggca   | ccttatt | cat    | cactgt  | catt   | cacaat  | gtgt   | ttaaa  | acagt | 660 |
| ttaaat   | gtag   | tttcct  | tg     |         |        |         |        |         |        |        |       |     |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ala | Phe | Ser | Asp | Arg | Ile | Ala | Asp | Gly | Glu | Met | Thr | Lys | Phe | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Leu | Gly | Arg | Pro | Ala | Gly | His | Arg | Met | Ser | Met | Leu | Arg | Thr | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Gln | Leu | Val | Gln | His | Glu | Arg | Ile | Glu | Thr | Thr | Val | Thr | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Ile | Glu | Val | Arg | Arg | Leu | Ala | Asp | Asn | Met | Ile | Gln | Leu | Gly | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Ser | Leu | Ala | Ala | Ala | Arg | Arg | Ala | Ala | Gly | Phe | Val | Arg | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Asp | Val | Leu | His | Lys | Ile | Phe | Thr | Glu | Leu | Xaa | His | Arg | Tyr | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Arg | Ala | Gly | Tyr | Thr | Arg | Met | Leu | Arg | Thr | Arg | Ile | Arg | Val |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe Ile Asp Arg Glu Asn  
115 120 125  
Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln Pro Pro Pro Arg Val  
130 135 140  
Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr Arg Gln Tyr Ala Pro  
145 150 155 160  
Pro Lys Glu Ala Lys Asn Phe  
165

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Lys Phe Arg Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser  
1 5 10 15  
Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg Ile Glu  
20 25 30  
Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp Asn Met  
35 40 45  
Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Arg Arg Ala Ala  
50 55 60  
Gly Phe Val Arg Gly Asp Asp Val Leu His Lys Ile Phe Thr Glu Leu  
65 70 75 80  
Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met Leu Arg  
85 90 95  
Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe  
100 105 110  
Ile Asp Arg Glu Asn Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln  
115 120 125  
Pro Pro Pro Arg Val Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr  
130 135 140  
Arg Gln Tyr Ala Pro Pro Lys Glu Ala Lys Asn Phe  
145 150 155

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ser Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg  
1 5 10 15  
Ile Glu Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp  
20 25 30  
Asn Met Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Arg Arg  
35 40 45  
Ala Ala Gly Phe Val Arg Gly Asp Asp Val Leu His Lys Ile Phe Thr  
50 55 60  
Glu Leu Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Arg | Thr | Arg | Ile | Arg | Val | Gly | Asp | Ala | Ala | Pro | Met | Ala | Tyr | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Phe | Ile | Asp | Arg | Glu | Asn | Glu | Leu | Arg | Gln | Ser | Lys | Pro | Ala | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Gln | Pro | Pro | Pro | Arg | Val | Pro | Leu | Asp | Pro | Trp | Ala | Arg | Ser | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Thr | Arg | Gln | Tyr | Ala | Pro | Pro | Lys | Glu | Ala | Lys | Asn | Phe |     |     |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..505  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| atcaatcggg | ttatctgcac | ttgtttcaat | ggtgcattca | atatctctca  | agctgggtgct | 60  |
| cttgcttgcc | ttacacccga | aggacttgag | gcaatgcata | agggtgattgg | attctataaaa | 120 |
| gaaaacacaa | acataatcat | tgacacattc | acatctctcg | ggtagatgt   | atatggagga  | 180 |
| aatgcgcctt | acgtatgggt | tcacttccc  | aaccaaagct | catgggatgt  | gtttgctgag  | 240 |
| attctggaga | agactcatgt | ggttacaact | ccaggaagt  | ggtttgacc   | aggggggtgaa | 300 |
| gggttcgttc | gtgtcagtg  | ctttggtcac | agagagaaca | tcttagaggc  | atgtcgaaga  | 360 |
| ttcaagcagc | tttacaattg | aagaaccttg | tttgtaatcg | ttctctcatca | tcataccctt  | 420 |
| ctttaatgac | atgattttag | ttaaaaatat | gtcgtttcca | ttgtkktstg  | gaatttgtag  | 480 |
| aagacacttt | tqacaccaqt | qtttc      |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..126  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Asn | Arg | Ile | Ile | Cys | Thr | Cys | Phe | Asn | Gly | Ala | Ser | Asn | Ile | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Ala | Gly | Ala | Leu | Ala | Cys | Leu | Thr | Pro | Glu | Gly | Leu | Glu | Ala | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Lys | Val | Ile | Gly | Phe | Tyr | Lys | Glu | Asn | Thr | Asn | Ile | Ile | Ile | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Phe | Thr | Ser | Leu | Gly | Tyr | Asp | Val | Tyr | Gly | Gly | Asn | Ala | Pro | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Trp | Val | His | Phe | Pro | Asn | Gln | Ser | Ser | Trp | Asp | Val | Phe | Ala | Glu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Leu | Glu | Lys | Thr | His | Val | Val | Thr | Thr | Pro | Gly | Ser | Gly | Phe | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Gly | Gly | Glu | Gly | Phe | Val | Arg | Val | Ser | Ala | Phe | Gly | His | Arg | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Ile | Leu | Glu | Ala | Cys | Arg | Arg | Phe | Lys | Gln | Leu | Tyr | Lys |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..95
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Lys | Val | Ile | Gly | Phe | Tyr | Lys | Glu | Asn | Thr | Asn | Ile | Ile | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | Thr | Phe | Thr | Ser | Leu | Gly | Tyr | Asp | Val | Tyr | Gly | Gly | Asn | Ala | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Val | Trp | Val | His | Phe | Pro | Asn | Gln | Ser | Ser | Trp | Asp | Val | Phe | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Ile | Leu | Glu | Lys | Thr | His | Val | Val | Thr | Thr | Pro | Gly | Ser | Gly | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Pro | Gly | Gly | Glu | Gly | Phe | Val | Arg | Val | Ser | Ala | Phe | Gly | His | Arg |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Glu | Asn | Ile | Leu | Glu | Ala | Cys | Arg | Arg | Phe | Lys | Gln | Leu | Tyr | Lys |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 431 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..431
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|              |            |            |             |            |            |     |
|--------------|------------|------------|-------------|------------|------------|-----|
| atttcctaaa   | agaacgaacg | acgccatata | caccgagaag  | ctcaacgttc | gtcatcactc | 60  |
| ttctcgcttc   | tcggcgcttc | catcgccgtc | tctatctaata | ttcgtcctgc | gtcgacctgg | 120 |
| tgagctactt   | cagattccgg | ccatcacgca | gctccagttg  | tatgctttgt | ggctaataca | 180 |
| aagatgacaa   | caatcaaaac | cggtcagaaa | actcaaaagt  | cttctccttc | cggttctgct | 240 |
| actaccgcta   | ctggtactct | taagcagtc  | tcagcatcgt  | ttaawaggtg | gggaaggaga | 300 |
| caccgcgttg   | taagatatgg | acttccgatg | atatctctca  | ctgtatttgg | agccctcgga | 360 |
| ctcggccaac   | tccttcaagg | cagtaaggat | attgcaaagg  | taaaagatga | ccaagaatgg | 420 |
| gagattatag a |            |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..61
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Pro | Lys | Arg | Thr | Asn | Asp | Ala | Ile | Tyr | Thr | Glu | Lys | Leu | Asn | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | His | His | Ser | Arg | Phe | Ser | Ala | Ser | Pro | Ser | Pro | Ser | Leu | Ser |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Phe | Val | Leu | Arg | Arg | Pro | Gly | Glu | Leu | Leu | Gln | Ile | Pro | Ala | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr | Gln | Leu | Gln | Leu | Tyr | Ala | Leu | Trp | Leu | Ile | Gln | Arg |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Phe Leu Lys Glu Arg Thr Thr Pro Tyr Thr Pro Arg Ser Ser Thr Phe
1 5 10 15
Val Ile Thr Leu Leu Ala Ser Arg Arg Leu His Arg Arg Leu Tyr Leu
20 25 30
Ile Ser Ser Cys Val Asp Leu Val Ser Tyr Phe Arg Phe Arg Pro Ser
35 40 45
Arg Ser Ser Ser Cys Met Leu Cys Gly
50 55
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Met Thr Thr Ile Lys Thr Gly Gln Lys Thr Gln Lys Ser Ser Pro Ser
1 5 10 15
Gly Ser Ala Thr Thr Ala Thr Gly Thr Leu Lys Gln Ser Ser Ala Ser
20 25 30
Phe Xaa Arg Trp Gly Arg Arg His Pro Phe Val Arg Tyr Gly Leu Pro
35 40 45
Met Ile Ser Leu Thr Val Phe Gly Ala Leu Gly Leu Gly Gln Leu Leu
50 55 60
Gln Gly Ser Lys Asp Ile Ala Lys Val Lys Asp Asp Gln Glu Trp Glu
65 70 75 80
Ile Ile
```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2584
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
aaacacacca aaatcaaaag ctgagagctc tcttacattg aagctacttt cgaagatagc 60
attcactgat tggtaaagag ttctagaagc gacgagcatc ttcttttagtt cccgagtttt 120
ctgcgtttga gaagtctggt ctagaaagta atgggtgaca gcgaggccat ggtttccgag 180
gggtatactt ctgctccata tggagactat aatgcttctg ctgctactgt ggaatcgacc 240
gggcaagaga ctgcaccaat tgttgatgca tcacactcgg tcaacaatga ttctttggtc 300
```

aatggtactg cgccagttga gaacggaagt gcaacagata atgtggctgt gactgctcca 360  
gcagcgagc atggagacaa tactggctct acactctcaa cggaagagga gcgcttggtg 420  
aatattgtaa gggcaaatc tttagagttt aatgcttgga ctgccttgat tgatgagacg 480  
gagaggaatag cgcaggacaa tatagcaaaa atccggaagg tctatgatgc tttcttagct 540  
gaatttcctc tgtgttatgg ctattggaaa aagtttgccg atcatgaggc tcgggtgggg 600  
gcaatggaca aagtcgtgga ggtttatgaa agagcagtgc tgggagtgc atattcagtg 660  
gatatctggt tgcattattg cacttttgcc atcaatacat atggagatcc agaaacgac 720  
agaaggcttt ttgaacgagc tttggtttac gttggaactg attttctttc ctctccgttg 780  
tgggacaaat acattgagta tgagtacatg cagcaggact ggagccgagt tgccttgatt 840  
tacaccagaa tattggagaa tccaattcaa aatctggata gatatttcag cagttttaag 900  
gagctagctg aaacacggcc tctgtcggaa ctaaggagtg ctgaggaatc cgcagctgct 960  
gctgttgctg ttgctggtga tgcttctgaa agtgcagcat ctgagtccgg tgaaaaggca 1020  
gatgaaggac gatctcaagt tgatggttcc accgaacaat cccctaaatt ggaaagtgc 1080  
agttcaactg aacctgagga gttgaagaag tatgtaggca tcagggaagc catgtacata 1140  
aaatcgaaag agtttgaatc taaaatcatt ggttatgaaa tggctataag gaggccctat 1200  
ttccatgtgc gtccctctgaa tgtcgcagaa ctggagaatt ggcacaacta tctggatttc 1260  
attgagaggg atggagactt caataagggt gtcaagctgt atgaaagatg tgtggttacc 1320  
tgtgcaaatt acccagaata ctggattcgt tatgtgacaa acatggaagc aagtggaggt 1380  
gcggaacctg cagaaaatgc ccttgctcga gcaactcaag tctttgtcaa gaaacaacca 1440  
gagattcacc tattgtctgc tcgattaaaa gagatatagc tgggtctaga 1500  
gctgcatacc aattagtgc ctctgaaatt tctcctggac ttcttgaagc agtaatcaag 1560  
catgcaataa tggaaataccg actaggtaat ctggatgatg ctttctcttt gtatgagcaa 1620  
gtgattgctg ttgaaaaggg gaaagaacat tccacaatac tgccactgct gtatgcgcag 1680  
tattcaaggt ttccatactt ggtctccagg gatgctgaga aagctaggag gattattgtc 1740  
gaagcacttg accatgtaca accgtcaaaa cctctcatgg aagcactgat tcattttgag 1800  
gcgattcagc caccaccaag agagattgat taccttgagc cacttgtaga gaaagttata 1860  
aagccagatg cagatgcccc aaacattgca agttccactg agaggaaga gctatcctta 1920  
atatatatag agttcctggg tatttttggg gatgtgaagt ccattaaaaa agcggaagat 1980  
caacatgtta aactgtttta tcctcatcgg agcacgtcgg agctgaaaaa gcgtagcgca 2040  
gatgattttc tcgcatcaga taggacgaaa atggcaaaaa cttacaacgg cactccacct 2100  
gctcagccag tatccaatgc atatccaaat gctcaggctc aatgggtctg tggttatgct 2160  
gcgagcctc agacttggcc accagcacia gctgctcctg ctcaaccaca gcaatggaac 2220  
cctgcctacg gtcaacaggc tgcttatggt gcatatgggg gatatacctgc tggctatacc 2280  
gctccacaag caccaacacc tgtgccacag gccgcagctt atggagcgta tctgtcctag 2340  
acatacccaa cgcagagtta tgcacctcca gttgcagcag cagcaccagc ggctgcaccg 2400  
gtgcagcaac cggctgctgc tgttgctcct caagcgtact acaacacgta ctactgagcc 2460  
tattactgct gctggctggt tttgtagtgt aattgataac catttgcttc tatctactca 2520  
aatttagtgt ctggatgttt acatgtctct ctttctcga tcagtgacaa tagatattta 2580  
cttt

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..768
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Gly Asp Ser Glu Ala Met Val Ser Glu Gly Tyr Thr Ser Ala Pro  
1 5 10 15  
Tyr Gly Asp Tyr Asn Ala Ser Ala Thr Val Glu Ser Thr Gly Gln  
20 25 30  
Glu Thr Ala Pro Ile Val Asp Ala Ser His Ser Val Asn Asn Asp Ser  
35 40 45  
Leu Val Asn Gly Thr Ala Pro Val Glu Asn Gly Ser Ala Thr Asp Asn  
50 55 60  
Val Ala Val Thr Ala Pro Ala Ala Glu His Gly Asp Asn Thr Gly Ser  
65 70 75 80

Thr Leu Ser Thr Glu Glu Glu Arg Leu Trp Asn Ile Val Arg Ala Asn  
85 90 95  
Ser Leu Glu Phe Asn Ala Trp Thr Ala Leu Ile Asp Glu Thr Glu Arg  
100 105 110  
Ile Ala Gln Asp Asn Ile Ala Lys Ile Arg Lys Val Tyr Asp Ala Phe  
115 120 125  
Leu Ala Glu Phe Pro Leu Cys Tyr Gly Tyr Trp Lys Lys Phe Ala Asp  
130 135 140  
His Glu Ala Arg Val Gly Ala Met Asp Lys Val Val Glu Val Tyr Glu  
145 150 155 160  
Arg Ala Val Leu Gly Val Thr Tyr Ser Val Asp Ile Trp Leu His Tyr  
165 170 175  
Cys Thr Phe Ala Ile Asn Thr Tyr Gly Asp Pro Glu Thr Ile Arg Arg  
180 185 190  
Leu Phe Glu Arg Ala Leu Val Tyr Val Gly Thr Asp Phe Leu Ser Ser  
195 200 205  
Pro Leu Trp Asp Lys Tyr Ile Glu Tyr Glu Tyr Met Gln Gln Asp Trp  
210 215 220  
Ser Arg Val Ala Leu Ile Tyr Thr Arg Ile Leu Glu Asn Pro Ile Gln  
225 230 235 240  
Asn Leu Asp Arg Tyr Phe Ser Ser Phe Lys Glu Leu Ala Glu Thr Arg  
245 250 255  
Pro Leu Ser Glu Leu Arg Ser Ala Glu Glu Ser Ala Ala Ala Val  
260 265 270  
Ala Val Ala Gly Asp Ala Ser Glu Ser Ala Ala Ser Glu Ser Gly Glu  
275 280 285  
Lys Ala Asp Glu Gly Arg Ser Gln Val Asp Gly Ser Thr Glu Gln Ser  
290 295 300  
Pro Lys Leu Glu Ser Ala Ser Ser Thr Glu Pro Glu Glu Leu Lys Lys  
305 310 315 320  
Tyr Val Gly Ile Arg Glu Ala Met Tyr Ile Lys Ser Lys Glu Phe Glu  
325 330 335  
Ser Lys Ile Ile Gly Tyr Glu Met Ala Ile Arg Arg Pro Tyr Phe His  
340 345 350  
Val Arg Pro Leu Asn Val Ala Glu Leu Glu Asn Trp His Asn Tyr Leu  
355 360 365  
Asp Phe Ile Glu Arg Asp Gly Asp Phe Asn Lys Val Val Lys Leu Tyr  
370 375 380  
Glu Arg Cys Val Val Thr Cys Ala Asn Tyr Pro Glu Tyr Trp Ile Arg  
385 390 395 400  
Tyr Val Thr Asn Met Glu Ala Ser Gly Ser Ala Asp Leu Ala Glu Asn  
405 410 415  
Ala Leu Ala Arg Ala Thr Gln Val Phe Val Lys Lys Gln Pro Glu Ile  
420 425 430  
His Leu Phe Ala Ala Arg Leu Lys Glu Gln Asn Gly Asp Ile Ala Gly  
435 440 445  
Ala Arg Ala Ala Tyr Gln Leu Val His Ser Glu Ile Ser Pro Gly Leu  
450 455 460  
Leu Glu Ala Val Ile Lys His Ala Asn Met Glu Tyr Arg Leu Gly Asn  
465 470 475 480  
Leu Asp Asp Ala Phe Ser Leu Tyr Glu Gln Val Ile Ala Val Glu Lys  
485 490 495  
Gly Lys Glu His Ser Thr Ile Leu Pro Leu Leu Tyr Ala Gln Tyr Ser  
500 505 510  
Arg Phe Ser Tyr Leu Val Ser Arg Asp Ala Glu Lys Ala Arg Arg Ile  
515 520 525  
Ile Val Glu Ala Leu Asp His Val Gln Pro Ser Lys Pro Leu Met Glu  
530 535 540  
Ala Leu Ile His Phe Glu Ala Ile Gln Pro Pro Pro Arg Glu Ile Asp  
545 550 555 560  
Tyr Leu Glu Pro Leu Val Glu Lys Val Ile Lys Pro Asp Ala Asp Ala

```
(2) INFORMATION FOR SEQ ID NO:21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..762
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497877
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
```

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21. |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                                      | Val | Ser | Glu | Gly | Tyr | Thr | Ser | Ala | Pro | Tyr | Gly | Asp | Tyr | Asn | Ala |  |
| 1                                        |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser                                      | Ala | Ala | Thr | Val | Glu | Ser | Thr | Gly | Gln | Glu | Thr | Ala | Pro | Ile | Val |  |
|                                          |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp                                      | Ala | Ser | His | Ser | Val | Asn | Asn | Asp | Ser | Leu | Val | Asn | Gly | Thr | Ala |  |
|                                          |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro                                      | Val | Glu | Asn | Gly | Ser | Ala | Thr | Asp | Asn | Val | Ala | Val | Thr | Ala | Pro |  |
|                                          | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ala                                      | Ala | Glu | His | Gly | Asp | Asn | Thr | Gly | Ser | Thr | Leu | Ser | Thr | Glu | Glu |  |
| 65                                       |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Glu                                      | Arg | Leu | Trp | Asn | Ile | Val | Arg | Ala | Asn | Ser | Leu | Glu | Phe | Asn | Ala |  |
|                                          |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Trp                                      | Thr | Ala | Leu | Ile | Asp | Glu | Thr | Glu | Arg | Ile | Ala | Gln | Asp | Asn | Ile |  |
|                                          |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala                                      | Lys | Ile | Arg | Lys | Val | Tyr | Asp | Ala | Phe | Leu | Ala | Glu | Phe | Pro | Leu |  |
|                                          |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Cys                                      | Tyr | Gly | Tyr | Trp | Lys | Lys | Phe | Ala | Asp | His | Glu | Ala | Arg | Val | Gly |  |
|                                          | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ala                                      | Met | Asp | Lys | Val | Val | Glu | Val | Tyr | Glu | Arg | Ala | Val | Leu | Gly | Val |  |
| 145                                      |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Thr                                      | Tyr | Ser | Val | Asp | Ile | Trp | Leu | His | Tyr | Cys | Thr | Phe | Ala | Ile | Asn |  |
|                                          |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |



Thr Tyr Gly Asp Pro Glu Thr Ile Arg Arg Leu Phe Glu Arg Ala Leu  
180 185 190  
Val Tyr Val Gly Thr Asp Phe Leu Ser Ser Pro Leu Trp Asp Lys Tyr  
195 200 205  
Ile Glu Tyr Glu Tyr Met Gln Gln Asp Trp Ser Arg Val Ala Leu Ile  
210 215 220  
Tyr Thr Arg Ile Leu Glu Asn Pro Ile Gln Asn Leu Asp Arg Tyr Phe  
225 230 235 240  
Ser Ser Phe Lys Glu Leu Ala Glu Thr Arg Pro Leu Ser Glu Leu Arg  
245 250 255  
Ser Ala Glu Glu Ser Ala Ala Ala Ala Val Ala Val Ala Gly Asp Ala  
260 265 270  
Ser Glu Ser Ala Ala Ser Glu Ser Gly Glu Lys Ala Asp Glu Gly Arg  
275 280 285  
Ser Gln Val Asp Gly Ser Thr Glu Gln Ser Pro Lys Leu Glu Ser Ala  
290 295 300  
Ser Ser Thr Glu Pro Glu Glu Leu Lys Lys Tyr Val Gly Ile Arg Glu  
305 310 315 320  
Ala Met Tyr Ile Lys Ser Lys Glu Phe Glu Ser Lys Ile Ile Gly Tyr  
325 330 335  
Glu Met Ala Ile Arg Arg Pro Tyr Phe His Val Arg Pro Leu Asn Val  
340 345 350  
Ala Glu Leu Glu Asn Trp His Asn Tyr Leu Asp Phe Ile Glu Arg Asp  
355 360 365  
Gly Asp Phe Asn Lys Val Val Lys Leu Tyr Glu Arg Cys Val Val Thr  
370 375 380  
Cys Ala Asn Tyr Pro Glu Tyr Trp Ile Arg Tyr Val Thr Asn Met Glu  
385 390 395 400  
Ala Ser Gly Ser Ala Asp Leu Ala Glu Asn Ala Leu Ala Arg Ala Thr  
405 410 415  
Gln Val Phe Val Lys Lys Gln Pro Glu Ile His Leu Phe Ala Ala Arg  
420 425 430  
Leu Lys Glu Gln Asn Gly Asp Ile Ala Gly Ala Arg Ala Ala Tyr Gln  
435 440 445  
Leu Val His Ser Glu Ile Ser Pro Gly Leu Leu Glu Ala Val Ile Lys  
450 455 460  
His Ala Asn Met Glu Tyr Arg Leu Gly Asn Leu Asp Asp Ala Phe Ser  
465 470 475 480  
Leu Tyr Glu Gln Val Ile Ala Val Glu Lys Gly Lys Glu His Ser Thr  
485 490 495  
Ile Leu Pro Leu Leu Tyr Ala Gln Tyr Ser Arg Phe Ser Tyr Leu Val  
500 505 510  
Ser Arg Asp Ala Glu Lys Ala Arg Arg Ile Ile Val Glu Ala Leu Asp  
515 520 525  
His Val Gln Pro Ser Lys Pro Leu Met Glu Ala Leu Ile His Phe Glu  
530 535 540  
Ala Ile Gln Pro Pro Pro Arg Glu Ile Asp Tyr Leu Glu Pro Leu Val  
545 550 555 560  
Glu Lys Val Ile Lys Pro Asp Ala Asp Ala Gln Asn Ile Ala Ser Ser  
565 570 575  
Thr Glu Arg Glu Glu Leu Ser Leu Ile Tyr Ile Glu Phe Leu Gly Ile  
580 585 590  
Phe Gly Asp Val Lys Ser Ile Lys Lys Ala Glu Asp Gln His Val Lys  
595 600 605  
Leu Phe Tyr Pro His Arg Ser Thr Ser Glu Leu Lys Lys Arg Ser Ala  
610 615 620  
Asp Asp Phe Leu Ala Ser Asp Arg Thr Lys Met Ala Lys Thr Tyr Asn  
625 630 635 640  
Gly Thr Pro Pro Ala Gln Pro Val Ser Asn Ala Tyr Pro Asn Ala Gln  
645 650 655  
Ala Gln Trp Ser Gly Gly Tyr Ala Ala Gln Pro Gln Thr Trp Pro Pro

(2) INFORMATION FOR SEQ ID NO:22:

(A) LENGTH: 617 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..617

(D) OTHER INFORMATION: / Ceres Seq. ID 1497878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|            |            |            |            |            |     |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Asp        | Lys        | Val        | Val<br>5   | Glu | Val        | Tyr        | Glu        | Arg<br>10  | Ala        | Val        | Leu        | Gly        | Val<br>15  | Thr        |
| Tyr        | Ser        | Val        | Asp<br>20  | Ile        | Trp | Leu        | His        | Tyr<br>25  | Cys        | Thr        | Phe        | Ala        | Ile<br>30  | Asn        | Thr        |
| Tyr        | Gly        | Asp<br>35  | Pro        | Glu        | Thr | Ile        | Arg<br>40  | Arg        | Leu        | Phe        | Glu        | Arg<br>45  | Ala        | Leu        | Val        |
| Tyr        | Val<br>50  | Gly        | Thr        | Asp        | Phe | Leu<br>55  | Ser        | Ser        | Pro        | Leu        | Trp<br>60  | Asp        | Lys        | Tyr        | Ile        |
| Glu<br>65  | Tyr        | Glu        | Tyr        | Met<br>70  | Gln | Gln        | Asp        | Trp        | Ser        | Arg<br>75  | Val        | Ala        | Leu        | Ile<br>80  | Tyr        |
| Thr        | Arg        | Ile        | Leu        | Glu<br>85  | Asn | Pro        | Ile        | Gln        | Asn<br>90  | Leu        | Asp        | Arg        | Tyr        | Phe<br>95  | Ser        |
| Ser        | Phe        | Lys        | Glu<br>100 | Leu        | Ala | Glu        | Thr        | Arg<br>105 | Pro        | Leu        | Ser        | Glu        | Leu<br>110 | Arg        | Ser        |
| Ala        | Glu        | Glu<br>115 | Ser        | Ala        | Ala | Ala        | Ala<br>120 | Val        | Ala        | Val        | Ala        | Gly<br>125 | Asp        | Ala        | Ser        |
| Glu        | Ser        | Ala<br>130 | Ala        | Ser        | Glu | Ser        | Gly<br>135 | Glu        | Lys        | Ala        | Asp<br>140 | Glu        | Gly        | Arg        | Ser        |
| Gln<br>145 | Val        | Asp        | Gly        | Ser<br>150 | Thr | Glu        | Gln        | Ser        | Pro        | Lys<br>155 | Leu        | Glu        | Ser        | Ala<br>160 | Ser        |
| Ser        | Thr        | Glu        | Pro        | Glu<br>165 | Glu | Leu        | Lys        | Lys        | Tyr<br>170 | Val        | Gly        | Ile        | Arg        | Glu<br>175 | Ala        |
| Met        | Tyr        | Ile        | Lys<br>180 | Ser        | Lys | Glu        | Phe        | Glu<br>185 | Ser        | Lys        | Ile        | Ile        | Gly<br>190 | Tyr        | Glu        |
| Met        | Ala        | Ile<br>195 | Arg        | Arg        | Pro | Tyr        | Phe<br>200 | His        | Val        | Arg        | Pro        | Leu<br>205 | Asn        | Val        | Ala        |
| Glu        | Leu<br>210 | Glu        | Asn        | Trp        | His | Asn<br>215 | Tyr        | Leu        | Asp        | Phe        | Ile<br>220 | Glu        | Arg        | Asp        | Gly        |
| Asp<br>225 | Phe        | Asn        | Lys        | Val<br>230 | Val | Lys        | Leu        | Tyr        | Glu        | Arg<br>235 | Cys        | Val        | Val        | Thr        | Cys<br>240 |
| Ala        | Asn        | Tyr        | Pro        | Glu<br>245 | Tyr | Trp        | Ile        | Arg        | Tyr<br>250 | Val        | Thr        | Asn        | Met        | Glu<br>255 | Ala        |
| Ser        | Gly        | Ser        | Ala<br>260 | Asp        | Leu | Ala        | Glu        | Asn<br>265 | Ala        | Leu        | Ala        | Arg        | Ala<br>270 | Thr        | Gln        |
| Val        | Phe        | Val<br>275 | Lys        | Lys        | Gln | Pro        | Glu<br>280 | Ile        | His        | Leu        | Phe        | Ala<br>285 | Ala        | Arg        | Leu        |

Lys Glu Gln Asn Gly Asp Ile Ala Gly Ala Arg Ala Ala Tyr Gln Leu  
290 295 300  
Val His Ser Glu Ile Ser Pro Gly Leu Leu Glu Ala Val Ile Lys His  
305 310 315 320  
Ala Asn Met Glu Tyr Arg Leu Gly Asn Leu Asp Asp Ala Phe Ser Leu  
325 330 335  
Tyr Glu Gln Val Ile Ala Val Glu Lys Gly Lys Glu His Ser Thr Ile  
340 345 350  
Leu Pro Leu Leu Tyr Ala Gln Tyr Ser Arg Phe Ser Tyr Leu Val Ser  
355 360 365  
Arg Asp Ala Glu Lys Ala Arg Arg Ile Ile Val Glu Ala Leu Asp His  
370 375 380  
Val Gln Pro Ser Lys Pro Leu Met Glu Ala Leu Ile His Phe Glu Ala  
385 390 395 400  
Ile Gln Pro Pro Pro Arg Glu Ile Asp Tyr Leu Glu Pro Leu Val Glu  
405 410 415  
Lys Val Ile Lys Pro Asp Ala Asp Ala Gln Asn Ile Ala Ser Ser Thr  
420 425 430  
Glu Arg Glu Glu Leu Ser Leu Ile Tyr Ile Glu Phe Leu Gly Ile Phe  
435 440 445  
Gly Asp Val Lys Ser Ile Lys Lys Ala Glu Asp Gln His Val Lys Leu  
450 455 460  
Phe Tyr Pro His Arg Ser Thr Ser Glu Leu Lys Lys Arg Ser Ala Asp  
465 470 475 480  
Asp Phe Leu Ala Ser Asp Arg Thr Lys Met Ala Lys Thr Tyr Asn Gly  
485 490 495  
Thr Pro Pro Ala Gln Pro Val Ser Asn Ala Tyr Pro Asn Ala Gln Ala  
500 505 510  
Gln Trp Ser Gly Gly Tyr Ala Ala Gln Pro Gln Thr Trp Pro Pro Ala  
515 520 525  
Gln Ala Ala Pro Ala Gln Pro Gln Gln Trp Asn Pro Ala Tyr Gly Gln  
530 535 540  
Gln Ala Ala Tyr Gly Ala Tyr Gly Gly Tyr Pro Ala Gly Tyr Thr Ala  
545 550 555 560  
Pro Gln Ala Pro Thr Pro Val Pro Gln Ala Ala Tyr Gly Ala Tyr  
565 570 575  
Pro Ala Gln Thr Tyr Pro Thr Gln Ser Tyr Ala Pro Pro Val Ala Ala  
580 585 590  
Ala Ala Pro Ala Ala Ala Pro Val Gln Gln Pro Ala Ala Val Ala  
595 600 605  
Pro Gln Ala Tyr Tyr Asn Thr Tyr Tyr  
610 615

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..833
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| caaaccaagt tttcttctaa gctgtatttg aaatggtata tatttcacac accaaacaga   | 60  |
| tcagaagcta aaaggtaata atataatggc ggatttgagg gacgaaaaag gtaacccaat   | 120 |
| ccatctaacc gacaçacagg gaaacccaat tgctcgacctg actgatgagc acggtaaccc  | 180 |
| catgtacctt accgggtgtg ttagctccac tcctcagcat aaggagagta ctaccagcga   | 240 |
| cattgcagag caccctacta gcaccgttg agaaacacat ccggcagctg ctccaactgg    | 300 |
| tgtctggtgct gccaccgctg ccactgcgac aggagtctct gctgggtactg gagcaaccac | 360 |
| cacagggcag caacaccatg ggtcgcttga agagcatctt cgtcggtctg gaagttcatc   | 420 |

```
tagctctagc tcggaggatg acgggcaagg agggaggagg aagaagagca taaaggagaa 480
aattaaagag aagttcagta gcggcaaaca caaggacgaa caaacaccaa ccaccgccac 540
aacaacagga cctgccacta ccgaccaacc tcacgagaag aagggcattc tcgagaagat 600
caaggacaag cttcccggcc accataacca caaccaccca tgaacaccaa tcatatgacg 660
tctttgttac atgaataaat cgtttgacg aatttcatta gggcttatga agaatacaata 720
tatatgtcta gtgaagttta ctaaatttta gttgtgtttg cttgcagttt gtgaatgtga 780
ccatcgtgtt atcatgttct tgtttattta taaagaagga actgtatttt gct
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1497884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Met Ala Asp Leu Arg Asp Glu Lys Gly Asn Pro Ile His Leu Thr Asp
1 5 10 15
Thr Gln Gly Asn Pro Ile Val Asp Leu Thr Asp Glu His Gly Asn Pro
20 25 30
Met Tyr Leu Thr Gly Val Val Ser Ser Thr Pro Gln His Lys Glu Ser
35 40 45
Thr Thr Ser Asp Ile Ala Glu His Pro Thr Ser Thr Val Gly Glu Thr
50 55 60
His Pro Ala Ala Ala Pro Thr Gly Ala Gly Ala Thr Ala Ala Thr
65 70 75 80
Ala Thr Gly Val Ser Ala Gly Thr Gly Ala Thr Thr Thr Gly Gln Gln
85 90 95
His His Gly Ser Leu Glu Glu His Leu Arg Arg Ser Gly Ser Ser Ser
100 105 110
Ser Ser Ser Ser Glu Asp Asp Gly Gln Gly Gly Arg Arg Lys Lys Ser
115 120 125
Ile Lys Glu Lys Ile Lys Glu Lys Phe Ser Ser Gly Lys His Lys Asp
130 135 140
Glu Gln Thr Pro Thr Thr Ala Thr Thr Thr Gly Pro Ala Thr Thr Asp
145 150 155 160
Gln Pro His Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Asp Lys Leu
165 170 175
Pro Gly His His Asn His Asn His Pro
180 185
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1497885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Met Tyr Leu Thr Gly Val Val Ser Ser Thr Pro Gln His Lys Glu Ser
1 5 10 15
Thr Thr Ser Asp Ile Ala Glu His Pro Thr Ser Thr Val Gly Glu Thr
20 25 30
His Pro Ala Ala Ala Pro Thr Gly Ala Gly Ala Ala Thr Ala Ala Thr
35 40 45
```

Ala Thr Gly Val Ser Ala Gly Thr Gly Ala Thr Thr Thr Gly Gln Gln  
50 55 60  
His His Gly Ser Leu Glu Glu His Leu Arg Arg Ser Gly Ser Ser Ser  
65 70 75 80  
Ser Ser Ser Ser Glu Asp Asp Gly Gln Gly Gly Arg Arg Lys Lys Ser  
85 90 95  
Ile Lys Glu Lys Ile Lys Glu Lys Phe Ser Ser Gly Lys His Lys Asp  
100 105 110  
Glu Gln Thr Pro Thr Thr Ala Thr Thr Thr Gly Pro Ala Thr Thr Asp  
115 120 125  
Gln Pro His Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Asp Lys Leu  
130 135 140  
Pro Gly His His Asn His Asn His Pro  
145 150

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

|            |             |            |            |             |             |      |
|------------|-------------|------------|------------|-------------|-------------|------|
| agtctagtca | tttctcagac  | tctgacctca | ctgatctcca | atggcgaaaa  | ccctagctcg  | 60   |
| ctccacagcg | tcacgcatca  | ccaagcgctt | attctccacc | tccggagcca  | ccactccttc  | 120  |
| cccttcttat | atcctctccc  | gtcgatcaac | cccgtgttc  | tcccatgccg  | tcggattcat  | 180  |
| ctcttccttg | aatcgtttca  | caacgattcg | aactcgaatg | gatagggtccg | gtggatcgta  | 240  |
| ctctcctcta | aaatccggtt  | cgaatttcag | cgaccgagca | cccactgaga  | tggcgccggt  | 300  |
| gtttcctggc | tgcgattatg  | agcattgggt | gattgtaatg | gacaaacctg  | gaggcgaaaa  | 360  |
| cgctactaag | cagcaaatga  | ttgattgtta | tgttcaaacc | ctagctaaaa  | ttatcggcag  | 420  |
| tgaggaagaa | gctaagaaga  | agatttataa | tgtatcgtgt | gaaagggtatt | ttggatttgg  | 480  |
| ttgtgagatt | gatgaagaga  | catcaaacaa | acttgaagga | cttcctgggtg | ttctcttcat  | 540  |
| caatctcaca | accaaattcca | aaaaactttt | ctcctccatc | aaaatcctcc  | gacgatgaca  | 600  |
| accatagctg | cagctggcct  | caacgtcgcg | actccacgag | tggtcggtcg  | acctgtggct  | 660  |
| cgtgtattag | gtccgggtccg | gttgaattac | ccgtggaaat | tcggttcgat  | gaagcggatg  | 720  |
| gttgtgggta | aggctacatc  | ggaaggagag | atatcgga   | aggtggagaa  | gagtatacaa  | 780  |
| gaagctaagg | agacatgcgc  | tgatgatccg | gtgagcgggg | agtgtgtagc  | ggcttggggac | 840  |
| gaggtggagg | agctgagtgc  | ggcggcgagt | catgctaggg | acaagaagaa  | agctggtggc  | 900  |
| tccgatcctt | tggaagagta  | ttgcaatgat | aaycctgaga | ctgatgagtg  | tcgtacttat  | 960  |
| gataattaaa | aaatatgttt  | ttgatgttcg | aattatgaaa | ctttaggtat  | ggatcaatgt  | 1020 |
| ttgttcttct | tgtcccttgt  | tgttatgttt | gtgttttttg | tttggttgat  | gattgtaatg  | 1080 |
| tgataaatga | atatgaatag  | tacaatacac | aacatatgtt | tc          |             |      |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Ala Lys Thr Leu Ala Arg Ser Thr Ala Ser Arg Ile Thr Lys Arg  
1 5 10 15  
Leu Phe Ser Thr Ser Gly Ala Thr Thr Pro Ser Pro Ser Tyr Ile Leu  
20 25 30

Ser Arg Arg Ser Thr Pro Val Phe Ser His Ala Val Gly Phe Ile Ser  
35 40 45  
Ser Leu Asn Arg Phe Thr Thr Ile Arg Thr Arg Met Asp Arg Ser Gly  
50 55 60  
Gly Ser Tyr Ser Pro Leu Lys Ser Gly Ser Asn Phe Ser Asp Arg Ala  
65 70 75 80  
Pro Thr Glu Met Ala Pro Leu Phe Pro Gly Cys Asp Tyr Glu His Trp  
85 90 95  
Leu Ile Val Met Asp Lys Pro Gly Gly Glu Asn Ala Thr Lys Gln Gln  
100 105 110  
Met Ile Asp Cys Tyr Val Gln Thr Leu Ala Lys Ile Ile Gly Ser Glu  
115 120 125  
Glu Glu Ala Lys Lys Lys Ile Tyr Asn Val Ser Cys Glu Arg Tyr Phe  
130 135 140  
Gly Phe Gly Cys Glu Ile Asp Glu Glu Thr Ser Asn Lys Leu Glu Gly  
145 150 155 160  
Leu Pro Gly Val Leu Phe Ile Asn Leu Thr Thr Lys Ser Lys Lys Leu  
165 170 175  
Phe Ser Ser Ile Lys Ile Leu Arg Arg  
180 185

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1497888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Asp Arg Ser Gly Gly Ser Tyr Ser Pro Leu Lys Ser Gly Ser Asn  
1 5 10 15  
Phe Ser Asp Arg Ala Pro Thr Glu Met Ala Pro Leu Phe Pro Gly Cys  
20 25 30  
Asp Tyr Glu His Trp Leu Ile Val Met Asp Lys Pro Gly Gly Glu Asn  
35 40 45  
Ala Thr Lys Gln Gln Met Ile Asp Cys Tyr Val Gln Thr Leu Ala Lys  
50 55 60  
Ile Ile Gly Ser Glu Glu Ala Lys Lys Lys Ile Tyr Asn Val Ser  
65 70 75 80  
Cys Glu Arg Tyr Phe Gly Phe Gly Cys Glu Ile Asp Glu Glu Thr Ser  
85 90 95  
Asn Lys Leu Glu Gly Leu Pro Gly Val Leu Phe Ile Asn Leu Thr Thr  
100 105 110  
Lys Ser Lys Lys Leu Phe Ser Ser Ile Lys Ile Leu Arg Arg  
115 120 125

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1497889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Thr Thr Ile Ala Ala Ala Gly Leu Asn Val Ala Thr Pro Arg Val

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```

1 5 10 15
Val Val Arg Pro Val Ala Arg Val Leu Gly Pro Val Arg Leu Asn Tyr
 20 25 30
Pro Trp Lys Phe Gly Ser Met Lys Arg Met Val Val Val Lys Ala Thr
 35 40 45
Ser Glu Gly Glu Ile Ser Glu Lys Val Glu Lys Ser Ile Gln Glu Ala
 50 55 60
Lys Glu Thr Cys Ala Asp Asp Pro Val Ser Gly Glu Cys Val Ala Ala
 65 70 75 80
Trp Asp Glu Val Glu Glu Leu Ser Ala Ala Ala Ser His Ala Arg Asp
 85 90 95
Lys Lys Lys Ala Gly Gly Ser Asp Pro Leu Glu Glu Tyr Cys Asn Asp
 100 105 110
Xaa Pro Glu Thr Asp Glu Cys Arg Thr Tyr Asp Asn
 115 120
```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1025
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

acccaccaa actttacttt ctattcagac aagacatttc gatagcttat ttctatggtc 60
tgatcacacg atagtgtatt ctgatatcat cactctacca aagagatacc aaattatgga 120
aggagaatct atcactttcc ggtgaagata aaccggagat ccaatctcca attccaccaa 180
atcagatctt catactctct ggacaaagca atatggccgg acgcggcggc gtcgtcaaag 240
atcaccacca caatcgctgg gtctgggata aaatcctccc accggaatgc gcaccaaact 300
catcgatcct ccgcctgtcc gcagatctcc ggtgggaaga agcacacgag ccactacacg 360
ttgacattga cacaggtaaa gtgtgtggag taggtccagg aatggcggtc gctaacgcgg 420
tgaagaatcg cgtggaacaa gattcggctg tgatcgggtt ggtgccgtgc gcttcgggtg 480
gaacggcgat aaaagagtgg gagcgtggaa gccacttgta cgagaggatg gtcaagagaa 540
cggaggagag taggaaatgc ggcggagaga tcaaggcggg gttgtggtat caaggagaga 600
gtgacgtgtt ggacatccat gacgccgaga gctacgggaa caatatggat cgtttgatta 660
agaacctccg tcatgatctc aaccttcctt ctcttcccat tattcagggtg gcaatagcat 720
cgggaggagg atacatagat aaggtgagag aagcacagtt gggactgaaa ctgtcgaatg 780
tggtctgtgt agatgctaag ggattgccgc taaagtccga caatcttcac ttaaccaccg 840
aggctcaagt ccagcttggt ctctccttag cacaagctta cctttccaac ttctgctaga 900
caatcaagta agttcgtgat aaggttcatg aatctttctg aatgtatgtg gtggactagt 960
tatatggata tcacaaaact ttgtaataat ggattggtaa aacattgatg ttcatagtga 1020
agaac
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..228
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

Met Ala Gly Arg Gly Gly Val Val Lys Asp His His His Asn Arg Trp
1 5 10 15
Val Trp Asp Lys Ile Leu Pro Pro Glu Cys Ala Pro Asn Ser Ser Ile
 20 25 30
```

Leu Arg Leu Ser Ala Asp Leu Arg Trp Glu Glu Ala His Glu Pro Leu  
35 40 45  
His Val Asp Ile Asp Thr Gly Lys Val Cys Gly Val Gly Pro Gly Met  
50 55 60  
Ala Phe Ala Asn Ala Val Lys Asn Arg Val Glu Thr Asp Ser Ala Val  
65 70 75 80  
Ile Gly Leu Val Pro Cys Ala Ser Gly Gly Thr Ala Ile Lys Glu Trp  
85 90 95  
Glu Arg Gly Ser His Leu Tyr Glu Arg Met Val Lys Arg Thr Glu Glu  
100 105 110  
Ser Arg Lys Cys Gly Gly Glu Ile Lys Ala Val Leu Trp Tyr Gln Gly  
115 120 125  
Glu Ser Asp Val Leu Asp Ile His Asp Ala Glu Ser Tyr Gly Asn Asn  
130 135 140  
Met Asp Arg Leu Ile Lys Asn Leu Arg His Asp Leu Asn Leu Pro Ser  
145 150 155 160  
Leu Pro Ile Ile Gln Val Ala Ile Ala Ser Gly Gly Gly Tyr Ile Asp  
165 170 175  
Lys Val Arg Glu Ala Gln Leu Gly Leu Lys Leu Ser Asn Val Val Cys  
180 185 190  
Val Asp Ala Lys Gly Leu Pro Leu Lys Ser Asp Asn Leu His Leu Thr  
195 200 205  
Thr Glu Ala Gln Val Gln Leu Gly Leu Ser Leu Ala Gln Ala Tyr Leu  
210 215 220  
Ser Asn Phe Cys  
225

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Phe Ala Asn Ala Val Lys Asn Arg Val Glu Thr Asp Ser Ala  
1 5 10 15  
Val Ile Gly Leu Val Pro Cys Ala Ser Gly Gly Thr Ala Ile Lys Glu  
20 25 30  
Trp Glu Arg Gly Ser His Leu Tyr Glu Arg Met Val Lys Arg Thr Glu  
35 40 45  
Glu Ser Arg Lys Cys Gly Gly Glu Ile Lys Ala Val Leu Trp Tyr Gln  
50 55 60  
Gly Glu Ser Asp Val Leu Asp Ile His Asp Ala Glu Ser Tyr Gly Asn  
65 70 75 80  
Asn Met Asp Arg Leu Ile Lys Asn Leu Arg His Asp Leu Asn Leu Pro  
85 90 95  
Ser Leu Pro Ile Ile Gln Val Ala Ile Ala Ser Gly Gly Gly Tyr Ile  
100 105 110  
Asp Lys Val Arg Glu Ala Gln Leu Gly Leu Lys Leu Ser Asn Val Val  
115 120 125  
Cys Val Asp Ala Lys Gly Leu Pro Leu Lys Ser Asp Asn Leu His Leu  
130 135 140  
Thr Thr Glu Ala Gln Val Gln Leu Gly Leu Ser Leu Ala Gln Ala Tyr  
145 150 155 160  
Leu Ser Asn Phe Cys  
165

(2) INFORMATION FOR SEQ ID NO:33:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 123 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..123  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497893  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Val Lys Arg Thr Glu Glu Ser Arg Lys Cys Gly Gly Glu Ile Lys  
1                  5                  10                  15  
Ala Val Leu Trp Tyr Gln Gly Glu Ser Asp Val Leu Asp Ile His Asp  
                  20                  25                  30  
Ala Glu Ser Tyr Gly Asn Asn Met Asp Arg Leu Ile Lys Asn Leu Arg  
                  35                  40                  45  
His Asp Leu Asn Leu Pro Ser Leu Pro Ile Ile Gln Val Ala Ile Ala  
                  50                  55                  60  
Ser Gly Gly Gly Tyr Ile Asp Lys Val Arg Glu Ala Gln Leu Gly Leu  
65                  70                  75                  80  
Lys Leu Ser Asn Val Val Cys Val Asp Ala Lys Gly Leu Pro Leu Lys  
                  85                  90                  95  
Ser Asp Asn Leu His Leu Thr Thr Glu Ala Gln Val Gln Leu Gly Leu  
                  100                 105                 110  
Ser Leu Ala Gln Ala Tyr Leu Ser Asn Phe Cys  
                 115                 120

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1166 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1166  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497894  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

atatatacaa cgaggaaaaa tagtactatt ttctacgaac ttcagaatct ttcgtctctc 60  
ttaattattt ttctcaaatt tctcgaaaca tctagttttc ttttcaacca gccaatcatg 120  
ggtagtgatc atcatcatcg aaagctccac gttatgttct tccctttcat ggcttatggt 180  
cacatgatac caactctaga catggctaag cttttctcta gcagaggagc caaatccaca 240  
atcctcacca catctctcaa ctccaagatc ctccaaaaac ccatcgacac attcaagaat 300  
ctgaatccgg gtctcgaaat cgacatccag atcttcgatt tcccttgctg ggagctgggg 360  
ttaccagaag gatgtgaaaa cgttgatttc ttcaattcaa acaacaatga tgataaaaac 420  
gagatgatcg tgaaattctt tttctcgaca aggtttttca aagaccagct tgagaaactc 480  
ctcgggacaa cgagaccaga ctgtcttata gccgacatgt tcttccctg ggctactgaa 540  
gctgctggga agttcaatgt gccaaagact gtgttccacg gcaactggcta cttctcttta 600  
tgcgctgggt attgcatcgg agtgcataaa ccacagaaga gagtggcttc aagctctgag 660  
ccattttgtga ttcccgagct ccctgggaac attgtgataa ctgaagaaca gatcatagat 720  
ggcgatggag aatccgacat gggaaagttt atgactgaag ttaggggaatc ggaagtgaag 780  
agctcaggag ttgttttgaa tagttttctac gagctagaac atgattacgc cgattttttac 840  
aaaagttgtg tacaaaagag agcgtggcat atcgggtccgc tatcggttta caacagggga 900  
tttgaggaga aggctgagag aggaagaaaa gccaacattg atgasgctga atgcctcaaa 960  
tggcttgact ccaagaaacc aaattcagtc atttatgttt cctttgggag cgtggctttc 1020  
ttcaagaatg aacagttatt cgagatcgct gcagggttag aagcttccgg tacaagtttc 1080  
at ttgggttg ttaggaaaac caaaggtatt gaaattgacg tttgaagcct atattatata 1140  
actgtaattt gggtagcttt gatttt

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..374
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497895
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Tyr | Thr | Thr | Arg | Lys | Asn | Ser | Thr | Ile | Phe | Tyr | Glu | Leu | Gln | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ser | Ser | Leu | Leu | Ile | Ile | Phe | Leu | Lys | Phe | Leu | Glu | Thr | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Leu | Phe | Asn | Gln | Pro | Ile | Met | Gly | Ser | Asp | His | His | His | Arg | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | His | Val | Met | Phe | Phe | Pro | Phe | Met | Ala | Tyr | Gly | His | Met | Ile | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Leu | Asp | Met | Ala | Lys | Leu | Phe | Ser | Ser | Arg | Gly | Ala | Lys | Ser | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Leu | Thr | Thr | Ser | Leu | Asn | Ser | Lys | Ile | Leu | Gln | Lys | Pro | Ile | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Lys | Asn | Leu | Asn | Pro | Gly | Leu | Glu | Ile | Asp | Ile | Gln | Ile | Phe |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asp | Phe | Pro | Cys | Val | Glu | Leu | Gly | Leu | Pro | Glu | Gly | Cys | Glu | Asn | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Phe | Phe | Thr | Ser | Asn | Asn | Asp | Asp | Lys | Asn | Glu | Met | Ile | Val |     |
|     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Lys | Phe | Phe | Phe | Ser | Thr | Arg | Phe | Phe | Lys | Asp | Gln | Leu | Glu | Lys | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Gly | Thr | Thr | Arg | Pro | Asp | Cys | Leu | Ile | Ala | Asp | Met | Phe | Phe | Pro |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Trp | Ala | Thr | Glu | Ala | Ala | Gly | Lys | Phe | Asn | Val | Pro | Arg | Leu | Val | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Gly | Thr | Gly | Tyr | Phe | Ser | Leu | Cys | Ala | Gly | Tyr | Cys | Ile | Gly | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Lys | Pro | Gln | Lys | Arg | Val | Ala | Ser | Ser | Ser | Glu | Pro | Phe | Val | Ile |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Glu | Leu | Pro | Gly | Asn | Ile | Val | Ile | Thr | Glu | Gln | Ile | Ile | Asp |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Asp | Gly | Glu | Ser | Asp | Met | Gly | Lys | Phe | Met | Thr | Glu | Val | Arg | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Glu | Val | Lys | Ser | Ser | Gly | Val | Val | Leu | Asn | Ser | Phe | Tyr | Glu | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | His | Asp | Tyr | Ala | Asp | Phe | Tyr | Lys | Ser | Cys | Val | Gln | Lys | Arg | Ala |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Trp | His | Ile | Gly | Pro | Leu | Ser | Val | Tyr | Asn | Arg | Gly | Phe | Glu | Glu | Lys |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Glu | Arg | Gly | Lys | Lys | Ala | Asn | Ile | Asp | Xaa | Ala | Glu | Cys | Leu | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Trp | Leu | Asp | Ser | Lys | Lys | Pro | Asn | Ser | Val | Ile | Tyr | Val | Ser | Phe | Gly |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Val | Ala | Phe | Phe | Lys | Asn | Glu | Gln | Leu | Phe | Glu | Ile | Ala | Ala | Gly |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Glu | Ala | Ser | Gly | Thr | Ser | Phe | Ile | Trp | Val | Val | Arg | Lys | Thr | Lys |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Gly | Ile | Glu | Ile | Asp | Val |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 370 |     |     |     |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:36:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 335 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..335  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497896  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Gly Ser Asp His His His Arg Lys Leu His Val Met Phe Phe Pro  
1                   5                   10                   15  
Phe Met Ala Tyr Gly His Met Ile Pro Thr Leu Asp Met Ala Lys Leu  
          20                   25                   30  
Phe Ser Ser Arg Gly Ala Lys Ser Thr Ile Leu Thr Thr Ser Leu Asn  
          35                   40                   45  
Ser Lys Ile Leu Gln Lys Pro Ile Asp Thr Phe Lys Asn Leu Asn Pro  
          50                   55                   60  
Gly Leu Glu Ile Asp Ile Gln Ile Phe Asp Phe Pro Cys Val Glu Leu  
65                   70                   75                   80  
Gly Leu Pro Glu Gly Cys Glu Asn Val Asp Phe Phe Thr Ser Asn Asn  
          85                   90                   95  
Asn Asp Asp Lys Asn Glu Met Ile Val Lys Phe Phe Phe Ser Thr Arg  
          100                   105                   110  
Phe Phe Lys Asp Gln Leu Glu Lys Leu Leu Gly Thr Thr Arg Pro Asp  
          115                   120                   125  
Cys Leu Ile Ala Asp Met Phe Phe Pro Trp Ala Thr Glu Ala Ala Gly  
          130                   135                   140  
Lys Phe Asn Val Pro Arg Leu Val Phe His Gly Thr Gly Tyr Phe Ser  
145                   150                   155                   160  
Leu Cys Ala Gly Tyr Cys Ile Gly Val His Lys Pro Gln Lys Arg Val  
          165                   170                   175  
Ala Ser Ser Ser Glu Pro Phe Val Ile Pro Glu Leu Pro Gly Asn Ile  
          180                   185                   190  
Val Ile Thr Glu Glu Gln Ile Ile Asp Gly Asp Gly Glu Ser Asp Met  
          195                   200                   205  
Gly Lys Phe Met Thr Glu Val Arg Glu Ser Glu Val Lys Ser Ser Gly  
          210                   215                   220  
Val Val Leu Asn Ser Phe Tyr Glu Leu Glu His Asp Tyr Ala Asp Phe  
225                   230                   235                   240  
Tyr Lys Ser Cys Val Gln Lys Arg Ala Trp His Ile Gly Pro Leu Ser  
          245                   250                   255  
Val Tyr Asn Arg Gly Phe Glu Glu Lys Ala Glu Arg Gly Lys Lys Ala  
          260                   265                   270  
Asn Ile Asp Xaa Ala Glu Cys Leu Lys Trp Leu Asp Ser Lys Lys Pro  
          275                   280                   285  
Asn Ser Val Ile Tyr Val Ser Phe Gly Ser Val Ala Phe Phe Lys Asn  
290                   295                   300  
Glu Gln Leu Phe Glu Ile Ala Ala Gly Leu Glu Ala Ser Gly Thr Ser  
305                   310                   315                   320  
Phe Ile Trp Val Val Arg Lys Thr Lys Gly Ile Glu Ile Asp Val  
          325                   330                   335

- (2) INFORMATION FOR SEQ ID NO:37:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 323 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..323

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(D) OTHER INFORMATION: / Ceres Seq. ID 1497897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Phe Phe Pro Phe Met Ala Tyr Gly His Met Ile Pro Thr Leu Asp  
1 5 10 15  
Met Ala Lys Leu Phe Ser Ser Arg Gly Ala Lys Ser Thr Ile Leu Thr  
20 25 30  
Thr Ser Leu Asn Ser Lys Ile Leu Gln Lys Pro Ile Asp Thr Phe Lys  
35 40 45  
Asn Leu Asn Pro Gly Leu Glu Ile Asp Ile Gln Ile Phe Asp Phe Pro  
50 55 60  
Cys Val Glu Leu Gly Leu Pro Glu Gly Cys Glu Asn Val Asp Phe Phe  
65 70 75 80  
Thr Ser Asn Asn Asn Asp Asp Lys Asn Glu Met Ile Val Lys Phe Phe  
85 90 95  
Phe Ser Thr Arg Phe Phe Lys Asp Gln Leu Glu Lys Leu Leu Gly Thr  
100 105 110  
Thr Arg Pro Asp Cys Leu Ile Ala Asp Met Phe Phe Pro Trp Ala Thr  
115 120 125  
Glu Ala Ala Gly Lys Phe Asn Val Pro Arg Leu Val Phe His Gly Thr  
130 135 140  
Gly Tyr Phe Ser Leu Cys Ala Gly Tyr Cys Ile Gly Val His Lys Pro  
145 150 155 160  
Gln Lys Arg Val Ala Ser Ser Ser Glu Pro Phe Val Ile Pro Glu Leu  
165 170 175  
Pro Gly Asn Ile Val Ile Thr Glu Glu Gln Ile Ile Asp Gly Asp Gly  
180 185 190  
Glu Ser Asp Met Gly Lys Phe Met Thr Glu Val Arg Glu Ser Glu Val  
195 200 205  
Lys Ser Ser Gly Val Val Leu Asn Ser Phe Tyr Glu Leu Glu His Asp  
210 215 220  
Tyr Ala Asp Phe Tyr Lys Ser Cys Val Gln Lys Arg Ala Trp His Ile  
225 230 235 240  
Gly Pro Leu Ser Val Tyr Asn Arg Gly Phe Glu Glu Lys Ala Glu Arg  
245 250 255  
Gly Lys Lys Ala Asn Ile Asp Xaa Ala Glu Cys Leu Lys Trp Leu Asp  
260 265 270  
Ser Lys Lys Pro Asn Ser Val Ile Tyr Val Ser Phe Gly Ser Val Ala  
275 280 285  
Phe Phe Lys Asn Glu Gln Leu Phe Glu Ile Ala Ala Gly Leu Glu Ala  
290 295 300  
Ser Gly Thr Ser Phe Ile Trp Val Val Arg Lys Thr Lys Gly Ile Glu  
305 310 315 320  
Ile Asp Val

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..584

(D) OTHER INFORMATION: / Ceres Seq. ID 1497898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aagtgattaa gcttatgcag agtttcaa ccaaggagta tgtagggag acaattgcct    | 60  |
| ggatgcatta ctattggttt ttgaccaatg aagggatcga gttcttgaga acttatctta | 120 |
| atcttccatc tgatgttggt cctgctactt tgaagaagtc agctaagcct ggtggctcgc | 180 |
| catttggttg cccacctggt gatcgctcaa gaggacctcg ccatgaagga ggagaccgtc | 240 |
| ccaggtttg tgaccgtgat gggatccgtg caggtcctcg agctggtggt gagtttggag  | 300 |

gtgaaaaggg tggagctcct gcagattacc agccatcttt ccaaggaagt gggcgtggtt 360  
ttggccgtgg tgctggtggc tacagcgcag ctgcaccatc tggttcaggt ttgccttgaa 420  
aaagaaatgt ctttaggtga cagtaagacc atggaggagt tttcagcttt aaattttgct 480  
tttgtaattc agattccgga atccttcata atctctatct gagtttagtt ttgttggtga 540  
atcaaacatc cgatttaaag ttatgttcat tccatcttct cttc

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Val Ile Lys Leu Met Gln Ser Phe Lys Ser Lys Glu Tyr Val Arg Glu  
1 5 10 15  
Thr Ile Ala Trp Met His Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile  
20 25 30  
Glu Phe Leu Arg Thr Tyr Leu Asn Leu Pro Ser Asp Val Val Pro Ala  
35 40 45  
Thr Leu Lys Lys Ser Ala Lys Pro Gly Gly Arg Pro Phe Gly Gly Pro  
50 55 60  
Pro Gly Asp Arg Ser Arg Gly Pro Arg His Glu Gly Gly Asp Arg Pro  
65 70 75 80  
Arg Phe Gly Asp Arg Asp Gly Tyr Arg Ala Gly Pro Arg Ala Gly Gly  
85 90 95  
Glu Phe Gly Gly Glu Lys Gly Gly Ala Pro Ala Asp Tyr Gln Pro Ser  
100 105 110  
Phe Gln Gly Ser Gly Arg Gly Phe Gly Arg Gly Ala Gly Gly Tyr Ser  
115 120 125  
Ala Ala Ala Pro Ser Gly Ser Gly Leu Pro  
130 135

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Gln Ser Phe Lys Ser Lys Glu Tyr Val Arg Glu Thr Ile Ala Trp  
1 5 10 15  
Met His Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile Glu Phe Leu Arg  
20 25 30  
Thr Tyr Leu Asn Leu Pro Ser Asp Val Val Pro Ala Thr Leu Lys Lys  
35 40 45  
Ser Ala Lys Pro Gly Gly Arg Pro Phe Gly Gly Pro Pro Gly Asp Arg  
50 55 60  
Ser Arg Gly Pro Arg His Glu Gly Gly Asp Arg Pro Arg Phe Gly Asp  
65 70 75 80  
Arg Asp Gly Tyr Arg Ala Gly Pro Arg Ala Gly Gly Glu Phe Gly Gly  
85 90 95  
Glu Lys Gly Gly Ala Pro Ala Asp Tyr Gln Pro Ser Phe Gln Gly Ser  
100 105 110

Gly Arg Gly Phe Gly Arg Gly Ala Gly Gly Tyr Ser Ala Ala Ala Pro  
115 120 125  
Ser Gly Ser Gly Leu Pro  
130

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met His Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile Glu Phe Leu Arg  
1 5 10 15  
Thr Tyr Leu Asn Leu Pro Ser Asp Val Val Pro Ala Thr Leu Lys Lys  
20 25 30  
Ser Ala Lys Pro Gly Gly Arg Pro Phe Gly Gly Pro Pro Gly Asp Arg  
35 40 45  
Ser Arg Gly Pro Arg His Glu Gly Gly Asp Arg Pro Arg Phe Gly Asp  
50 55 60  
Arg Asp Gly Tyr Arg Ala Gly Pro Arg Ala Gly Gly Glu Phe Gly Gly  
65 70 75 80  
Glu Lys Gly Gly Ala Pro Ala Asp Tyr Gln Pro Ser Phe Gln Gly Ser  
85 90 95  
Gly Arg Gly Phe Gly Arg Gly Ala Gly Gly Tyr Ser Ala Ala Ala Pro  
100 105 110  
Ser Gly Ser Gly Leu Pro  
115

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

acatccttag tttttctaaa ccacaaaata aaaactttcg ttcattgaaat cttatggtaa 60  
gttttgagag aaatatccga gtattgcttc agtccgtagc atacgaatca agcgagacga 120  
tggtgcagcc tggaaccgag ataaaagcaa gcgacctaac cctactagta atcacgatta 180  
tactcttcgc aatcttcacg gttggcttgg smttcggttt gcttccgctg gacctctcgc 240  
caattttact cacaagaatc catcaaccct ttcactgact ccgacgttga atcccgtacg 300  
agtattacgg cggtgcgtgg gctcgacgag gctatcatca actcatttcc gacgtttctc 360  
tactcggagg tgaaggagcg gagaatcggg atagggtggc tcgagtgtgc agtgtgtatc 420  
tgtgagttcg aagaccatga aacgctccgt ttgatgcctg aatgctgccca cgtgtttcat 480  
gctgattgtg taagtgtctg gctctctgat cactccacgt gtccactctg tcgtgtggat 540  
ctttgcttac aaccgggtga gagaagctac ttgaatccgg aaccggatct tgtagaatct 600  
acaaactcgc atttgtttga tgggtgacg tggaccaata ggaacagacc gtctcgggtca 660  
tggtcaacga gattgtctca atgtcgagtc tcccagatat taatctcgag atcgcatctg 720  
accggacatt ctgtggttca accgctagat aatttagacc ggtttacgct tcggttacca 780  
gaagaagtcc ggaggcaact gacgaagaaa acggtggaca acgtggcatt ttctcaggct 840  
aggagctcac ggcgtggtta cagaagcaga agtgccggaa gcgagaggag tgtcttctcg 900  
taccaacggc ggatgcattc cttctctgat tgtgcatggt ccacctcctg tggcggagaa 960  
gcggtggctc cgtcaaagga ttttcgccga atatcagttg aacaatcyca gntagatgat 1020

cgagtgtagt agataggcaa ttttcttggt gtgtgttttn tgctaacaac atttgtgttt 1080  
gtctgtttgc tatcatttgc ttttcgaaca tgaccaatat tcaagtcc

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Glu | Cys | Cys | His | Val | Phe | His | Ala | Asp | Cys | Val | Ser | Val | Trp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Leu | Ser | Asp | His | Ser | Thr | Cys | Pro | Leu | Cys | Arg | Val | Asp | Leu | Cys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Pro | Gly | Glu | Arg | Ser | Tyr | Leu | Asn | Pro | Glu | Pro | Asp | Leu | Val | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Thr | Asn | Ser | His | Leu | Phe | Asp | Gly | Val | Thr | Trp | Thr | Asn | Arg | Asn |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Arg | Pro | Ser | Arg | Ser | Trp | Ser | Thr | Arg | Leu | Ser | Gln | Cys | Arg | Val | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Gln | Ile | Leu | Ile | Ser | Arg | Ser | His | Ser | Thr | Gly | His | Ser | Val | Val | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Leu | Asp | Asn | Leu | Asp | Arg | Phe | Thr | Leu | Arg | Leu | Pro | Glu | Glu | Val |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Arg | Arg | Gln | Leu | Thr | Lys | Lys | Thr | Val | Asp | Asn | Val | Ala | Phe | Ser | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Ala | Arg | Ser | Ser | Arg | Arg | Gly | Tyr | Arg | Ser | Arg | Ser | Ala | Gly | Ser | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |
| Arg | Ser | Val | Phe | Ser | Tyr | Gln | Arg | Arg | Met | His | Ser | Phe | Ser | Asp | Cys |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Ala | Trp | Ser | Thr | Ser | Cys | Gly | Gly | Glu | Ala | Val | Ala | Pro | Ser | Lys | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |
| Phe | Arg | Arg | Ile | Ser | Val | Glu | Gln | Xaa | Gln | Xaa | Asp | Asp | Arg | Val |     |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     |     | 190 |     |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| ataacgaagc  | ggttggaaga  | agatgaaact | gttcgacgcg  | cactgtcacc | ttcaagaccc | 60  |
| gaggattatc  | accaaagctc  | ctcagataat | cacctccgcc  | gttgcttccg | gcgtctctgc | 120 |
| tttcgccgctc | aatggagtct  | ccgagaaaga | ttggagtttg  | gtcaaagaga | tgggagctaa | 180 |
| atacccttct  | gttggttcctt | gctttgggat | ccatccatgg  | tatgtagcag | agaggagtcc | 240 |
| tcaatggttt  | gagacataag  | agtttctttg | agaccactcc  | tactgctgct | gttggagaaa | 300 |
| ttggtttgga  | caaagggtct  | aagggaaggg | agattgattt  | ctcagaacag | gttaccgtct | 360 |
| ttcgtcaaca  | gcttgaactt  | gcaaaggaat | tgaagaaacc  | tgcgtcagtt | cattgtgttc | 420 |
| gtgcatttgg  | ggatctactc  | gagatattaa | aatctgtagg  | gccttttcct | tctggggcca | 480 |
| tgcttcactc  | gtatttgggt  | tytgctgaga | tggttcctga  | atttgctaag | ctcgggtgat | 540 |
| atttctcctt  | ctccggtttc  | cttatgtcca | tgagtgaagaa | aaaagccaag | aagatgttga | 600 |
| aagcagttcc  | atctgatagg  | atcttattgg | agacggattc  | accagatgca | ctaccaaagg | 660 |

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| cagagtcagg | ttgtctctac | tttgtagacg | gagatccttc  | tctacccgaa | gaaggaaatt | 720  |
| cagctcagga | tcttgattct | gcttcatatg | ataagcctaa  | tgtgtctagt | gactcgatga | 780  |
| agttaacaaa | ggaaacactt | aatcacccgg | ctaataattca | tatcgtactc | ggatatgtag | 840  |
| cgcagttggt | ggatatgaag | aatgaagaac | tcgcggaaact | aagttatcaa | aatgctgttc | 900  |
| ggttattctc | ttacgaaggt | tcaaagatac | ttcttgacag  | aggtactggg | gatgtctctg | 960  |
| gtcacactca | aaaccagtca | acaacacatg | tatcatgagt  | tcttacttct | taagaaatcg | 1020 |
| tagtgtttct | catcactcta | ttacgagtct | ttgaatttgg  | actctctctt | tttttttctt | 1080 |
| ttttttttga | atgtttgaat | ttggaattat | tgtactagtg  | ttatagacaa | tcacactttt | 1140 |
| ctttgtacaa | actacaaagg | ttctgatttt | gtgtgaaaat  | taattcagtt | aatgatgtga | 1200 |
| ttagagcc   |            |            |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1497905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | His | Ser | Tyr | Leu | Gly | Xaa | Ala | Glu | Met | Val | Pro | Glu | Phe | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Leu | Gly | Ala | Tyr | Phe | Ser | Phe | Ser | Gly | Phe | Leu | Met | Ser | Met | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Glu | Lys | Lys | Ala | Lys | Lys | Met | Leu | Lys | Ala | Val | Pro | Ser | Asp | Arg | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Leu | Glu | Thr | Asp | Ser | Pro | Asp | Ala | Leu | Pro | Lys | Ala | Glu | Ser | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Leu | Tyr | Phe | Val | Asp | Gly | Asp | Pro | Ser | Leu | Pro | Glu | Glu | Gly | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Ala | Gln | Asp | Leu | Asp | Ser | Ala | Ser | Tyr | Asp | Lys | Pro | Asn | Val | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Asp | Ser | Met | Lys | Leu | Thr | Lys | Glu | Thr | Leu | Asn | His | Pro | Ala | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | His | Ile | Val | Leu | Gly | Tyr | Val | Ala | Gln | Leu | Leu | Asp | Met | Lys | Asn |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Glu | Glu | Leu | Ala | Glu | Leu | Ser | Tyr | Gln | Asn | Ala | Val | Arg | Leu | Phe | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Tyr | Glu | Gly | Ser | Lys | Ile | Leu | Leu | Asp | Arg | Gly | Thr | Gly | Asp | Val | Ser |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Gly | His | Thr | Gln | Asn | Gln | Ser | Thr | Thr | His | Val | Ser |     |     |     |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1497906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Pro | Glu | Phe | Ala | Lys | Leu | Gly | Ala | Tyr | Phe | Ser | Phe | Ser | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Leu | Met | Ser | Met | Ser | Glu | Lys | Lys | Ala | Lys | Lys | Met | Leu | Lys | Ala |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Val | Pro | Ser | Asp | Arg | Ile | Leu | Leu | Glu | Thr | Asp | Ser | Pro | Asp | Ala | Leu |



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Pro Lys Ala Glu Ser Gly Cys Leu Tyr Phe Val Asp Gly Asp Pro Ser |     |     |
| 50                                                              | 55  | 60  |
| Leu Pro Glu Glu Gly Asn Ser Ala Gln Asp Leu Asp Ser Ala Ser Tyr |     |     |
| 65                                                              | 70  | 75  |
| Asp Lys Pro Asn Val Ser Ser Asp Ser Met Lys Leu Thr Lys Glu Thr |     |     |
| 85                                                              | 90  | 95  |
| Leu Asn His Pro Ala Asn Ile His Ile Val Leu Gly Tyr Val Ala Gln |     |     |
| 100                                                             | 105 | 110 |
| Leu Leu Asp Met Lys Asn Glu Glu Leu Ala Glu Leu Ser Tyr Gln Asn |     |     |
| 115                                                             | 120 | 125 |
| Ala Val Arg Leu Phe Ser Tyr Glu Gly Ser Lys Ile Leu Leu Asp Arg |     |     |
| 130                                                             | 135 | 140 |
| Gly Thr Gly Asp Val Ser Gly His Thr Gln Asn Gln Ser Thr Thr His |     |     |
| 145                                                             | 150 | 155 |
| Val Ser                                                         |     | 160 |

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1497907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Ser Met Ser Glu Lys Lys Ala Lys Lys Met Leu Lys Ala Val Pro |     |     |
| 1                                                               | 5   | 10  |
| Ser Asp Arg Ile Leu Leu Glu Thr Asp Ser Pro Asp Ala Leu Pro Lys |     |     |
| 20                                                              | 25  | 30  |
| Ala Glu Ser Gly Cys Leu Tyr Phe Val Asp Gly Asp Pro Ser Leu Pro |     |     |
| 35                                                              | 40  | 45  |
| Glu Glu Gly Asn Ser Ala Gln Asp Leu Asp Ser Ala Ser Tyr Asp Lys |     |     |
| 50                                                              | 55  | 60  |
| Pro Asn Val Ser Ser Asp Ser Met Lys Leu Thr Lys Glu Thr Leu Asn |     |     |
| 65                                                              | 70  | 75  |
| His Pro Ala Asn Ile His Ile Val Leu Gly Tyr Val Ala Gln Leu Leu |     |     |
| 85                                                              | 90  | 95  |
| Asp Met Lys Asn Glu Glu Leu Ala Glu Leu Ser Tyr Gln Asn Ala Val |     |     |
| 100                                                             | 105 | 110 |
| Arg Leu Phe Ser Tyr Glu Gly Ser Lys Ile Leu Leu Asp Arg Gly Thr |     |     |
| 115                                                             | 120 | 125 |
| Gly Asp Val Ser Gly His Thr Gln Asn Gln Ser Thr Thr His Val Ser |     |     |
| 130                                                             | 135 | 140 |

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 765 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..765

(D) OTHER INFORMATION: / Ceres Seq. ID 1497908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| gttcgattga | tgaacagact | cttactgctt | ctaaaccggg  | aaccggtgtg | gttattgctg  | 60  |
| tcaaaaaact | taaccaagat | ggttggcaag | gtcaccagga  | atggctggcg | gaagtgaatt  | 120 |
| acttggggca | gttttcgcat | cctaactctt | tgaactgat   | tggttattgc | ttagaggatg  | 180 |
| agcatcgtct | tcttgtttat | gagttcatgc | ctcgtggaag  | cttagagaat | catttgttca  | 240 |
| gaagagggtc | ttattttcaa | cctttatctt | ggactctccg  | gttgaaagtt | gctcttggtg  | 300 |
| cagcgaaagg | tcttgcgttt | cttcataacg | ccgagactag  | tgtcatatac | cgcgatttca  | 360 |
| aaacgtcgaa | tatactgctt | gattcggagt | acaatgctaa  | gctttctgat | ttcgggctag  | 420 |
| ctaaagacgg | tccaacgggt | gataaaagcc | atgtctctac  | gcggatcatg | gggtacttacg | 480 |
| gatacgagc  | tcctgaatat | cttgcaactg | gtcattttaac | aaccaaaagt | gatgtctata  | 540 |
| gctacgggtg | tgtgcttttg | gaggtgttgt | ctggacggag  | agctgtagac | aagaaccgtc  | 600 |
| caccaggaga | gcaaaagcta | gtggaatggg | caagaccgtt  | acttgctaac | aaaaggraag  | 660 |
| ttattccgag | ttatcgataa | ccgtctacaa | gatcaatac   | caatggaaga | agcttgtaag  | 720 |
| tagctactct | tgcgctgaga | tgccacacat | tcgagataag  | ctgag      |             |     |

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Asp | Glu | Gln | Thr | Leu | Thr | Ala | Ser | Lys | Pro | Gly | Thr | Gly | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ile | Ala | Val | Lys | Lys | Leu | Asn | Gln | Asp | Gly | Trp | Gln | Gly | His | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Trp | Leu | Ala | Glu | Val | Asn | Tyr | Leu | Gly | Gln | Phe | Ser | His | Pro | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Val | Lys | Leu | Ile | Gly | Tyr | Cys | Leu | Glu | Asp | Glu | His | Arg | Leu | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Tyr | Glu | Phe | Met | Pro | Arg | Gly | Ser | Leu | Glu | Asn | His | Leu | Phe | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Gly | Ser | Tyr | Phe | Gln | Pro | Leu | Ser | Trp | Thr | Leu | Arg | Leu | Lys | Val |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Leu | Gly | Ala | Ala | Lys | Gly | Leu | Ala | Phe | Leu | His | Asn | Ala | Glu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Val | Ile | Tyr | Arg | Asp | Phe | Lys | Thr | Ser | Asn | Ile | Leu | Leu | Asp | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Tyr | Asn | Ala | Lys | Leu | Ser | Asp | Phe | Gly | Leu | Ala | Lys | Asp | Gly | Pro |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Thr | Gly | Asp | Lys | Ser | His | Val | Ser | Thr | Arg | Ile | Met | Gly | Thr | Tyr | Gly |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Tyr | Ala | Ala | Pro | Glu | Tyr | Leu | Ala | Thr | Gly | His | Leu | Thr | Thr | Lys | Ser |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asp | Val | Tyr | Ser | Tyr | Gly | Val | Val | Leu | Glu | Val | Leu | Ser | Gly | Arg |     |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Arg | Ala | Val | Asp | Lys | Asn | Arg | Pro | Pro | Gly | Glu | Gln | Lys | Leu | Val | Glu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Trp | Ala | Arg | Pro | Leu | Leu | Ala | Asn | Lys | Arg | Xaa | Val | Ile | Pro | Ser | Tyr |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1497910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Arg | Gly | Ser | Leu | Glu | Asn | His | Leu | Phe | Arg | Arg | Gly | Ser | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Gln | Pro | Leu | Ser | Trp | Thr | Leu | Arg | Leu | Lys | Val | Ala | Leu | Gly | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Lys | Gly | Leu | Ala | Phe | Leu | His | Asn | Ala | Glu | Thr | Ser | Val | Ile | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Asp | Phe | Lys | Thr | Ser | Asn | Ile | Leu | Leu | Asp | Ser | Glu | Tyr | Asn | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Leu | Ser | Asp | Phe | Gly | Leu | Ala | Lys | Asp | Gly | Pro | Thr | Gly | Asp | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | His | Val | Ser | Thr | Arg | Ile | Met | Gly | Thr | Tyr | Gly | Tyr | Ala | Ala | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Tyr | Leu | Ala | Thr | Gly | His | Leu | Thr | Lys | Ser | Asp | Val | Tyr | Ser |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Gly | Val | Val | Leu | Leu | Glu | Val | Leu | Ser | Gly | Arg | Arg | Ala | Val | Asp |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Lys | Asn | Arg | Pro | Pro | Gly | Glu | Gln | Lys | Leu | Val | Glu | Trp | Ala | Arg | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Leu | Ala | Asn | Lys | Arg | Xaa | Val | Ile | Pro | Ser | Tyr | Arg |     |     |     |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..888

(D) OTHER INFORMATION: / Ceres Seq. ID 1497911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| atccttataa  | cctttcttct | cctcttctcc | ttcttcctct | tatgcaaaca  | tatatattaca | 60  |
| taaacaacaca | catatatata | gtaagagaga | gagagagaga | tctagcaaga  | tagtgaaagc  | 120 |
| ttcataatca  | atggaagggg | ttgacaacac | aaatcctatg | ttaaccctag  | aagaaggcga  | 180 |
| aaacaacaat  | cctttttctt | ccttagatga | caaaacatta | atgatgatgg  | ctccttcggt  | 240 |
| aatcttttcg  | ggcgatgtag | gtccatcttc | ttcttcttgt | actccagcag  | gttatcatct  | 300 |
| atctgctcag  | ctggagaact | ttcgaggagg | tggaggagag | atggcaggat  | tagtgagtaa  | 360 |
| taatagcaat  | aatagtgate | ataataagaa | ttgcaacaaa | ggaaaaggga  | agagaacttc  | 420 |
| ggcaatgcag  | aggatagctt | tccatacaag | gagtgatgat | gatgttcttg  | atgatggtta  | 480 |
| tcgttggcga  | aagtacggtc | agaaatctgt | caagaacaat | gctcatccca  | ggagctatta  | 540 |
| tagatgtaca  | taccacacat | gcaacgtgaa | gaaacaagtg | caaagactgg  | caaaagatcc  | 600 |
| aaacgttgtc  | gtaacaacct | acgaagggtg | tcataatcat | ccttgatgaga | agctcatgga  | 660 |
| gactcttagc  | cctctcctta | agcaacttca | gttcctctca | agagtttctg  | atctgtaatt  | 720 |
| attgaatggt  | aattagtggg | gtaatacatt | aattatgctt | taatctctcc  | attgaccctc  | 780 |
| aatctccaaa  | gagacaaatg | tatagaataa | atctcataac | atacatgctt  | taggtttatt  | 840 |
| gagacattga  | tctatgtttt | gctttaattt | gattcgtcta | attgtccc    |             |     |

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1497912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Val | Asp | Asn | Thr | Asn | Pro | Met | Leu | Thr | Leu | Glu | Glu | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Asn | Asn | Asn | Pro | Phe | Ser | Ser | Leu | Asp | Asp | Lys | Thr | Leu | Met | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ala | Pro | Ser | Leu | Ile | Phe | Ser | Gly | Asp | Val | Gly | Pro | Ser | Ser | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Cys | Thr | Pro | Ala | Gly | Tyr | His | Leu | Ser | Ala | Gln | Leu | Glu | Asn | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Gly | Gly | Gly | Gly | Glu | Met | Ala | Gly | Leu | Val | Ser | Asn | Asn | Ser | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Ser | Asp | His | Asn | Lys | Asn | Cys | Asn | Lys | Gly | Lys | Gly | Lys | Arg | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Ala | Met | Gln | Arg | Ile | Ala | Phe | His | Thr | Arg | Ser | Asp | Asp | Asp | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Asp | Asp | Gly | Tyr | Arg | Trp | Arg | Lys | Tyr | Gly | Gln | Lys | Ser | Val | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Asn | Ala | His | Pro | Arg | Ser | Tyr | Tyr | Arg | Cys | Thr | Tyr | His | Thr | Cys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Val | Lys | Lys | Gln | Val | Gln | Arg | Leu | Ala | Lys | Asp | Pro | Asn | Val | Val |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Val | Thr | Thr | Tyr | Glu | Gly | Val | His | Asn | His | Pro | Cys | Glu | Lys | Leu | Met |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Thr | Leu | Ser | Pro | Leu | Leu | Lys | Gln | Leu | Gln | Phe | Leu | Ser | Arg | Val |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ser | Asp | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1497913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Thr | Leu | Glu | Glu | Gly | Glu | Asn | Asn | Asn | Pro | Phe | Ser | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | Asp | Lys | Thr | Leu | Met | Met | Met | Ala | Pro | Ser | Leu | Ile | Phe | Ser | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Val | Gly | Pro | Ser | Ser | Ser | Ser | Cys | Thr | Pro | Ala | Gly | Tyr | His | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Gln | Leu | Glu | Asn | Phe | Arg | Gly | Gly | Gly | Gly | Glu | Met | Ala | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Val | Ser | Asn | Asn | Ser | Asn | Asn | Ser | Asp | His | Asn | Lys | Asn | Cys | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Gly | Lys | Gly | Lys | Arg | Thr | Ser | Ala | Met | Gln | Arg | Ile | Ala | Phe | His |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Arg | Ser | Asp | Asp | Asp | Val | Leu | Asp | Asp | Gly | Tyr | Arg | Trp | Arg | Lys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Tyr | Gly | Gln | Lys | Ser | Val | Lys | Asn | Asn | Ala | His | Pro | Arg | Ser | Tyr | Tyr |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Cys | Thr | Tyr | His | Thr | Cys | Asn | Val | Lys | Lys | Gln | Val | Gln | Arg | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Lys | Asp | Pro | Asn | Val | Val | Thr | Thr | Tyr | Glu | Gly | Val | His | Asn |     |

145                      150                      155                      160  
His Pro Cys Glu Lys Leu Met Glu Thr Leu Ser Pro Leu Leu Lys Gln  
                                 165                      170                      175  
Leu Gln Phe Leu Ser Arg Val Ser Asp Leu  
                                 180                      185

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Met Met Ala Pro Ser Leu Ile Phe Ser Gly Asp Val Gly Pro Ser  
1                      5                      10                      15  
Ser Ser Ser Cys Thr Pro Ala Gly Tyr His Leu Ser Ala Gln Leu Glu  
                                 20                      25                      30  
Asn Phe Arg Gly Gly Gly Gly Glu Met Ala Gly Leu Val Ser Asn Asn  
                                 35                      40                      45  
Ser Asn Asn Ser Asp His Asn Lys Asn Cys Asn Lys Gly Lys Gly Lys  
                                 50                      55                      60  
Arg Thr Ser Ala Met Gln Arg Ile Ala Phe His Thr Arg Ser Asp Asp  
65                      70                      75                      80  
Asp Val Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser  
                                 85                      90                      95  
Val Lys Asn Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His  
                                 100                      105                      110  
Thr Cys Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn  
                                 115                      120                      125  
Val Val Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys  
                                 130                      135                      140  
Leu Met Glu Thr Leu Ser Pro Leu Leu Lys Gln Leu Gln Phe Leu Ser  
145                      150                      155                      160  
Arg Val Ser Asp Leu  
                                 165

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1257
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

aaagaaactc aacttttttt ctttatcttt aacatcaaaa aacttttatcg atatctttac 60  
aaccattaaa caaaaaattt ggccactaca agttgaaaaa gttttgatta tatctaatacg 120  
ctgaaatgga ttacaaggta tcaagaagtg gggagatagt agaaggagaa gtagaagatt 180  
cagaaaagat tgattttacca cctggtttca gatttcaccc aactgatgaa gaacttataa 240  
cacactatct aagaccaaag gttgtaaact cttttttctc tgctatagct attggtgaag 300  
ttgatctcaa caaagtcgag ccttgggact tgccttgga ggctaagctt ggggaaaaag 360  
agtggactct cttttgcgta agagaccgaa aataccgcac tggtttaaga acgaatcgtg 420  
ctactaaagc cggttatttg aaagctacag ggaaagataa agagatcttc aaagggaaat 480  
ctcttggttg tatgaagaaa acattggttt tctacaaagg aagagctcct aaaggagtaa 540  
aaacaaattg ggtcatgcat gagtatcgat tagaaggcaa atacggtatc gataatctcc 600

```
ctaaaaccgc taagaacgaa tgtgttatta gtcgtgtttt tcataaacgg actgatggta 660
cgaaggagca tatgtccgtt ggtttacctc cgctgatgga ttcttctcca tatctaaaga 720
gtagaggaca agactcttta gccgggacca cccttggtgg gttgttgtct cacgttacct 780
acttctccga ccaaacaacc gatgacaaga gtcttggtgc cgattttaaa actaccatgt 840
ttggttccgg atcgactaac tttttaccaa acataggttc tctactagac ttcgatcctc 900
tgtttctaca aaacaattct tcagtactaa agatgttgct tgacaatgaa gaaacccaat 960
ttaagaagaa tcttcacaat tcaggttcat cagagagtga actaacagcg agttcttggc 1020
aaggtcacaa ttcttatggt tccactggtc cagtgaatct tgattgcgtt tggaaattct 1080
gaatttgga aatcgaaaat ttggatgta actagggggt atataggggt tttaaaaaca 1140
gtgtatatat gcgttatgtg ttagcttttag attctaggat atacaaagat gacactaata 1200
gattcttata acattttgta aaaaaaaatc attgtagtga atactctctt gccattt
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
Met Asp Tyr Lys Val Ser Arg Ser Gly Glu Ile Val Glu Gly Glu Val
1 5 10 15
Glu Asp Ser Glu Lys Ile Asp Leu Pro Gly Phe Arg Phe His Pro
20 25 30
Thr Asp Glu Glu Leu Ile Thr His Tyr Leu Arg Pro Lys Val Val Asn
35 40 45
Ser Phe Phe Ser Ala Ile Ala Ile Gly Glu Val Asp Leu Asn Lys Val
50 55 60
Glu Pro Trp Asp Leu Pro Trp Lys Ala Lys Leu Gly Glu Lys Glu Trp
65 70 75 80
Tyr Phe Phe Cys Val Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr
85 90 95
Asn Arg Ala Thr Lys Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys
100 105 110
Glu Ile Phe Lys Gly Lys Ser Leu Val Gly Met Lys Lys Thr Leu Val
115 120 125
Phe Tyr Lys Gly Arg Ala Pro Lys Gly Val Lys Thr Asn Trp Val Met
130 135 140
His Glu Tyr Arg Leu Glu Gly Lys Tyr Gly Ile Asp Asn Leu Pro Lys
145 150 155 160
Thr Ala Lys Asn Glu Cys Val Ile Ser Arg Val Phe His Lys Arg Thr
165 170 175
Asp Gly Thr Lys Glu His Met Ser Val Gly Leu Pro Pro Leu Met Asp
180 185 190
Ser Ser Pro Tyr Leu Lys Ser Arg Gly Gln Asp Ser Leu Ala Gly Thr
195 200 205
Thr Leu Gly Gly Leu Leu Ser His Val Thr Tyr Phe Ser Asp Gln Thr
210 215 220
Thr Asp Asp Lys Ser Leu Val Ala Asp Phe Lys Thr Thr Met Phe Gly
225 230 235 240
Ser Gly Ser Thr Asn Phe Leu Pro Asn Ile Gly Ser Leu Leu Asp Phe
245 250 255
Asp Pro Leu Phe Leu Gln Asn Asn Ser Ser Val Leu Lys Met Leu Leu
260 265 270
Asp Asn Glu Glu Thr Gln Phe Lys Lys Asn Leu His Asn Ser Gly Ser
275 280 285
Ser Glu Ser Glu Leu Thr Ala Ser Ser Trp Gln Gly His Asn Ser Tyr
290 295 300
```

Gly Ser Thr Gly Pro Val Asn Leu Asp Cys Val Trp Lys Phe  
305 310 315

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Lys | Thr | Leu | Val | Phe | Tyr | Lys | Gly | Arg | Ala | Pro | Lys | Gly | Val |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Thr | Asn | Trp | Val | Met | His | Glu | Tyr | Arg | Leu | Glu | Gly | Lys | Tyr | Gly |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Ile | Asp | Asn | Leu | Pro | Lys | Thr | Ala | Lys | Asn | Glu | Cys | Val | Ile | Ser | Arg |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Phe | His | Lys | Arg | Thr | Asp | Gly | Thr | Lys | Glu | His | Met | Ser | Val | Gly |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Pro | Pro | Leu | Met | Asp | Ser | Ser | Pro | Tyr | Leu | Lys | Ser | Arg | Gly | Gln |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Asp | Ser | Leu | Ala | Gly | Thr | Thr | Leu | Gly | Gly | Leu | Leu | Ser | His | Val | Thr |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Tyr | Phe | Ser | Asp | Gln | Thr | Thr | Asp | Asp | Lys | Ser | Leu | Val | Ala | Asp | Phe |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Lys | Thr | Thr | Met | Phe | Gly | Ser | Gly | Ser | Thr | Asn | Phe | Leu | Pro | Asn | Ile |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Ser | Leu | Leu | Asp | Phe | Asp | Pro | Leu | Phe | Leu | Gln | Asn | Asn | Ser | Ser |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | Leu | Lys | Met | Leu | Leu | Asp | Asn | Glu | Glu | Thr | Gln | Phe | Lys | Lys | Asn |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Leu | His | Asn | Ser | Gly | Ser | Ser | Glu | Ser | Glu | Leu | Thr | Ala | Ser | Ser | Trp |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Gln | Gly | His | Asn | Ser | Tyr | Gly | Ser | Thr | Gly | Pro | Val | Asn | Leu | Asp | Cys |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Val | Trp | Lys | Phe |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | His | Glu | Tyr | Arg | Leu | Glu | Gly | Lys | Tyr | Gly | Ile | Asp | Asn | Leu | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Thr | Ala | Lys | Asn | Glu | Cys | Val | Ile | Ser | Arg | Val | Phe | His | Lys | Arg |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Asp | Gly | Thr | Lys | Glu | His | Met | Ser | Val | Gly | Leu | Pro | Pro | Leu | Met |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asp | Ser | Ser | Pro | Tyr | Leu | Lys | Ser | Arg | Gly | Gln | Asp | Ser | Leu | Ala | Gly |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Thr | Thr | Leu | Gly | Gly | Leu | Leu | Ser | His | Val | Thr | Tyr | Phe | Ser | Asp | Gln |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Thr | Asp | Asp | Lys | Ser | Leu | Val | Ala | Asp | Phe | Lys | Thr | Thr | Met | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ser | Gly | Ser | Thr | Asn | Phe | Leu | Pro | Asn | Ile | Gly | Ser | Leu | Leu | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Asp | Pro | Leu | Phe | Leu | Gln | Asn | Asn | Ser | Ser | Val | Leu | Lys | Met | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Asp | Asn | Glu | Glu | Thr | Gln | Phe | Lys | Lys | Asn | Leu | His | Asn | Ser | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Ser | Glu | Ser | Glu | Leu | Thr | Ala | Ser | Ser | Trp | Gln | Gly | His | Asn | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Gly | Ser | Thr | Gly | Pro | Val | Asn | Leu | Asp | Cys | Val | Trp | Lys | Phe |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| aacccaaaca | aaacaaaaca | aaaaaaacac | gagtgggaagc | ttttaaacaa | aattagaaaa | 60  |
| agagagagag | aaatggcgac | gtcgggaaca | tacgtgacgg  | aggtgccgct | aaaaggaacg | 120 |
| gtggagaaac | acttcaagag | gtacaggaac | gagaactatc  | tcttccctga | cactatcggc | 180 |
| caccacatcc | aaagtgttac | tgttcacgat | ggcgaatggg  | acactcaagg | aggcatcaag | 240 |
| atttgaact  | acacactcgg | agatggaaag | gaggaggtat  | tcaaggagag | gagagagata | 300 |
| gacgatgaca | ataagatagt | aaaggttgta | ggattggaag  | gtcacgtgat | ggagcagttc | 360 |
| aagggtgatg | agattgactt | ccaatttatt | cccaagtctg  | aagaagattg | cgtctgcaaa | 420 |
| atcactatga | tatgggagaa | gcgcaacgat | gatttccccg  | aaccaagcag | ctacatgcaa | 480 |
| ctcctcaaga | gtatggttat | tgatatggag | gaccacgtcc  | ttaaagctta | atcaatatca | 540 |
| caaccaccac | catcatcaca | accaccatca | tcatcatcct  | atatgtttat | taaattgttt | 600 |
| tcatttatat | ataatagact | agataagaac | ctgtataatg  | tgcgggataa | aatgattgaa | 660 |
| ataaattatt | atgcgtaaac | ttattgtatg | agatatcata  | tatgtttgta | tacaagaaaa | 720 |
| tatgtaatta | aagtbttttg | ttttattt   |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gln | Asn | Lys | Thr | Lys | Gln | Lys | Lys | His | Glu | Trp | Lys | Leu | Leu | Asn |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Ile | Arg | Lys | Arg | Glu | Arg | Glu | Met | Ala | Thr | Ser | Gly | Thr | Tyr | Val |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Thr | Glu | Val | Pro | Leu | Lys | Gly | Thr | Val | Glu | Lys | His | Phe | Lys | Arg | Tyr |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Asn | Glu | Asn | Tyr | Leu | Phe | Pro | Asp | Thr | Ile | Gly | His | His | Ile | Gln |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ser | Val | Thr | Val | His | Asp | Gly | Glu | Trp | Asp | Thr | Gln | Gly | Gly | Ile | Lys |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Ile | Trp | Asn | Tyr | Thr | Leu | Gly | Asp | Gly | Lys | Glu | Glu | Val | Phe | Lys | Glu |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |
| Arg | Arg | Glu | Ile | Asp | Asp | Asp | Asn | Lys | Ile | Val | Lys | Val | Val | Gly | Leu |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |  |  |
| Glu | Gly | His | Val | Met | Glu | Gln | Phe | Lys | Val | Tyr | Glu | Ile | Asp | Phe | Gln |  |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |  |  |
| Phe | Ile | Pro | Lys | Ser | Glu | Glu | Asp | Cys | Val | Cys | Lys | Ile | Thr | Met | Ile |  |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |
| Trp | Glu | Lys | Arg | Asn | Asp | Phe | Pro | Glu | Pro | Ser | Ser | Tyr | Met | Gln |     |  |  |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |  |  |
| Leu | Leu | Lys | Ser | Met | Val | Ile | Asp | Met | Glu | Asp | His | Val | Leu | Lys | Ala |  |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |  |

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1497926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Ala | Thr | Ser | Gly | Thr | Tyr | Val | Thr | Glu | Val | Pro | Leu | Lys | Gly | Thr |  |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |  |
| Val | Glu | Lys | His | Phe | Lys | Arg | Tyr | Arg | Asn | Glu | Asn | Tyr | Leu | Phe | Pro |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |
| Asp | Thr | Ile | Gly | His | His | Ile | Gln | Ser | Val | Thr | Val | His | Asp | Gly | Glu |  |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |  |
| Trp | Asp | Thr | Gln | Gly | Gly | Ile | Lys | Ile | Trp | Asn | Tyr | Thr | Leu | Gly | Asp |  |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |
| Gly | Lys | Glu | Glu | Val | Phe | Lys | Glu | Arg | Arg | Glu | Ile | Asp | Asp | Asp | Asn |  |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |  |
| Lys | Ile | Val | Lys | Val | Val | Gly | Leu | Glu | Gly | His | Val | Met | Glu | Gln | Phe |  |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |  |
| Lys | Val | Tyr | Glu | Ile | Asp | Phe | Gln | Phe | Ile | Pro | Lys | Ser | Glu | Glu | Asp |  |  |  |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |  |  |
| Cys | Val | Cys | Lys | Ile | Thr | Met | Ile | Trp | Glu | Lys | Arg | Asn | Asp | Asp | Phe |  |  |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |  |  |
| Pro | Glu | Pro | Ser | Ser | Tyr | Met | Gln | Leu | Leu | Lys | Ser | Met | Val | Ile | Asp |  |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |
| Met | Glu | Asp | His | Val | Leu | Lys | Ala |     |     |     |     |     |     |     |     |  |  |  |
| 145 |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |     |  |  |  |

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 591 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..591

(D) OTHER INFORMATION: / Ceres Seq. ID 1497927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtgattcagt | tttggttttg | gaacctaat  | ctctctcaag | agattcagct | aagatgagta | 60  |
| ctatgaaatt | ttgccgcgaa | tgtaataaca | ttctgtatcc | taaggaggac | aaagaacaga | 120 |
| agatcctcct | ctatgcttgc | cgtaattgtg | atcaccagga | ggtagctgat | aacagctgtg | 180 |
| tgtacagaaa | cgaggttcat | cactctgtaa | gtgagcgaac | tcagatctta | acagacgtgg | 240 |

```
cttctgaccb tactcttccc sgaaccaagg ctgtgcgttg ctctaagtgt cagcataggg 300
aggccgtttt cttccaggct acggttagag gtgaagaagg aatgacactg ttctttgtct 360
gttgcaaccc gaattgtggt catcgctgga gagaataaag agcttttcgg tttcaattgg 420
tgagttctta agagtttttag gagttgatgt agttaccagt aagtgtataa tgtggaatga 480
cgggaacaac cttctgcccc agtcagagac aaatccgtat tcatgtaatc tgttatgaaa 540
ccataatctc aacttctggt tcaccaaaaca taaagattgg aacttgtttc t
```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1497928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
Asp Ser Val Leu Val Leu Glu Pro Asn Ser Leu Ser Arg Asp Ser Ala
1 5 10 15
Lys Met Ser Thr Met Lys Phe Cys Arg Glu Cys Asn Asn Ile Leu Tyr
 20 25 30
Pro Lys Glu Asp Lys Glu Gln Lys Ile Leu Leu Tyr Ala Cys Arg Asn
 35 40 45
Cys Asp His Gln Glu Val Ala Asp Asn Ser Cys Val Tyr Arg Asn Glu
 50 55 60
Val His His Ser Val Ser Glu Arg Thr Gln Ile Leu Thr Asp Val Ala
 65 70 75 80
Ser Asp Xaa Thr Leu Pro Xaa Thr Lys Ala Val Arg Cys Ser Lys Cys
 85 90 95
Gln His Arg Glu Ala Val Phe Phe Gln Ala Thr Val Arg Gly Glu Glu
 100 105 110
Gly Met Thr Leu Phe Phe Val Cys Cys Asn Pro Asn Cys Gly His Arg
 115 120 125
Trp Arg Glu
 130
```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1497929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
Met Ser Thr Met Lys Phe Cys Arg Glu Cys Asn Asn Ile Leu Tyr Pro
1 5 10 15
Lys Glu Asp Lys Glu Gln Lys Ile Leu Leu Tyr Ala Cys Arg Asn Cys
 20 25 30
Asp His Gln Glu Val Ala Asp Asn Ser Cys Val Tyr Arg Asn Glu Val
 35 40 45
His His Ser Val Ser Glu Arg Thr Gln Ile Leu Thr Asp Val Ala Ser
 50 55 60
Asp Xaa Thr Leu Pro Xaa Thr Lys Ala Val Arg Cys Ser Lys Cys Gln
 65 70 75 80
His Arg Glu Ala Val Phe Phe Gln Ala Thr Val Arg Gly Glu Glu Gly
 85 90 95
Met Thr Leu Phe Phe Val Cys Cys Asn Pro Asn Cys Gly His Arg Trp
```

Arg Glu 100 105 110

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Cys | Arg | Glu | Cys | Asn | Asn | Ile | Leu | Tyr | Pro | Lys | Glu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Glu | Gln | Lys | Ile | Leu | Leu | Tyr | Ala | Cys | Arg | Asn | Cys | Asp | His | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Val | Ala | Asp | Asn | Ser | Cys | Val | Tyr | Arg | Asn | Glu | Val | His | His | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ser | Glu | Arg | Thr | Gln | Ile | Leu | Thr | Asp | Val | Ala | Ser | Asp | Xaa | Thr |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Pro | Xaa | Thr | Lys | Ala | Val | Arg | Cys | Ser | Lys | Cys | Gln | His | Arg | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Val | Phe | Phe | Gln | Ala | Thr | Val | Arg | Gly | Glu | Glu | Gly | Met | Thr | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Phe | Val | Cys | Cys | Asn | Pro | Asn | Cys | Gly | His | Arg | Trp | Arg | Glu |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..568
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

|            |             |             |            |             |            |     |
|------------|-------------|-------------|------------|-------------|------------|-----|
| ccttggttag | ccatgggaag  | catctctcct  | cgttccatgt | tcgatgagct  | gaagaaaaca | 60  |
| atctccgcac | caaccacctc  | cacaactcca  | aggaacggac | cgggagatac  | aggactcaac | 120 |
| tggttaatgt | atgagttgct  | atggagggat  | ttcttcaggt | ttataaccaa  | gaaatacagc | 180 |
| tcagcgaaga | cgcagggtcga | ggctgggtccg | gctacagcct | gtaccgggtgc | ctttgcttaa | 240 |
| acatttgaaa | acttttcaggt | gaccggaaaa  | gttagaagcg | acctgtttct  | ttgccctact | 300 |
| ctgggtgatg | gtggattaat  | ttgctatccg  | gacaggactt | tactgctctc  | ttttgaaact | 360 |
| tgagtgtcag | gagaataaaa  | tctaagcttc  | tttttttggc | tcaatcaagt  | tgtccgttcc | 420 |
| ctgttctaaa | catttcggat  | actcattcca  | taaaaagtct | ctacaatttg  | agacgctctc | 480 |
| ctttgtgggt | aagacttgag  | aatgtatctt  | agaaartaay | cgaagtmgtt  | gtgtctatga | 540 |
| atattaaatt | caggaatatt  | aagatgtc    |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1497932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Pro Trp Leu Ala Met Gly Ser Ile Ser Pro Arg Ser Met Phe Asp Glu  
1 5 10 15  
Leu Lys Lys Thr Ile Ser Ala Ser Thr Thr Ser Thr Thr Pro Arg Asn  
20 25 30  
Gly Pro Gly Asp Thr Gly Leu Asn Trp Leu Met Tyr Glu Leu Leu Trp  
35 40 45  
Arg Asp Phe Phe Arg Phe Ile Thr Lys Lys Tyr Ser Ser Ala Lys Thr  
50 55 60  
Gln Val Glu Ala Gly Pro Ala Thr Ala Cys Thr Gly Ala Phe Ala  
65 70 75

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1497933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Gly Ser Ile Ser Pro Arg Ser Met Phe Asp Glu Leu Lys Lys Thr  
1 5 10 15  
Ile Ser Ala Ser Thr Thr Ser Thr Thr Pro Arg Asn Gly Pro Gly Asp  
20 25 30  
Thr Gly Leu Asn Trp Leu Met Tyr Glu Leu Leu Trp Arg Asp Phe Phe  
35 40 45  
Arg Phe Ile Thr Lys Lys Tyr Ser Ser Ala Lys Thr Gln Val Glu Ala  
50 55 60  
Gly Pro Ala Thr Ala Cys Thr Gly Ala Phe Ala  
65 70 75

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1497934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Phe Asp Glu Leu Lys Lys Thr Ile Ser Ala Ser Thr Thr Ser Thr  
1 5 10 15  
Thr Pro Arg Asn Gly Pro Gly Asp Thr Gly Leu Asn Trp Leu Met Tyr  
20 25 30  
Glu Leu Leu Trp Arg Asp Phe Phe Arg Phe Ile Thr Lys Lys Tyr Ser  
35 40 45  
Ser Ala Lys Thr Gln Val Glu Ala Gly Pro Ala Thr Ala Cys Thr Gly  
50 55 60  
Ala Phe Ala  
65

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1012 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1012  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497939  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| acttcagcaa | aaccactaca  | cctttcttat | ctctcagatt | ttctcaagaa | gatttgtgtgg | 60  |
| aagatgatga | gacggaagat  | ttttctcttt | ggtgattcca | tcactgaaga | atccttttagt | 120 |
| gacggtggct | ggggtgcttc  | tctcgccgat | cttctccgcc | gcaaggctga | tatggtgcta  | 180 |
| cgaggataca | gtggatataa  | cacgaggtgg | gcactgaaag | tggtggagag | agtttttccg  | 240 |
| gtggcagaag | aagacggcgg  | agattctccg | gcagctgtga | ctgttttctt | tgaggcgaac  | 300 |
| gacgcgtgtc | ttccggagag  | atgctcgggg | tttcagcatg | tgccacttca | cgagtacaag  | 360 |
| cagaatcttc | gctctattgt  | ttcgtttctc | aagaatcggt | ggccacaaac | ggccattatt  | 420 |
| cttataactc | cgcttccaat  | agacgaagag | gcccgcctca | gatatcctta | tatcgaaaac  | 480 |
| acaacggggg | tgccggaaaag | aacgaatgaa | gtagccggac | tatacgcaaa | agcatgtata  | 540 |
| gcagtagctg | aggaatgtca  | aatttcggtc | actgatcttt | ggtccaaaat | gcagcaaaat  | 600 |
| scaaattggs | aaacagaatg  | tctatgggac | gggttacatt | tgagtcgggt | cggtaacaaa  | 660 |
| gtattgtttg | aagaagtagc  | aaagaagctt | aaagaagaag | gcattggagc | tgaggactta  | 720 |
| gctgtgggac | ttcccttat   | agaagatggt | gaccctaagg | atcctctcaa | atcctttgat  | 780 |
| gagttttgat | gctttatatt  | actaccatgc | agtttggttc | ttctatcttt | gattacttct  | 840 |
| taatttcgat | attaatttag  | ggaatgtgac | attattaggc | actttgtgag | aatctttttg  | 900 |
| tgagaatctt | tttacgtttg  | aggcacttgt | gagagagagg | gcactttgcc | atcttttttt  | 960 |
| agaggagatt | gaaccaattt  | gcccctgaag | tgatgaaaac | acaataattt | tt          |     |

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 262 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..262  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497940  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Ser | Ala | Lys | Pro | Leu | His | Leu | Ser | Tyr | Leu | Ser | Asp | Phe | Leu | Lys |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Lys | Ile | Val | Trp | Lys | Met | Met | Arg | Arg | Lys | Ile | Phe | Leu | Phe | Gly | Asp |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Ser | Ile | Thr | Glu | Glu | Ser | Phe | Ser | Asp | Gly | Gly | Trp | Gly | Ala | Ser | Leu |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Ala | Asp | Leu | Leu | Arg | Arg | Lys | Ala | Asp | Met | Val | Leu | Arg | Gly | Tyr | Ser |  |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |  |
| Gly | Tyr | Asn | Thr | Arg | Trp | Ala | Leu | Lys | Val | Val | Glu | Arg | Val | Phe | Pro |  |
| 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Val | Ala | Glu | Glu | Asp | Gly | Gly | Asp | Ser | Pro | Ala | Ala | Val | Thr | Val | Phe |  |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |
| Phe | Gly | Ala | Asn | Asp | Ala | Cys | Leu | Pro | Glu | Arg | Cys | Ser | Gly | Phe | Gln |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| His | Val | Pro | Leu | His | Glu | Tyr | Lys | Gln | Asn | Leu | Arg | Ser | Ile | Val | Ser |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Phe | Leu | Lys | Asn | Arg | Trp | Pro | Gln | Thr | Ala | Ile | Ile | Leu | Ile | Thr | Pro |  |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |
| Pro | Pro | Ile | Asp | Glu | Glu | Ala | Arg | Leu | Arg | Tyr | Pro | Tyr | Ile | Glu | Asn |  |
| 145 |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Thr | Thr | Gly | Leu | Pro | Glu | Arg | Thr | Asn | Glu | Val | Ala | Gly | Leu | Tyr | Ala |  |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |     |  |
| Lys | Ala | Cys | Ile | Ala | Val | Ala | Glu | Glu | Cys | Gln | Ile | Ser | Val | Thr | Asp |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Leu | Trp | Ser | Lys | Met | Gln | Gln | Xaa | Xaa | Asn | Trp | Xaa | Thr | Glu | Cys | Leu |  |

195 200 205  
Trp Asp Gly Leu His Leu Ser Arg Val Gly Asn Lys Val Leu Phe Glu  
210 215 220  
Glu Val Ala Lys Lys Leu Lys Glu Glu Gly Ile Gly Ala Glu Asp Leu  
225 230 235 240  
Ala Val Asp Leu Pro Leu Ile Glu Asp Val Asp Pro Lys Asp Pro Leu  
245 250 255  
Lys Ser Phe Asp Glu Phe  
260

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1497941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Met Arg Arg Lys Ile Phe Leu Phe Gly Asp Ser Ile Thr Glu Glu  
1 5 10 15  
Ser Phe Ser Asp Gly Gly Trp Gly Ala Ser Leu Ala Asp Leu Leu Arg  
20 25 30  
Arg Lys Ala Asp Met Val Leu Arg Gly Tyr Ser Gly Tyr Asn Thr Arg  
35 40 45  
Trp Ala Leu Lys Val Val Glu Arg Val Phe Pro Val Ala Glu Glu Asp  
50 55 60  
Gly Gly Asp Ser Pro Ala Ala Val Thr Val Phe Phe Gly Ala Asn Asp  
65 70 75 80  
Ala Cys Leu Pro Glu Arg Cys Ser Gly Phe Gln His Val Pro Leu His  
85 90 95  
Glu Tyr Lys Gln Asn Leu Arg Ser Ile Val Ser Phe Leu Lys Asn Arg  
100 105 110  
Trp Pro Gln Thr Ala Ile Ile Leu Ile Thr Pro Pro Pro Ile Asp Glu  
115 120 125  
Glu Ala Arg Leu Arg Tyr Pro Tyr Ile Glu Asn Thr Thr Gly Leu Pro  
130 135 140  
Glu Arg Thr Asn Glu Val Ala Gly Leu Tyr Ala Lys Ala Cys Ile Ala  
145 150 155 160  
Val Ala Glu Glu Cys Gln Ile Ser Val Thr Asp Leu Trp Ser Lys Met  
165 170 175  
Gln Gln Xaa Xaa Asn Trp Xaa Thr Glu Cys Leu Trp Asp Gly Leu His  
180 185 190  
Leu Ser Arg Val Gly Asn Lys Val Leu Phe Glu Glu Val Ala Lys Lys  
195 200 205  
Leu Lys Glu Glu Gly Ile Gly Ala Glu Asp Leu Ala Val Asp Leu Pro  
210 215 220  
Leu Ile Glu Asp Val Asp Pro Lys Asp Pro Leu Lys Ser Phe Asp Glu  
225 230 235 240  
Phe

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1497942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Arg | Lys | Ile | Phe | Leu | Phe | Gly | Asp | Ser | Ile | Thr | Glu | Glu | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Ser | Asp | Gly | Gly | Trp | Gly | Ala | Ser | Leu | Ala | Asp | Leu | Leu | Arg | Arg |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Lys | Ala | Asp | Met | Val | Leu | Arg | Gly | Tyr | Ser | Gly | Tyr | Asn | Thr | Arg | Trp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Lys | Val | Val | Glu | Arg | Val | Phe | Pro | Val | Ala | Glu | Glu | Asp | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Asp | Ser | Pro | Ala | Ala | Val | Thr | Val | Phe | Phe | Gly | Ala | Asn | Asp | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Cys | Leu | Pro | Glu | Arg | Cys | Ser | Gly | Phe | Gln | His | Val | Pro | Leu | His | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Tyr | Lys | Gln | Asn | Leu | Arg | Ser | Ile | Val | Ser | Phe | Leu | Lys | Asn | Arg | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Gln | Thr | Ala | Ile | Ile | Leu | Ile | Thr | Pro | Pro | Pro | Ile | Asp | Glu | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Ala | Arg | Leu | Arg | Tyr | Pro | Tyr | Ile | Glu | Asn | Thr | Thr | Gly | Leu | Pro | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Arg | Thr | Asn | Glu | Val | Ala | Gly | Leu | Tyr | Ala | Lys | Ala | Cys | Ile | Ala | Val |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Glu | Glu | Cys | Gln | Ile | Ser | Val | Thr | Asp | Leu | Trp | Ser | Lys | Met | Gln |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Xaa | Xaa | Asn | Trp | Xaa | Thr | Glu | Cys | Leu | Trp | Asp | Gly | Leu | His | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Arg | Val | Gly | Asn | Lys | Val | Leu | Phe | Glu | Glu | Val | Ala | Lys | Lys | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Glu | Glu | Gly | Ile | Gly | Ala | Glu | Asp | Leu | Ala | Val | Asp | Leu | Pro | Leu |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ile | Glu | Asp | Val | Asp | Pro | Lys | Asp | Pro | Leu | Lys | Ser | Phe | Asp | Glu | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1380

(D) OTHER INFORMATION: / Ceres Seq. ID 1497943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

|             |              |            |             |            |             |     |
|-------------|--------------|------------|-------------|------------|-------------|-----|
| atatttattcc | tttctccgct   | ataaaaagcg | atattttctat | tgtagctcga | tttgcgggaa  | 60  |
| aatcttgcac  | ctgcctcaga   | aaattttctg | gggagctttc  | accaattagt | tcttctcgtc  | 120 |
| tctctctctc  | tctttgggta   | atgtttctac | agattctctc  | ctcctaattc | agagacgaca  | 180 |
| aaacgctata  | aacaacattt   | ttacagtttg | gaggaggaag  | gagaaatgat | aggttttatta | 240 |
| actgagagta  | gcagcagtc    | tatggtggta | aatgtggatg  | ggttgatgcg | tccgataccg  | 300 |
| atgtctccgg  | ttaatgcgga   | ggttgaggag | atgagatcag  | agtcgccggg | ggttaatgat  | 360 |
| aaggcgtag   | atatttctga   | tgatgatcat | gatgatgaga  | atgaaccgct | tattgtttct  | 420 |
| ggtgaatgtc  | gtatttggtc   | tgatgagtct | cctgttgaga  | atcttgagag | cccttggtgct | 480 |
| tgcagtggca  | gcctaaagta   | tgctcataga | aaatgtgttc  | agcgttggtg | caatgaaaag  | 540 |
| aaaaacatta  | tatgcgagat   | ttgtcaccag | ccttatcaac  | ctggatatac | cgctccacca  | 600 |
| cctccacttc  | agcctgaaga   | aacaactatt | gacattgggtg | gaggatggac | aatctcaggt  | 660 |
| ttggatgtgc  | atgatcctcg   | tctccttgca | attgctgaag  | ctgaacgtcg | gtatttagag  | 720 |
| tctgaatatg  | tggaatatatac | agcttcaagt | gcaagcgggg  | ccgcattctg | tcgctcagct  | 780 |

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| gctctaatat | taatggctct | tcttctctta  | cgacacgcac  | tgaccataac  | agatgatact  | 840  |
| gatggcgaag | aagacgaccc | atcttcgata  | ctatctcttg  | tcctgctccg  | agctgctgga  | 900  |
| tttcttcttc | catgctatat | catggctkkg  | gccatcagta  | ttctacagcg  | ccgaagacag  | 960  |
| agacaggaag | ctgcagcttt | ggctacacag  | tttgcgtttg  | tgcttcagtc  | agggcagcct  | 1020 |
| agaacagttc | acttcacggt | atcaccggga  | atatcatcat  | cctccgtggc  | tcattgcgact | 1080 |
| acatctacac | aacaacagca | tgacgatcct  | gtctgaattc  | tgatctaattg | tcacaagcat  | 1140 |
| ggagccatta | caaggtacga | tgtaaataca  | atgaagaatt  | tggtgtccgt  | aaattgtatg  | 1200 |
| agtaaaggat | tgaaatcatt | tgaattcgtg  | gaagggttaga | tctttcattt  | tacttgtatg  | 1260 |
| cvaatgtgc  | aaataggttt | tgacacaaatt | tgtaaattct  | gctttactat  | ttttcacaca  | 1320 |
| ttgtcttgaa | acttgagtgt | atTTTTTTTT  | aaaaaataat  | tcgtctttta  | ggaagaaaac  | 1380 |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1497944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Gly | Leu | Leu | Thr | Glu | Ser | Ser | Ser | Ser | His | Met | Val | Val | Asn |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Asp | Gly | Leu | Met | Arg | Pro | Ile | Pro | Met | Ser | Pro | Val | Asn | Ala | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Glu | Glu | Met | Arg | Ser | Glu | Ser | Pro | Val | Val | Asn | Asp | Lys | Ala | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ile | Ser | Asp | Asp | Asp | His | Asp | Asp | Glu | Asn | Glu | Pro | Leu | Ile | Val |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Gly | Glu | Cys | Arg | Ile | Cys | Ser | Asp | Glu | Ser | Pro | Val | Glu | Asn | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Ser | Pro | Cys | Ala | Cys | Ser | Gly | Ser | Leu | Lys | Tyr | Ala | His | Arg | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Cys | Val | Gln | Arg | Trp | Cys | Asn | Glu | Lys | Lys | Asn | Ile | Ile | Cys | Glu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | His | Gln | Pro | Tyr | Gln | Pro | Gly | Tyr | Thr | Ala | Pro | Pro | Pro | Pro | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Gln | Pro | Glu | Glu | Thr | Thr | Ile | Asp | Ile | Gly | Gly | Gly | Trp | Thr | Ile | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Gly | Leu | Asp | Val | His | Asp | Pro | Arg | Leu | Leu | Ala | Ile | Ala | Glu | Ala | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Arg | Tyr | Leu | Glu | Ser | Glu | Tyr | Val | Glu | Tyr | Thr | Ala | Ser | Ser | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ser | Gly | Ala | Ala | Phe | Cys | Arg | Ser | Ala | Ala | Leu | Ile | Leu | Met | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Leu | Leu | Arg | His | Ala | Leu | Thr | Ile | Thr | Asp | Asp | Thr | Asp | Gly | Glu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Asp | Asp | Pro | Ser | Ser | Ile | Leu | Ser | Leu | Val | Leu | Leu | Arg | Ala | Ala |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Gly | Phe | Leu | Leu | Pro | Cys | Tyr | Ile | Met | Ala | Xaa | Ala | Ile | Ser | Ile | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Arg | Arg | Arg | Gln | Arg | Gln | Glu | Ala | Ala | Ala | Leu | Ala | Thr | Gln | Phe |
|     |     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |
| Ala | Phe | Val | Leu | Gln | Ser | Gly | Gln | Pro | Arg | Thr | Val | His | Phe | Thr | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Pro | Gly | Ile | Ser | Ser | Ser | Ser | Val | Ala | His | Ala | Thr | Thr | Ser | Thr |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Gln | Gln | Gln | His | Asp | Asp | Pro | Val |     |     |     |     |     |     |     |     |
|     |     |     | 290 |     |     |     | 295 |     |     |     |     |     |     |     |     |



(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..284

(D) OTHER INFORMATION: / Ceres Seq. ID 1497945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Val | Asn | Val | Asp | Gly | Leu | Met | Arg | Pro | Ile | Pro | Met | Ser | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Asn | Ala | Glu | Val | Glu | Glu | Met | Arg | Ser | Glu | Ser | Pro | Val | Val | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Lys | Ala | Leu | Asp | Ile | Ser | Asp | Asp | His | Asp | Asp | Glu | Asn | Glu |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Leu | Ile | Val | Ser | Gly | Glu | Cys | Arg | Ile | Cys | Ser | Asp | Glu | Ser | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Glu | Asn | Leu | Glu | Ser | Pro | Cys | Ala | Cys | Ser | Gly | Ser | Leu | Lys | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | His | Arg | Lys | Cys | Val | Gln | Arg | Trp | Cys | Asn | Glu | Lys | Lys | Asn | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Cys | Glu | Ile | Cys | His | Gln | Pro | Tyr | Gln | Pro | Gly | Tyr | Thr | Ala | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Pro | Pro | Leu | Gln | Pro | Glu | Glu | Thr | Thr | Ile | Asp | Ile | Gly | Gly | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Trp | Thr | Ile | Ser | Gly | Leu | Asp | Val | His | Asp | Pro | Arg | Leu | Leu | Ala | Ile |
|     |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ala | Glu | Ala | Glu | Arg | Arg | Tyr | Leu | Glu | Ser | Glu | Tyr | Val | Glu | Tyr | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ser | Ser | Ala | Ser | Gly | Ala | Ala | Phe | Cys | Arg | Ser | Ala | Ala | Leu | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Met | Ala | Leu | Leu | Leu | Leu | Arg | His | Ala | Leu | Thr | Ile | Thr | Asp | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Asp | Gly | Glu | Glu | Asp | Asp | Pro | Ser | Ser | Ile | Leu | Ser | Leu | Val | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Arg | Ala | Ala | Gly | Phe | Leu | Leu | Pro | Cys | Tyr | Ile | Met | Ala | Xaa | Ala |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Ser | Ile | Leu | Gln | Arg | Arg | Arg | Gln | Arg | Gln | Glu | Ala | Ala | Ala | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Thr | Gln | Phe | Ala | Phe | Val | Leu | Gln | Ser | Gly | Gln | Pro | Arg | Thr | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| His | Phe | Thr | Val | Ser | Pro | Gly | Ile | Ser | Ser | Ser | Ser | Val | Ala | His | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Thr | Ser | Thr | Gln | Gln | Gln | His | Asp | Pro | Val |     |     |     |     |     |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1497946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Arg Pro Ile Pro Met Ser Pro Val Asn Ala Glu Val Glu Glu Met

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Arg Ser Glu Ser Pro Val Val Asn Asp Lys Ala Leu Asp Ile Ser Asp |     |     |     |
| 20                                                              | 25  | 30  |     |
| Asp Asp His Asp Asp Glu Asn Glu Pro Leu Ile Val Ser Gly Glu Cys |     |     |     |
| 35                                                              | 40  | 45  |     |
| Arg Ile Cys Ser Asp Glu Ser Pro Val Glu Asn Leu Glu Ser Pro Cys |     |     |     |
| 50                                                              | 55  | 60  |     |
| Ala Cys Ser Gly Ser Leu Lys Tyr Ala His Arg Lys Cys Val Gln Arg |     |     |     |
| 65                                                              | 70  | 75  | 80  |
| Trp Cys Asn Glu Lys Lys Asn Ile Ile Cys Glu Ile Cys His Gln Pro |     |     |     |
| 85                                                              | 90  | 95  |     |
| Tyr Gln Pro Gly Tyr Thr Ala Pro Pro Pro Leu Gln Pro Glu Glu     |     |     |     |
| 100                                                             | 105 | 110 |     |
| Thr Thr Ile Asp Ile Gly Gly Gly Trp Thr Ile Ser Gly Leu Asp Val |     |     |     |
| 115                                                             | 120 | 125 |     |
| His Asp Pro Arg Leu Leu Ala Ile Ala Glu Ala Glu Arg Arg Tyr Leu |     |     |     |
| 130                                                             | 135 | 140 |     |
| Glu Ser Glu Tyr Val Glu Tyr Thr Ala Ser Ser Ala Ser Gly Ala Ala |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| Phe Cys Arg Ser Ala Ala Leu Ile Leu Met Ala Leu Leu Leu Leu Arg |     |     |     |
| 165                                                             | 170 | 175 |     |
| His Ala Leu Thr Ile Thr Asp Asp Thr Asp Gly Glu Glu Asp Asp Pro |     |     |     |
| 180                                                             | 185 | 190 |     |
| Ser Ser Ile Leu Ser Leu Val Leu Leu Arg Ala Ala Gly Phe Leu Leu |     |     |     |
| 195                                                             | 200 | 205 |     |
| Pro Cys Tyr Ile Met Ala Xaa Ala Ile Ser Ile Leu Gln Arg Arg Arg |     |     |     |
| 210                                                             | 215 | 220 |     |
| Gln Arg Gln Glu Ala Ala Leu Ala Thr Gln Phe Ala Phe Val Leu     |     |     |     |
| 225                                                             | 230 | 235 | 240 |
| Gln Ser Gly Gln Pro Arg Thr Val His Phe Thr Val Ser Pro Gly Ile |     |     |     |
| 245                                                             | 250 | 255 |     |
| Ser Ser Ser Ser Val Ala His Ala Thr Thr Ser Thr Gln Gln Gln His |     |     |     |
| 260                                                             | 265 | 270 |     |
| Asp Asp Pro Val                                                 |     |     |     |
| 275                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| aaaatttcgc  | aaactaat    | tttcaatt   | ttcttcgt   | atctctctga  | aagcttctct | 60  |
| tcttcttctc  | accatgtctg  | gttatcctcc | atcaagccaa | ggttacggtt  | acggcggtaa | 120 |
| tccaccacct  | cctcagccac  | cgtaaggatc | aaccggcaat | aacctcctc   | cgtgcggatc | 180 |
| atccggcagc  | aatcctcctc  | ctccgtacgg | atcatcagcc | tcctcaccgt  | acgcagttcc | 240 |
| ctacggagct  | cagcccgtc   | cttacgggtg | accaccgtca | gcaccgtacg  | cgtctcctcc | 300 |
| aggagaccat  | aataagccgc  | acaaagagaa | acctcacggc | gcctcctacg  | gatctccatc | 360 |
| tcccgggtggc | tacgggtgctc | atccatcgtc | tggaccttcc | gactacgggtg | gttacggagg | 420 |
| agcgcgcgag  | cagtcctggac | atggaggagg | ttacggagga | gcgccgcagc  | agtctggaca | 480 |
| tggaggaggt  | tacggagctc  | ctcctccgca | agcttcttat | ggaagtccgt  | ttgcgtctct | 540 |
| ggttccgctcg | gcgtttcctc  | ccggaacaga | tccgaacatt | gtggcttggt  | tccaagctgc | 600 |
| ggatcgggac  | aatagtggat  | tcatcgatga | taaggagctt | caaggagctc  | tatcttcgta | 660 |
| taatcagagc  | ttcagcataa  | gaactgttca | tctccttatg | tatctattca  | ccaacagcaa | 720 |
| tgctcaggaag | attggaccaa  | aagagtttac | ttcacttttc | tkkagtcttc  | agaattggag | 780 |
| gtctatcttt  | gagaggtttg  | ataaggacag | aagcggtaga | atagatacaa  | acgagctgag | 840 |

```
agatgcactc atgagccttg ggttttctgt gtctcctgtg attttggatc tgctggtttc 900
aaagtttgac aaaagcggag gcaggaacag ggctatcgaa tatgacaatt tcatcgagtg 960
ttgtttgact gtaaaggggc tcaccgagaa gttcaaggag aaggatacgg cgttatcagg 1020
ctcagctact ttcaattacg agaacttcat gctcactgtt ttaccattcc tcgtcgcttg 1080
agtgattgtt tttttttttt ttgttgacca aasagattgt tttctaactc tattttcttt 1140
gtgagctttt ggatatttta tttgttgtct tttt
```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1497948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```
Lys Phe Arg Lys Leu Ile Phe Ser Leu Ser Ser Ser Leu Ile Ser Leu
1 5 10 15
Lys Ala Ser Leu Leu Leu Thr Met Ser Gly Tyr Pro Pro Ser Ser
20 25 30
Gln Gly Tyr Gly Tyr Gly Gly Asn Pro Pro Pro Pro Gln Pro Pro Tyr
35 40 45
Gly Ser Thr Gly Asn Asn Pro Pro Cys Gly Ser Ser Gly Ser Asn
50 55 60
Pro Pro Pro Pro Tyr Gly Ser Ser Ala Ser Ser Pro Tyr Ala Val Pro
65 70 75 80
Tyr Gly Ala Gln Pro Ala Pro Tyr Gly Ala Pro Pro Ser Ala Pro Tyr
85 90 95
Ala Ser Pro Pro Gly Asp His Asn Lys Pro His Lys Glu Lys Pro His
100 105 110
Gly Ala Ser Tyr Gly Ser Pro Ser Pro Gly Gly Tyr Gly Ala His Pro
115 120 125
Ser Ser Gly Pro Ser Asp Tyr Gly Gly Tyr Gly Gly Ala Pro Gln Gln
130 135 140
Ser Gly His Gly Gly Gly Tyr Gly Gly Ala Pro Gln Gln Ser Gly His
145 150 155 160
Gly Gly Gly Tyr Gly Ala Pro Pro Pro Gln Ala Ser Tyr Gly Ser Pro
165 170 175
Phe Ala Ser Leu Val Pro Ser Ala Phe Pro Pro Gly Thr Asp Pro Asn
180 185 190
Ile Val Ala Cys Phe Gln Ala Ala Asp Arg Asp Asn Ser Gly Phe Ile
195 200 205
Asp Asp Lys Glu Leu Gln Gly Ala Leu Ser Ser Tyr Asn Gln Ser Phe
210 215 220
Ser Ile Arg Thr Val His Leu Leu Met Tyr Leu Phe Thr Asn Ser Asn
225 230 235 240
Val Arg Lys Ile Gly Pro Lys Glu Phe Thr Ser Leu Phe Xaa Ser Leu
245 250 255
Gln Asn Trp Arg Ser Ile Phe Glu Arg Phe Asp Lys Asp Arg Ser Gly
260 265 270
Arg Ile Asp Thr Asn Glu Leu Arg Asp Ala Leu Met Ser Leu Gly Phe
275 280 285
Ser Val Ser Pro Val Ile Leu Asp Leu Leu Val Ser Lys Phe Asp Lys
290 295 300
Ser Gly Gly Arg Asn Arg Ala Ile Glu Tyr Asp Asn Phe Ile Glu Cys
305 310 315 320
Cys Leu Thr Val Lys Gly Leu Thr Glu Lys Phe Lys Glu Lys Asp Thr
325 330 335
Ala Leu Ser Gly Ser Ala Thr Phe Asn Tyr Glu Asn Phe Met Leu Thr
```

340 345 350  
Val Leu Pro Phe Leu Val Ala  
355  
(2) INFORMATION FOR SEQ ID NO:80:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 335 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..335  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497949  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:  
Met Ser Gly Tyr Pro Pro Ser Ser Gln Gly Tyr Gly Tyr Gly Gly Asn  
1 5 10 15  
Pro Pro Pro Pro Gln Pro Pro Tyr Gly Ser Thr Gly Asn Asn Pro Pro  
20 25 30  
Pro Cys Gly Ser Ser Gly Ser Asn Pro Pro Pro Pro Tyr Gly Ser Ser  
35 40 45  
Ala Ser Ser Pro Tyr Ala Val Pro Tyr Gly Ala Gln Pro Ala Pro Tyr  
50 55 60  
Gly Ala Pro Pro Ser Ala Pro Tyr Ala Ser Pro Gly Asp His Asn  
65 70 75 80  
Lys Pro His Lys Glu Lys Pro His Gly Ala Ser Tyr Gly Ser Pro Ser  
85 90 95  
Pro Gly Gly Tyr Gly Ala His Pro Ser Ser Gly Pro Ser Asp Tyr Gly  
100 105 110  
Gly Tyr Gly Gly Ala Pro Gln Gln Ser Gly His Gly Gly Gly Tyr Gly  
115 120 125  
Gly Ala Pro Gln Gln Ser Gly His Gly Gly Gly Tyr Gly Ala Pro Pro  
130 135 140  
Pro Gln Ala Ser Tyr Gly Ser Pro Phe Ala Ser Leu Val Pro Ser Ala  
145 150 155 160  
Phe Pro Pro Gly Thr Asp Pro Asn Ile Val Ala Cys Phe Gln Ala Ala  
165 170 175  
Asp Arg Asp Asn Ser Gly Phe Ile Asp Asp Lys Glu Leu Gln Gly Ala  
180 185 190  
Leu Ser Ser Tyr Asn Gln Ser Phe Ser Ile Arg Thr Val His Leu Leu  
195 200 205  
Met Tyr Leu Phe Thr Asn Ser Asn Val Arg Lys Ile Gly Pro Lys Glu  
210 215 220  
Phe Thr Ser Leu Phe Xaa Ser Leu Gln Asn Trp Arg Ser Ile Phe Glu  
225 230 235 240  
Arg Phe Asp Lys Asp Arg Ser Gly Arg Ile Asp Thr Asn Glu Leu Arg  
245 250 255  
Asp Ala Leu Met Ser Leu Gly Phe Ser Val Ser Pro Val Ile Leu Asp  
260 265 270  
Leu Leu Val Ser Lys Phe Asp Lys Ser Gly Gly Arg Asn Arg Ala Ile  
275 280 285  
Glu Tyr Asp Asn Phe Ile Glu Cys Cys Leu Thr Val Lys Gly Leu Thr  
290 295 300  
Glu Lys Phe Lys Glu Lys Asp Thr Ala Leu Ser Gly Ser Ala Thr Phe  
305 310 315 320  
Asn Tyr Glu Asn Phe Met Leu Thr Val Leu Pro Phe Leu Val Ala  
325 330 335

(2) INFORMATION FOR SEQ ID NO:81:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 748 base pairs  
(B) TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

(2) INFORMATION FOR SEQ ID NO:82:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1497954

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | His | Tyr | Ser | Ser | Arg | Arg | Leu | His | Arg | Arg | Leu | Tyr | Leu | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Cys | Val | Asp | Leu | Val | Ser | Tyr | Phe | Ser | Phe | Arg | Pro | Ser | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Ser | Cys | Met | Phe | Cys | Gly | Leu | Tyr | Lys | Asp | Asp | Asn | Asn | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Arg | Ser | Glu | Asn | Ser | Lys | Val | Phe | Ser | Phe | Arg | Phe | Cys | Tyr | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Tyr | Trp | Tyr | Thr | Gln | Ala | Val | Ile | Ser | Ile | Val |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Ile | Glu | Thr | Gly | Gln | Lys | Thr | Gln | Lys | Ser | Ser | Pro | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Ala | Thr | Thr | Ala | Thr | Gly | Thr | Leu | Lys | Gln | Ser | Ser | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Lys | Arg | Trp | Gly | Gly | Arg | His | Pro | Phe | Val | Arg | Tyr | Gly | Leu | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Met Ile Ser Leu Thr Val Phe Gly Ala Leu Gly Leu Gly Gln Leu Leu  
50 55 60  
Gln Gly Ser Lys Asp Ile Ala Lys Val Lys Asp Asp Gln Glu Trp Glu  
65 70 75 80  
Ile Ile Glu Thr Arg Lys Ala Leu Ser Arg Thr Gly Pro Val Asp Ala  
85 90 95  
Tyr Lys Pro Lys Asn Thr Ser Ile Glu Asp Glu Leu Lys Ala Met Gln  
100 105 110  
Glu Lys Val Asp Ile Asn Thr Tyr Glu Tyr Lys Lys Ile Pro Lys Leu  
115 120 125  
Asn Glu Ser Lys Ser Ser  
130

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met Ile Ser Leu Thr Val Phe Gly Ala Leu Gly Leu Gly Gln Leu Leu  
1 5 10 15  
Gln Gly Ser Lys Asp Ile Ala Lys Val Lys Asp Asp Gln Glu Trp Glu  
20 25 30  
Ile Ile Glu Thr Arg Lys Ala Leu Ser Arg Thr Gly Pro Val Asp Ala  
35 40 45  
Tyr Lys Pro Lys Asn Thr Ser Ile Glu Asp Glu Leu Lys Ala Met Gln  
50 55 60  
Glu Lys Val Asp Ile Asn Thr Tyr Glu Tyr Lys Lys Ile Pro Lys Leu  
65 70 75 80  
Asn Glu Ser Lys Ser Ser  
85

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..563
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| attcaccaga gaaatggtcg tcgctgacta ctaaccagag ccatcggtgg ttgatttcgc  | 60  |
| gatttcgagc tccattccta cttgtctcac cttaatctcc ggcgatcgaa ttacacggtt  | 120 |
| ccggttaatc aatctctccg tggccatgga caaagaagtt acaaagattg aaagtgatga  | 180 |
| cacttcacgc gtggagatca aagtgttgtt attcgccaga gcacgagagc tcacaggtgt  | 240 |
| gcctgatcta acactgaaga tgscatgagg tagtacaaca cagaaatgcc tggatgagtt  | 300 |
| ggtgcttaag tttccaagct tggaagaggt acgtagctgt gttgttctcg ctttgaacga  | 360 |
| ggaatataca accgattccg ccattgttca acatagagat gagttagcca tcatacctcc  | 420 |
| gataagcggc ggctaattgca tcgacacttc ttaaatccct ttaactcggg gattgtatct | 480 |
| cattggcgat gatccaaat gtaacttttg tcataataac acagaaatat ctgtctttta   | 540 |
| taatggaaag aaaatgttac atc                                          |     |

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497958  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:  
Ser Pro Glu Lys Trp Ser Ser Leu Thr Thr Asn Gln Ser His Arg Trp  
1 5 10 15  
Leu Ile Ser Arg Phe Arg Ala Pro Phe Leu Leu Val Ser Pro  
20 25 30

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..40  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497959  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:  
Met Asp Lys Glu Val Thr Lys Ile Glu Ser Asp Asp Thr Ser Ser Val  
1 5 10 15  
Glu Ile Lys Val Leu Leu Phe Ala Arg Ala Arg Glu Leu Thr Gly Val  
20 25 30  
Pro Asp Leu Thr Leu Lys Met Xaa  
35 40

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 933 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..933  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497963  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:  
acaattcaga tttcaatttc tcmaaaatsc ttaaaaaactt tchctcaatt ctctckaggc 60  
ttcgtgrtca ggtatgcaga tctttygtya agacgtctsa cyggaaarac tatcacyyts 120  
gaggtggava gytctgacac catygayaac gtkaargcca agatccagga yaargarggt 180  
atyccwccgg aycagcagag gmttgatctt cgcyygaaag caasttggar gatggmagma 240  
ckttggctga ytacaacaty cagaaggagt ccacacttca cttggtcttg cgtctgcgtg 300  
gaggtatgca gatcttcgk aagactctva ccggaagac catcactytk gaggtrgaga 360  
gctctgacac cattgacaac gtgaaggcca agatccagga taaggaaggt atccctccgg 420  
accagcagag gttgatcttt gccggaaaac aattggagga yggcagaact ttrgcggatt 480  
acaacatcca gaaggagtct acccttcaact tggctctgct tctbcgtgga ggtatgcaga 540  
tcttygttaa gactttgacc ggvaagacca tcaactcttga agtggagagc tcygacacca 600  
ttgacaacgt gaaggcyaa atccaggaya aggaaggwat ccctccggac cagcagasgt 660  
ctsatctts gkggaaagca gcttgaggat ggacgtacat tggccgacta caacatccag 720  
aaggagtcta cccttcaactt ggtcctccgt ctctgtggag gtttctaaat ctctgtctctg 780  
ttatgcttta agaagttcaa tgtctcgttt ctgttaaaac tttgggtggct tgtgttttgg 840  
ggccttgat aatcccctga tgaataattg ttccaactat gtttccattc ctgttatctc 900  
tttctttcta atgacaagtc gaacgtcttc ttt

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..127
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Gln | Ile | Ser | Ile | Ser | Xaa | Lys | Xaa | Leu | Lys | Thr | Phe | Xaa | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ser | Xaa | Gly | Phe | Val | Xaa | Arg | Tyr | Ala | Asp | Leu | Xaa | Xaa | Arg | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Xaa | Xaa | Gly | Xaa | Thr | Ile | Xaa | Xaa | Glu | Val | Xaa | Xaa | Ser | Asp | Thr | Xaa |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Xaa | Asn | Xaa | Xaa | Ala | Lys | Ile | Gln | Xaa | Xaa | Xaa | Gly | Xaa | Xaa | Pro | Xaa |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gln | Arg | Xaa | Asp | Leu | Arg | Xaa | Lys | Ala | Xaa | Trp | Xaa | Met | Xaa | Xaa |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Xaa | Trp | Leu | Xaa | Thr | Thr | Xaa | Arg | Arg | Ser | Pro | His | Phe | Thr | Trp | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Val | Cys | Val | Glu | Val | Cys | Arg | Ser | Ser | Xaa | Arg | Leu | Xaa | Pro | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Pro | Ser | Xaa | Xaa | Arg | Xaa | Arg | Ala | Leu | Thr | Pro | Leu | Thr | Thr |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..126
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1497965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ile | Phe | Xaa | Lys | Thr | Xaa | Thr | Gly | Lys | Thr | Ile | Thr | Xaa | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Xaa | Glu | Ser | Ser | Asp | Thr | Ile | Asp | Asn | Val | Lys | Ala | Lys | Ile | Gln | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Glu | Gly | Ile | Pro | Pro | Asp | Gln | Gln | Arg | Leu | Ile | Phe | Ala | Gly | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Leu | Glu | Xaa | Gly | Arg | Thr | Xaa | Ala | Asp | Tyr | Asn | Ile | Gln | Lys | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Thr | Leu | His | Leu | Val | Leu | Arg | Xaa | Arg | Gly | Gly | Met | Gln | Ile | Xaa |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Lys | Thr | Leu | Thr | Xaa | Lys | Thr | Ile | Thr | Leu | Glu | Val | Glu | Ser | Xaa |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Thr | Ile | Asp | Asn | Val | Lys | Xaa | Lys | Ile | Gln | Xaa | Lys | Glu | Xaa | Ile |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Pro | Asp | Gln | Gln | Xaa | Ser | Xaa | Leu | Xaa | Xaa | Lys | Ala | Ala |     |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1251 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)



(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1251

(D) OTHER INFORMATION: / Ceres Seq. ID 1497966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

|             |             |             |            |             |            |      |
|-------------|-------------|-------------|------------|-------------|------------|------|
| acgcaggcaa  | atgtctcgta  | atttaaatcta | tagaagaaac | agagctctct  | gttttgtttt | 60   |
| aatcttggtc  | tgcttccctt  | accggttttg  | cgctagaaac | acgccggagg  | cggancaatc | 120  |
| cacagcaaaa  | gcaactcaaa  | taatacacgt  | cagcaattcc | acgtggcatg  | atttctctcg | 180  |
| tcttgtagat  | gtccaaatag  | gtagccacgt  | cagcggcgta | tcagagctca  | aaagatacct | 240  |
| ccaccgattc  | ggttacgtca  | aggatggctc  | cgaaatat   | tccgacgtgt  | tcgatgggtc | 300  |
| tctggaatcg  | gcaatctctc  | tgtatcaaga  | aaatctcggg | ttaccaataa  | cgggaagact | 360  |
| cgacacgagt  | acagttactc  | tcagtgcgtt  | accgcgatgt | ggcgttagsg  | atacgcacat | 420  |
| gaccatcaac  | aacgatttcc  | tccacacaac  | ggcgattat  | acgtatttca  | acggtaaacc | 480  |
| gaaatggaac  | cgtgatacgc  | taacctacgc  | tatctccaaa | actcacaac   | tcgattactt | 540  |
| gacgtcagaa  | gacgtcaaaa  | ccgttttccg  | gcgagctttt | tcacagtggg  | caagcgtgat | 600  |
| tccgggtgagt | ttcgaggaag  | tcgacgattt  | cacgacggct | gatttaaaga  | tcggattcta | 660  |
| cgctgggtgat | cacgggtgacg | ggcttccgtt  | tgacgggtga | cttgggaact  | tagcacacgc | 720  |
| ttttgcgccg  | gagaacggga  | ggcttcacct  | cgacggcg   | gagacgtgga  | tcgtcgacga | 780  |
| tgacttgaaa  | ggatcttcag  | aggtggccgt  | tgacttgag  | tctgtggcga  | ctcacgagat | 840  |
| cggtcacttg  | ttgggattag  | gacatagctc  | gcaggagtcg | gcggttatgt  | atccgagtct | 900  |
| ccgaccgagg  | accaagaaag  | ttgatcttac  | ggttgatgac | gtggcagggt  | tacttaagct | 960  |
| atatggtccg  | aatcctaaac  | tacggttgga  | ttcactaacg | cagtcggaag  | attctattaa | 1020 |
| aaacggcacc  | gtatcacata  | gattcttgtc  | ggggaatttt | atcggttatg  | ttctgttggt | 1080 |
| tgttggtttg  | attcttttcc  | tataggttta  | taggcataaa | aaatactgtt  | tttattcatt | 1140 |
| tatttttaat  | taaatgtaca  | tatatttttc  | aactatgtaa | atgtaaatat  | atagttgaac | 1200 |
| aaaaaaagat  | gtacatatat  | agttaggctt  | ataattaggt | ttatgggtctt | g          |      |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1497967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Gln | Met | Ser | Arg | Asn | Leu | Ile | Tyr | Arg | Arg | Asn | Arg | Ala | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Phe | Val | Leu | Ile | Leu | Phe | Cys | Phe | Pro | Tyr | Arg | Phe | Gly | Ala | Arg |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Asn | Thr | Pro | Glu | Ala | Xaa | Gln | Ser | Thr | Ala | Lys | Ala | Thr | Gln | Ile | Ile |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |
| His | Val | Ser | Asn | Ser | Thr | Trp | His | Asp | Phe | Ser | Arg | Leu | Val | Asp | Val |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     | 60  |     |     |     |
| Gln | Ile | Gly | Ser | His | Val | Ser | Gly | Val | Ser | Glu | Leu | Lys | Arg | Tyr | Leu |
|     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| His | Arg | Phe | Gly | Tyr | Val | Lys | Asp | Gly | Ser | Glu | Ile | Phe | Ser | Asp | Val |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Asp | Gly | Pro | Leu | Glu | Ser | Ala | Ile | Ser | Leu | Tyr | Gln | Glu | Asn | Leu |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |
| Gly | Leu | Pro | Ile | Thr | Gly | Arg | Leu | Asp | Thr | Ser | Thr | Val | Thr | Leu | Met |
|     |     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |
| Ser | Leu | Pro | Arg | Cys | Gly | Val | Xaa | Asp | Thr | His | Met | Thr | Ile | Asn | Asn |
|     |     |     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |
| Asp | Phe | Leu | His | Thr | Thr | Ala | His | Tyr | Thr | Tyr | Phe | Asn | Gly | Lys | Pro |
|     |     |     |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Trp | Asn | Arg | Asp | Thr | Leu | Thr | Tyr | Ala | Ile | Ser | Lys | Thr | His | Lys |
|     |     |     |     |     |     | 165 |     |     |     | 170 |     |     |     | 175 |     |
| Leu | Asp | Tyr | Leu | Thr | Ser | Glu | Asp | Val | Lys | Thr | Val | Phe | Arg | Arg | Ala |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Arg | Asn | Leu | Ile | Tyr | Arg | Arg | Asn | Arg | Ala | Leu | Cys | Phe | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ile | Leu | Phe | Cys | Phe | Pro | Tyr | Arg | Phe | Gly | Ala | Arg | Asn | Thr | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ala | Xaa | Gln | Ser | Thr | Ala | Lys | Ala | Thr | Gln | Ile | Ile | His | Val | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Ser | Thr | Trp | His | Asp | Phe | Ser | Arg | Leu | Val | Asp | Val | Gln | Ile | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | His | Val | Ser | Gly | Val | Ser | Glu | Leu | Lys | Arg | Tyr | Leu | His | Arg | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Tyr | Val | Lys | Asp | Gly | Ser | Glu | Ile | Phe | Ser | Asp | Val | Phe | Asp | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Leu | Glu | Ser | Ala | Ile | Ser | Leu | Tyr | Gln | Glu | Asn | Leu | Gly | Leu | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Thr | Gly | Arg | Leu | Asp | Thr | Ser | Thr | Val | Thr | Leu | Met | Ser | Leu | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Cys | Gly | Val | Xaa | Asp | Thr | His | Met | Thr | Ile | Asn | Asn | Asp | Phe | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Thr | Thr | Ala | His | Tyr | Thr | Tyr | Phe | Asn | Gly | Lys | Pro | Lys | Trp | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Asp | Thr | Leu | Thr | Tyr | Ala | Ile | Ser | Lys | Thr | His | Lys | Leu | Asp | Tyr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Thr | Ser | Glu | Asp | Val | Lys | Thr | Val | Phe | Arg | Arg | Ala | Phe | Ser | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Trp | Ser | Ser | Val | Ile | Pro | Val | Ser | Phe | Glu | Glu | Val | Asp | Asp | Phe | Thr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

```

Thr Ala Asp Leu Lys Ile Gly Phe Tyr Ala Gly Asp His Gly Asp Gly
210 215 220
Leu Pro Phe Asp Gly Val Leu Gly Thr Leu Ala His Ala Phe Ala Pro
225 230 235 240
Glu Asn Gly Arg Leu His Leu Asp Ala Ala Glu Thr Trp Ile Val Asp
245 250 255
Asp Asp Leu Lys Gly Ser Ser Glu Val Ala Val Asp Leu Glu Ser Val
260 265 270
Ala Thr His Glu Ile Gly His Leu Leu Gly Leu Gly His Ser Ser Gln
275 280 285
Glu Ser Ala Val Met Tyr Pro Ser Leu Arg Pro Arg Thr Lys Lys Val
290 295 300
Asp Leu Thr Val Asp Asp Val Ala Gly Val Leu Lys Leu Tyr Gly Pro
305 310 315 320
Asn Pro Lys Leu Arg Leu Asp Ser Leu Thr Gln Ser Glu Asp Ser Ile
325 330 335
Lys Asn Gly Thr Val Ser His Arg Phe Leu Ser Gly Asn Phe Ile Gly
340 345 350
Tyr Val Leu Leu Val Val Gly Leu Ile Leu Phe Leu
355 360

```

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1497969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```

Met Ser Leu Pro Arg Cys Gly Val Xaa Asp Thr His Met Thr Ile Asn
1 5 10 15
Asn Asp Phe Leu His Thr Thr Ala His Tyr Thr Tyr Phe Asn Gly Lys
20 25 30
Pro Lys Trp Asn Arg Asp Thr Leu Thr Tyr Ala Ile Ser Lys Thr His
35 40 45
Lys Leu Asp Tyr Leu Thr Ser Glu Asp Val Lys Thr Val Phe Arg Arg
50 55 60
Ala Phe Ser Gln Trp Ser Ser Val Ile Pro Val Ser Phe Glu Glu Val
65 70 75 80
Asp Asp Phe Thr Thr Ala Asp Leu Lys Ile Gly Phe Tyr Ala Gly Asp
85 90 95
His Gly Asp Gly Leu Pro Phe Asp Gly Val Leu Gly Thr Leu Ala His
100 105 110
Ala Phe Ala Pro Glu Asn Gly Arg Leu His Leu Asp Ala Ala Glu Thr
115 120 125
Trp Ile Val Asp Asp Asp Leu Lys Gly Ser Ser Glu Val Ala Val Asp
130 135 140
Leu Glu Ser Val Ala Thr His Glu Ile Gly His Leu Leu Gly Leu Gly
145 150 155 160
His Ser Ser Gln Glu Ser Ala Val Met Tyr Pro Ser Leu Arg Pro Arg
165 170 175
Thr Lys Lys Val Asp Leu Thr Val Asp Asp Val Ala Gly Val Leu Lys
180 185 190
Leu Tyr Gly Pro Asn Pro Lys Leu Arg Leu Asp Ser Leu Thr Gln Ser
195 200 205
Glu Asp Ser Ile Lys Asn Gly Thr Val Ser His Arg Phe Leu Ser Gly
210 215 220
Asn Phe Ile Gly Tyr Val Leu Leu Val Val Gly Leu Ile Leu Phe Leu

```

2025 RELEASE UNDER E.O. 14176

225

230

235

240

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1457
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
gattgggtcaa aaaaatggaa gcgggcgaaga aacagagtgt tacaaatcag cttctcgccg 60
tgaaatcagc ttccggcaag acttttagcc agttagccgc ggagacaggt ctaaccaacg 120
tatacgtagc tcagcttctc cgctcgtaag ctcagctcaa accggacaca gtcccaaagc 180
ttaaggaagc tttaccagct ctgaccgatg aactaatcgg agatatgatg tctccaccgt 240
ggagatccta cgatcctaata ctcatccaag aaccactat ctacagggtg aatgaagcag 300
tgatgcattt tggtagagag ataaaggaga ttatcaatga agattttgga gatggcatca 360
tgctcgcgat agattttctat tgctctgtcg acaaaatcaa aggagtggat ggtaacaatc 420
gcgtgggtgt gacgcttgat ggaaagtmct ttcgcattc cgaacagagg acggagaata 480
tggtctcaag gctaaatctc aaggaggagta caagcgaatg ataagaaagc ctttacgtat 540
ccatgaaggc cttattgtaa gtggtaacgt tgtaataacct atgtgtttgt ttatctgtaa 600
tatatgcaac ttcagcatct agattaaaag ctgttttcagg ttgaataaca gtgaataaac 660
aaaacttata aaacctttct atgtttatct tcaaaaaaaaa aaaaaaaaaa cggcacgaga 720
agcttttttt tttttttttt tattaaatct ctcttttatg tgtttggttg ctttgacacg 780
ttgagaggct taacttggtg aaattagccc ctgggtggtc ccttggtagg tttgtgattt 840
ggactaagtc tgcttttgag aagcttgaat ctatctatgg ctcgtttgag aaaccatcag 900
agaagaagaa gggttacgtc ttgcctcgtg cgaagatggt gaatgctgat cttgctagga 960
ttattaactc cgatgaggta cagagtgtgg tgaaccgat taaggatggt tccaagagag 1020
cggttctgaa gaagaatcca ttgaagaacc ttaatgtgat gttcaagttg aatccttatg 1080
ctaagaccgc aaagagaatg tctctgttgg ctgaagcttc aagggttaag gctaagaagg 1140
agaagctcga gaagaagagg aaagtcgtca ctaaggagga ggcccaagcg atcaaagcag 1200
caggcaaggc ttggtatcag actatgattt cagacagtga ctacaccgag ttcgataact 1260
tcaccaagtg gcttggcgct agtcagtaat gatgctctcg tcatcgcaaa gtctcttata 1320
tctaggcaaa gattttgggt ttctgattta tgttcttcgt ttgtattgga tttatctggg 1380
attttatgtt gttgagttgg taagacgatt ttaagaact atgatggtgt ttttcaaact 1440
cttttcaatc tgtttcc
```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```
Leu Val Lys Lys Met Glu Ala Ala Lys Lys Gln Ser Val Thr Asn Gln
1 5 10 15
Leu Leu Ala Val Lys Ser Ala Ser Gly Lys Thr Phe Ser Gln Leu Ala
20 25 30
Ala Glu Thr Gly Leu Thr Asn Val Tyr Val Ala Gln Leu Leu Arg Arg
35 40 45
Gln Ala Gln Leu Lys Pro Asp Thr Val Pro Lys Leu Lys Glu Ala Leu
50 55 60
Pro Ala Leu Thr Asp Glu Leu Ile Gly Asp Met Met Ser Pro Pro Trp
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Ser | Tyr | Asp | Pro | Asn | Leu | Ile | Gln | Glu | Pro | Thr | Ile | Tyr | Arg | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Glu | Ala | Val | Met | His | Phe | Gly | Glu | Ser | Ile | Lys | Glu | Ile | Ile | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Asp | Phe | Gly | Asp | Gly | Ile | Met | Ser | Ala | Ile | Asp | Phe | Tyr | Cys | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Asp | Lys | Ile | Lys | Gly | Val | Asp | Gly | Asn | Asn | Arg | Val | Val | Val | Thr |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Leu | Asp | Gly | Lys | Xaa | Leu | Ser | His | Ser | Glu | Gln | Arg | Thr | Glu | Asn | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Ser | Arg | Leu | Asn | Leu | Lys | Gly | Gly | Thr | Ser | Glu |     |     |     |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ala | Ala | Lys | Lys | Gln | Ser | Val | Thr | Asn | Gln | Leu | Leu | Ala | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Ser | Ala | Ser | Gly | Lys | Thr | Phe | Ser | Gln | Leu | Ala | Ala | Glu | Thr | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Thr | Asn | Val | Tyr | Val | Ala | Gln | Leu | Leu | Arg | Arg | Gln | Ala | Gln | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Lys | Pro | Asp | Thr | Val | Pro | Lys | Leu | Lys | Glu | Ala | Leu | Pro | Ala | Leu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Glu | Leu | Ile | Gly | Asp | Met | Met | Ser | Pro | Pro | Trp | Arg | Ser | Tyr | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Asn | Leu | Ile | Gln | Glu | Pro | Thr | Ile | Tyr | Arg | Leu | Asn | Glu | Ala | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | His | Phe | Gly | Glu | Ser | Ile | Lys | Glu | Ile | Ile | Asn | Glu | Asp | Phe | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Gly | Ile | Met | Ser | Ala | Ile | Asp | Phe | Tyr | Cys | Ser | Val | Asp | Lys | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Gly | Val | Asp | Gly | Asn | Asn | Arg | Val | Val | Val | Thr | Leu | Asp | Gly | Lys |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Xaa | Leu | Ser | His | Ser | Glu | Gln | Arg | Thr | Glu | Asn | Met | Val | Ser | Arg | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Leu | Lys | Gly | Gly | Thr | Ser | Glu |     |     |     |     |     |     |     |     |
|     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asn | Ala | Asp | Leu | Ala | Arg | Ile | Ile | Asn | Ser | Asp | Glu | Val | Gln |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |

Ser Val Val Asn Pro Ile Lys Asp Gly Ser Lys Arg Ala Val Leu Lys  
20 25 30  
Lys Asn Pro Leu Lys Asn Leu Asn Val Met Phe Lys Leu Asn Pro Tyr  
35 40 45  
Ala Lys Thr Ala Lys Arg Met Ser Leu Leu Ala Glu Ala Ser Arg Val  
50 55 60  
Lys Ala Lys Lys Glu Lys Leu Glu Lys Lys Arg Lys Val Val Thr Lys  
65 70 75 80  
Glu Glu Ala Gln Ala Ile Lys Ala Ala Gly Lys Ala Trp Tyr Gln Thr  
85 90 95  
Met Ile Ser Asp Ser Asp Tyr Thr Glu Phe Asp Asn Phe Thr Lys Trp  
100 105 110  
Leu Gly Ala Ser Gln  
115

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..732
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| agaaacagtt ccgtgtaggc aaccattagg aaaaccctaa ctaaattcca ttattaattt   | 60  |
| cttttataat ccctttctct tgacattgac ttctctctct cgattcttct tctccagttt   | 120 |
| caatcaaaact caatttcttc tcaacgaacc ctaatttcca acaaatcgga ttcagtttct  | 180 |
| tcttcggaga ctaatcgaat cgcaatggct aagagttcct tcaagatctc taaccctctc   | 240 |
| gaggcaagga tgagtgaatc ttctcgaatc agagagaagt accctgacag aattcccgtg   | 300 |
| attgtggaga aggctggaca aagtgatgtt cctgacattg acaagaagaa gtatcktgta   | 360 |
| ccagctgatc taacagtggg acaatttgta tacgtggttc gtaaaagaat caagcttgga   | 420 |
| gctgagaaaag ctatttttgt ctttgtttaag aacacattgc ctccaactgc tgcattgatg | 480 |
| tctgcgatct atgaasaaca caaagatgag gatgggttcc tctacatgac ttacagtgga   | 540 |
| gagaacactt ttggatctct taccgttgct tgaataaaaa tcgatctttg gatgactttg   | 600 |
| atgtacatac ataaatcagg aagataaaga tgtacattgc ttcttctttt tctctggctt   | 660 |
| ttaactttgc tttggatgtt tggatatctt tccctttggg tttattaatc gtcagaaact   | 720 |
| tctccttttc tt                                                       |     |

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Ala Lys Ser Ser Phe Lys Ile Ser Asn Pro Leu Glu Ala Arg Met  
1 5 10 15  
Ser Glu Ser Ser Arg Ile Arg Glu Lys Tyr Pro Asp Arg Ile Pro Val  
20 25 30  
Ile Val Glu Lys Ala Gly Gln Ser Asp Val Pro Asp Ile Asp Lys Lys  
35 40 45  
Lys Tyr Xaa Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val  
50 55 60  
Val Arg Lys Arg Ile Lys Leu Gly Ala Glu Lys Ala Ile Phe Val Phe  
65 70 75 80

Val Lys Asn Thr Leu Pro Pro Thr Ala Ala Leu Met Ser Ala Ile Tyr  
85 90 95  
Glu Xaa His Lys Asp Glu Asp Gly Phe Leu Tyr Met Thr Tyr Ser Gly  
100 105 110  
Glu Asn Thr Phe Gly Ser Leu Thr Val Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met Ser Glu Ser Ser Arg Ile Arg Glu Lys Tyr Pro Asp Arg Ile Pro  
1 5 10 15  
Val Ile Val Glu Lys Ala Gly Gln Ser Asp Val Pro Asp Ile Asp Lys  
20 25 30  
Lys Lys Tyr Xaa Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr  
35 40 45  
Val Val Arg Lys Arg Ile Lys Leu Gly Ala Glu Lys Ala Ile Phe Val  
50 55 60  
Phe Val Lys Asn Thr Leu Pro Pro Thr Ala Ala Leu Met Ser Ala Ile  
65 70 75 80  
Tyr Glu Xaa His Lys Asp Glu Asp Gly Phe Leu Tyr Met Thr Tyr Ser  
85 90 95  
Gly Glu Asn Thr Phe Gly Ser Leu Thr Val Ala  
100 105

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..494
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| taacattgtg gtacttaatg gagggaggat agtagaggaa ggtacacatg attcttttagc | 60  |
| agcaaaaaat gggttgtatg tacgtttgat gcaaccacac tttggtaaag gtctacgccca | 120 |
| acatcgactg atatagagtt ttgaggctcc atcaatgata atgatttttg catctctgat  | 180 |
| caatgattct ccggaggatt acaagatggt caaaaaaac cctatacaac cacgggtagt   | 240 |
| tctctagcag atagggscgt tagatgtaga ttccatagt cttcgagctg cttattcttt   | 300 |
| ttttggagac gaagcatcag aagtaggtca tggtcattgc ttcgttctcc aaagtatatc  | 360 |
| gattttgtct attgaatctg aatatatttag gaggttggtg aatcattttg gaggctgttt | 420 |
| atttgccttt cttttatatg tgtctgtgct ggtttgttct tgcaaaaaca tggatgatgt  | 480 |
| atgtaaagct taag                                                    |     |

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..44  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Asn Ile Val Val Leu Asn Gly Gly Arg Ile Val Glu Glu Gly Thr His  
1 5 10 15  
Asp Ser Leu Ala Ala Lys Asn Gly Leu Tyr Val Arg Leu Met Gln Pro  
20 25 30  
His Phe Gly Lys Gly Leu Arg Gln His Arg Leu Ile  
35 40

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Ile Met Ile Leu Ala Ser Leu Ile Asn Asp Ser Pro Glu Asp Tyr  
1 5 10 15  
Lys Met Phe Lys Lys Asn Pro Ile Gln Pro Arg Val Val Leu  
20 25 30

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1592 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1592  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

aagactctct ctgctttcga ccmaaaaacc ttctcctctc ctctggggaga tctccatctt 60  
cttcgcttct tcgcttcccc gcctgaaaca attactcgat ctcgccggcg gaacaagctc 120  
tccgtttctc tttccggcag atcgattctt ccaattcctt attcctttct aggtcttcct 180  
taagaaaccc ttactttctt caaaatctgc atttatggcg attagggtta ccttcaccta 240  
ctccagctat gttgctagga gcattgcttc atccgccggg actcgtgtcg gtaccggcga 300  
cgttagatca tgcttcgaaa catgggttcg tcccaggttc tgccggccaca atcagatacc 360  
agatattgtt gataaatctc ccgcatccaa cacatggggt ccaagctcag gccctcgtgc 420  
tcgaccagct tcatcaatgt atagcaccat tgcgagggaa atcctcgaag aaggctgcaa 480  
gagtcacact gtcttggtta tgatctctct catgaatttg actggagctc cacagttttc 540  
gggtgtgacc ggtctcggga tctctccctt taagacttct tctgtcatcc cgttccttag 600  
gggttccaag tggatgcctt gtagtattcc ggcgacgtta tcaacggata ttgctgaggt 660  
tgatagagga ggaaaggctt gtgatcctaa agtgaagttg gagttgagt ataaagtctc 720  
gaatggtgga aacggatggg ttaataagct gttgaatatc tgctcggagg atgctaaggc 780  
tgctttcacg gcggttactt tttctctcct tttccgatcg gctttggccg agccaaagtc 840  
tataccttca tcactatgc ttctactctc cgtgtgggt gatcgtgtta tagccgagaa 900  
gggtctatac tttttcagga agccagaggt ttcagacata gttatcttca aggtccttcc 960  
tattttggtg gaacatggtt acagttgtgc tgatgttttc ataaaaagga tagttgctag 1020  
cgaagggtgac tgggttgaag tttgtgatgg aaagctctta gtaaatgaca ctgttcaagc 1080  
agaggatttt gtcttagagc caattgacta tgaaatggaa ccaatgtttg tccctgaagg 1140  
ttatgtcttc gtcctaggag acaaccgcaa caaaagcttt gattctcata actgggggtcc 1200  
acttccaata aagaacatca tagggagatc tgtgtttcgc tattggccac caagcaaagt 1260  
gtcagacata atacaccatg acaagttag ccaaaagaga gctgttgatg tatcttgacc 1320  
aacgcagatg gtatcttagg attaagcaga aaatttgatt agatgagctg tgccatgcc 1380



accatttttg cgctgaaggc aacagagcaa ttctttcttc ctgtctaggc ttgatggcgg 1440  
acatggaatg cactgggaaa tccatataaa aagaacaaga aaattgatat ttttgctttg 1500  
attttttttg atgtgttgaa acctaaatgc atccagtga attggcagta gctgtcaaac 1560  
ataaaagggg aaactttctt ttttgagtat tt

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ile | Arg | Val | Thr | Phe | Thr | Tyr | Ser | Ser | Tyr | Val | Ala | Arg | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Ala | Ser | Ser | Ala | Gly | Thr | Arg | Val | Gly | Thr | Gly | Asp | Val | Arg | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Phe | Glu | Thr | Trp | Val | Arg | Pro | Arg | Phe | Cys | Gly | His | Asn | Gln | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Asp | Ile | Val | Asp | Lys | Ser | Pro | Gly | Ser | Asn | Thr | Trp | Gly | Pro | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Gly | Pro | Arg | Ala | Arg | Pro | Ala | Ser | Ser | Met | Tyr | Ser | Thr | Ile | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Glu | Ile | Leu | Glu | Gly | Cys | Lys | Ser | Pro | Leu | Val | Leu | Gly | Met |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Ser | Leu | Met | Asn | Leu | Thr | Gly | Ala | Pro | Gln | Phe | Ser | Gly | Val | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Leu | Gly | Ile | Ser | Pro | Phe | Lys | Thr | Ser | Ser | Val | Ile | Pro | Phe | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Gly | Ser | Lys | Trp | Met | Pro | Cys | Ser | Ile | Pro | Ala | Thr | Leu | Ser | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Ile | Ala | Glu | Val | Asp | Arg | Gly | Gly | Lys | Val | Cys | Asp | Pro | Lys | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Leu | Glu | Leu | Ser | Asp | Lys | Val | Ser | Asn | Gly | Gly | Asn | Gly | Trp | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asn | Lys | Leu | Leu | Asn | Ile | Cys | Ser | Glu | Asp | Ala | Lys | Ala | Ala | Phe | Thr |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Val | Thr | Phe | Ser | Leu | Leu | Phe | Arg | Ser | Ala | Leu | Ala | Glu | Pro | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Ile | Pro | Ser | Thr | Ser | Met | Leu | Pro | Thr | Leu | Asp | Val | Gly | Asp | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Ile | Ala | Glu | Lys | Val | Ser | Tyr | Phe | Phe | Arg | Lys | Pro | Glu | Val | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Asp | Ile | Val | Ile | Phe | Lys | Ala | Pro | Pro | Ile | Leu | Val | Glu | His | Gly | Tyr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Cys | Ala | Asp | Val | Phe | Ile | Lys | Arg | Ile | Val | Ala | Ser | Glu | Gly | Asp |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Trp | Val | Glu | Val | Cys | Asp | Gly | Lys | Leu | Leu | Val | Asn | Asp | Thr | Val | Gln |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Glu | Asp | Phe | Val | Leu | Glu | Pro | Ile | Asp | Tyr | Glu | Met | Glu | Pro | Met |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | Val | Pro | Glu | Gly | Tyr | Val | Phe | Val | Leu | Gly | Asp | Asn | Arg | Asn | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Ser | Phe | Asp | Ser | His | Asn | Trp | Gly | Pro | Leu | Pro | Ile | Lys | Asn | Ile | Ile |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Gly | Arg | Ser | Val | Phe | Arg | Tyr | Trp | Pro | Pro | Ser | Lys | Val | Ser | Asp | Ile |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     | 350 |     |     |     |
| Ile | His | His | Glu | Gln | Val | Ser | Gln | Lys | Arg | Ala | Val | Asp | Val | Ser |     |

355 360 365

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1497989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Ser | Thr | Ile | Ala | Arg | Glu | Ile | Leu | Glu | Glu | Gly | Cys | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Leu | Val | Leu | Gly | Met | Ile | Ser | Leu | Met | Asn | Leu | Thr | Gly | Ala | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Phe | Ser | Gly | Val | Thr | Gly | Leu | Gly | Ile | Ser | Pro | Phe | Lys | Thr | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Val | Ile | Pro | Phe | Leu | Arg | Gly | Ser | Lys | Trp | Met | Pro | Cys | Ser | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Ala | Thr | Leu | Ser | Thr | Asp | Ile | Ala | Glu | Val | Asp | Arg | Gly | Gly | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Cys | Asp | Pro | Lys | Val | Lys | Leu | Glu | Leu | Ser | Asp | Lys | Val | Ser | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Gly | Asn | Gly | Trp | Val | Asn | Lys | Leu | Leu | Asn | Ile | Cys | Ser | Glu | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ala | Lys | Ala | Ala | Phe | Thr | Ala | Val | Thr | Phe | Ser | Leu | Leu | Phe | Arg | Ser |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Ala | Leu | Ala | Glu | Pro | Lys | Ser | Ile | Pro | Ser | Thr | Ser | Met | Leu | Pro | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Asp | Val | Gly | Asp | Arg | Val | Ile | Ala | Glu | Lys | Val | Ser | Tyr | Phe | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Lys | Pro | Glu | Val | Ser | Asp | Ile | Val | Ile | Phe | Lys | Ala | Pro | Pro | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Val | Glu | His | Gly | Tyr | Ser | Cys | Ala | Asp | Val | Phe | Ile | Lys | Arg | Ile |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |
| Val | Ala | Ser | Glu | Gly | Asp | Trp | Val | Glu | Val | Cys | Asp | Gly | Lys | Leu | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Asn | Asp | Thr | Val | Gln | Ala | Glu | Asp | Phe | Val | Leu | Glu | Pro | Ile | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Glu | Met | Glu | Pro | Met | Phe | Val | Pro | Glu | Gly | Tyr | Val | Phe | Val | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Asp | Asn | Arg | Asn | Lys | Ser | Phe | Asp | Ser | His | Asn | Trp | Gly | Pro | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Ile | Lys | Asn | Ile | Ile | Gly | Arg | Ser | Val | Phe | Arg | Tyr | Trp | Pro | Pro |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Lys | Val | Ser | Asp | Ile | Ile | His | Glu | Gln | Val | Ser | Gln | Lys | Arg |     |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ala | Val | Asp | Val | Ser |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 290 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1497990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Ile Ser Leu Met Asn Leu Thr Gly Ala Pro Gln Phe Ser Gly Val  
1 5 10 15  
Thr Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser Ser Val Ile Pro Phe  
20 25 30  
Leu Arg Gly Ser Lys Trp Met Pro Cys Ser Ile Pro Ala Thr Leu Ser  
35 40 45  
Thr Asp Ile Ala Glu Val Asp Arg Gly Gly Lys Val Cys Asp Pro Lys  
50 55 60  
Val Lys Leu Glu Leu Ser Asp Lys Val Ser Asn Gly Gly Asn Gly Trp  
65 70 75 80  
Val Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp Ala Lys Ala Ala Phe  
85 90 95  
Thr Ala Val Thr Phe Ser Leu Leu Phe Arg Ser Ala Leu Ala Glu Pro  
100 105 110  
Lys Ser Ile Pro Ser Thr Ser Met Leu Pro Thr Leu Asp Val Gly Asp  
115 120 125  
Arg Val Ile Ala Glu Lys Val Ser Tyr Phe Phe Arg Lys Pro Glu Val  
130 135 140  
Ser Asp Ile Val Ile Phe Lys Ala Pro Pro Ile Leu Val Glu His Gly  
145 150 155 160  
Tyr Ser Cys Ala Asp Val Phe Ile Lys Arg Ile Val Ala Ser Glu Gly  
165 170 175  
Asp Trp Val Glu Val Cys Asp Gly Lys Leu Leu Val Asn Asp Thr Val  
180 185 190  
Gln Ala Glu Asp Phe Val Leu Glu Pro Ile Asp Tyr Glu Met Glu Pro  
195 200 205  
Met Phe Val Pro Glu Gly Tyr Val Phe Val Leu Gly Asp Asn Arg Asn  
210 215 220  
Lys Ser Phe Asp Ser His Asn Trp Gly Pro Leu Pro Ile Lys Asn Ile  
225 230 235 240  
Ile Gly Arg Ser Val Phe Arg Tyr Trp Pro Ser Lys Val Ser Asp  
245 250 255  
Ile Ile His His Glu Gln Val Ser Gln Lys Arg Ala Val Asp Val Ser  
260 265 270

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..591

(D) OTHER INFORMATION: / Ceres Seq. ID 1497991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

aatttcacat ctttctcacc caaatctact cttaaccgta cttcttcttc tacagacatc 60  
aatttctctc gagataaact aaatcttcgc tgaaaaaatg tcgggtcgtg gaaagggagg 120  
aaaagggttg ggtaaaggag gagccaagcg tcacaggaag gttctgagag acaacatcca 180  
aggaatcacc aagcctgcga ttcgaagatt ggctcgtaga ggtggagtca agcgtatcag 240  
tggtctcctc tacgaggaga ctcggtggcg cctcaagatc tttctcgaga acgtgattcg 300  
tgatgctgtc acttacaccg agcacgctag gaggaagact gtgaccgccca tggatgttgt 360  
ctacgctctc aagaggcaag gaaggactct ttacggattc ggtggttaat tagagttttt 420  
cagatccgcg tttgtgtttt ctgggtttct cacttaagcg tctgcgtttt acttttgtat 480  
tgggtttggc gtttagtagt ttgcggtagc gttcttgtaa tgtgtaatta cgctttttct 540  
tcttgcttca gcagtttcgg ttgaaatata aatcgaatca agtttcactt c

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 103 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..103  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497992  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:  
Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala  
1                    5                    10                    15  
Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys  
                    20                    25                    30  
Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser  
                    35                    40                    45  
Gly Leu Ile Tyr Glu Glu Thr Arg Gly Val Leu Lys Ile Phe Leu Glu  
50                    55                    60  
Asn Val Ile Arg Asp Ala Val Thr Tyr Thr Glu His Ala Arg Arg Lys  
65                    70                    75                    80  
Thr Val Thr Ala Met Asp Val Val Tyr Ala Leu Lys Arg Gln Gly Arg  
                    85                    90                    95  
Thr Leu Tyr Gly Phe Gly Gly  
                    100

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1508 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1508  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| gcncnagncc  | nttnscskggg | nsggcnnkrr  | ksggrrrrrrk | srsqkkkkkkk | gatcactttt | 60   |
| tttggtttct  | ttcgcggaagc | caaaaaaaaaa | caagacaaaaa | agaaataaac  | gacgaggcct | 120  |
| ttgtttat    | tataaagctc  | cttcaccggt  | aaaagccttg  | gtcctcatga  | aaccgggaag | 180  |
| cccaagtact  | tacttccacc  | atcaaatcgt  | caaaccattt  | gcaaccatcg  | atggtgtgca | 240  |
| tgtcacgagt  | aagcttctac  | tcttctttct  | tgctactact  | gttagagggtc | gttgtcgcta | 300  |
| gcagcgagtt  | tgatgatgag  | aagaacatcg  | ttcagtcctaa | ccacggctat  | aatcatgatc | 360  |
| gtactcggtta | gtgttttctt  | cgcacttgga  | tgtatctccg  | tctacatgag  | gaggtgtctc | 420  |
| cagcacgctc  | tggggatgga  | cagcgggtgt  | ggtccaggaa  | actggcttaa  | cgtgaggcaa | 480  |
| acgacggagc  | ctgggctaga  | cgcgtctgtt  | atagaaacgt  | ttccaacgtt  | tccttactct | 540  |
| acagtgaaga  | cgttgaggat  | cggtaaagaa  | gctttggagt  | gtcccgtttg  | tctcaacgag | 600  |
| ttcgaggacg  | acgaaacgct  | gcgtttgatt  | cctcagtggt  | gtcacgtgtt  | tcattcctgt | 660  |
| tgcattgatg  | cctggctccg  | ttctcagacc  | acatgtcctc  | tttgccgagc  | caatctcggt | 720  |
| cctgtaccgg  | gtgagtcgtt  | ttcttcggag  | ataccgggtt  | tagctagaga  | aaccggtcag | 780  |
| aactctctca  | gaacgccgat  | tgatgataac  | cggaaaaggg  | ttttaacttc  | acctgacgag | 840  |
| cggttgattg  | actcagtggt  | ttggacgggt  | aaccaaagca  | tgccacgtaa  | atccatgtct | 900  |
| acaggttgag  | aactagctga  | attgtacagc  | cgggctagtt  | caccgggcca  | accggaggag | 960  |
| aatctcgacc  | ggtatagcgt  | gaggttacc   | caagagatac  | atgaccagct  | tgtgaactcc | 1020 |
| agcctgggaa  | agcaagggtc  | aaaaggccaa  | ctggccttac  | ctcaagaaag  | gagctcggtt | 1080 |
| agaggggttc  | gaaccggaag  | cctagggaact | gaaaagaact  | atttctactt  | tgaacgggtt | 1140 |
| gatcaagacg  | gtcgggttga  | cgggagacca  | ttttctataa  | ctcctccata  | ccatacccg  | 1200 |
| tcgatacagt  | ctccggatga  | gattatcaac  | gctagtggta  | attatcagga  | tcgtgctggt | 1260 |
| tcacctaaag  | gtttgcttct  | agcaataaag  | tcaccgtttg  | atcggttatt  | tactgggaag | 1320 |
| aaaaatgccg  | gtgagcggtc  | gtaccttcaa  | tccggcgatg  | cgagccctgt  | ctaggcgaat | 1380 |
| tactactatt  | gggggttatta | agaatatctt  | gaaataaaga  | aaatctgtat  | atgtattttc | 1440 |

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tttcttctag tttctttatg ttatatgaga aattcaattc cttcaccaat ataatgcac 1500  
tggtactg

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..353

(D) OTHER INFORMATION: / Ceres Seq. ID 1497994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Arg | Arg | Thr | Ser | Phe | Ser | Pro | Thr | Thr | Ala | Ile | Ile | Met | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Val | Ser | Val | Phe | Phe | Ala | Leu | Gly | Cys | Ile | Ser | Val | Tyr | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Cys | Leu | Gln | His | Ala | Leu | Gly | Met | Asp | Ser | Gly | Gly | Gly | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Asn | Trp | Leu | Asn | Val | Arg | Gln | Thr | Thr | Glu | Pro | Gly | Leu | Asp | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Val | Ile | Glu | Thr | Phe | Pro | Thr | Phe | Pro | Tyr | Ser | Thr | Val | Lys | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Arg | Ile | Gly | Lys | Glu | Ala | Leu | Glu | Cys | Pro | Val | Cys | Leu | Asn | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Glu | Asp | Asp | Glu | Thr | Leu | Arg | Leu | Ile | Pro | Gln | Cys | Cys | His | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | His | Pro | Gly | Cys | Ile | Asp | Ala | Trp | Leu | Arg | Ser | Gln | Thr | Thr | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Leu | Cys | Arg | Ala | Asn | Leu | Val | Pro | Val | Pro | Gly | Glu | Ser | Val | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Glu | Ile | Pro | Gly | Leu | Ala | Arg | Glu | Thr | Gly | Gln | Asn | Ser | Leu | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Pro | Ile | Asp | Asp | Asn | Arg | Lys | Arg | Val | Leu | Thr | Ser | Pro | Asp | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Leu | Ile | Asp | Ser | Val | Ala | Trp | Thr | Gly | Asn | Gln | Ser | Met | Pro | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Ser | Met | Ser | Thr | Gly | Trp | Lys | Leu | Ala | Glu | Leu | Tyr | Ser | Pro | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Ser | Pro | Gly | Gln | Pro | Glu | Glu | Asn | Leu | Asp | Arg | Tyr | Thr | Leu | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Pro | Gln | Glu | Ile | His | Asp | Gln | Leu | Val | Asn | Ser | Ser | Leu | Gly | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gln | Gly | Ser | Lys | Gly | Gln | Leu | Ala | Leu | Pro | Gln | Glu | Arg | Ser | Ser | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Arg | Gly | Phe | Arg | Thr | Gly | Ser | Leu | Gly | Thr | Glu | Lys | Asn | Tyr | Phe | Tyr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Glu | Arg | Phe | Asp | Gln | Asp | Gly | Arg | Leu | Asp | Arg | Arg | Pro | Phe | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Thr | Pro | Pro | Tyr | His | Thr | Arg | Ser | Ile | Gln | Ser | Pro | Asp | Glu | Ile |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Asn | Ala | Ser | Gly | Asn | Tyr | Gln | Asp | Arg | Ala | Gly | Ser | Pro | Lys | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Leu | Leu | Leu | Ala | Ile | Arg | Ser | Pro | Phe | Asp | Arg | Leu | Phe | Thr | Gly | Lys |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Asn | Ala | Gly | Glu | Arg | Ser | Tyr | Leu | Gln | Ser | Gly | Asp | Ala | Ser | Pro |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 352 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..352  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1497995  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Arg | Thr | Ser | Phe | Ser | Pro | Thr | Thr | Ala | Ile | Ile | Met | Ile | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Val | Ser | Val | Phe | Phe | Ala | Leu | Gly | Cys | Ile | Ser | Val | Tyr | Met | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Cys | Leu | Gln | His | Ala | Leu | Gly | Met | Asp | Ser | Gly | Gly | Gly | Pro | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Trp | Leu | Asn | Val | Arg | Gln | Thr | Thr | Glu | Pro | Gly | Leu | Asp | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ile | Glu | Thr | Phe | Pro | Thr | Phe | Pro | Tyr | Ser | Thr | Val | Lys | Thr | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Arg | Ile | Gly | Lys | Glu | Ala | Leu | Glu | Cys | Pro | Val | Cys | Leu | Asn | Glu | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Asp | Asp | Glu | Thr | Leu | Arg | Leu | Ile | Pro | Gln | Cys | Cys | His | Val | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Pro | Gly | Cys | Ile | Asp | Ala | Trp | Leu | Arg | Ser | Gln | Thr | Thr | Cys | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Cys | Arg | Ala | Asn | Leu | Val | Pro | Val | Pro | Gly | Glu | Ser | Val | Ser | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ile | Pro | Gly | Leu | Ala | Arg | Glu | Thr | Gly | Gln | Asn | Ser | Leu | Arg | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Ile | Asp | Asp | Asn | Arg | Lys | Arg | Val | Leu | Thr | Ser | Pro | Asp | Glu | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Ile | Asp | Ser | Val | Ala | Trp | Thr | Gly | Asn | Gln | Ser | Met | Pro | Arg | Lys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Met | Ser | Thr | Gly | Trp | Lys | Leu | Ala | Glu | Leu | Tyr | Ser | Pro | Ala | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Pro | Gly | Gln | Pro | Glu | Glu | Asn | Leu | Asp | Arg | Tyr | Thr | Leu | Arg | Leu |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Gln | Glu | Ile | His | Asp | Gln | Leu | Val | Asn | Ser | Ser | Leu | Gly | Lys | Gln |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Ser | Lys | Gly | Gln | Leu | Ala | Leu | Pro | Gln | Glu | Arg | Ser | Ser | Val | Arg |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Phe | Arg | Thr | Gly | Ser | Leu | Gly | Thr | Glu | Lys | Asn | Tyr | Phe | Tyr | Phe |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Arg | Phe | Asp | Gln | Asp | Gly | Arg | Leu | Asp | Arg | Arg | Pro | Phe | Ser | Ile |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Pro | Pro | Tyr | His | Thr | Arg | Ser | Ile | Gln | Ser | Pro | Asp | Glu | Ile | Ile |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Ala | Ser | Gly | Asn | Tyr | Gln | Asp | Arg | Ala | Gly | Ser | Pro | Lys | Gly | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Leu | Ala | Ile | Arg | Ser | Pro | Phe | Asp | Arg | Leu | Phe | Thr | Gly | Lys | Lys |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Asn | Ala | Gly | Glu | Arg | Ser | Tyr | Leu | Gln | Ser | Gly | Asp | Ala | Ser | Pro | Val |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 339 amino acids  
    (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..339  
(D) OTHER INFORMATION: / Ceres Seq. ID 1497996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Val | Leu | Val | Ser | Val | Phe | Phe | Ala | Leu | Gly | Cys | Ile | Ser | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Met | Arg | Arg | Cys | Leu | Gln | His | Ala | Leu | Gly | Met | Asp | Ser | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Pro | Gly | Asn | Trp | Leu | Asn | Val | Arg | Gln | Thr | Thr | Glu | Pro | Gly | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ala | Ser | Val | Ile | Glu | Thr | Phe | Pro | Thr | Phe | Pro | Tyr | Ser | Thr | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Thr | Leu | Arg | Ile | Gly | Lys | Glu | Ala | Leu | Glu | Cys | Pro | Val | Cys | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Glu | Phe | Glu | Asp | Asp | Glu | Thr | Leu | Arg | Leu | Ile | Pro | Gln | Cys | Cys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| His | Val | Phe | His | Pro | Gly | Cys | Ile | Asp | Ala | Trp | Leu | Arg | Ser | Gln | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Thr | Cys | Pro | Leu | Cys | Arg | Ala | Asn | Leu | Val | Pro | Val | Pro | Gly | Glu | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Val | Ser | Ser | Glu | Ile | Pro | Gly | Leu | Ala | Arg | Glu | Thr | Gly | Gln | Asn | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Leu | Arg | Thr | Pro | Ile | Asp | Asp | Asn | Arg | Lys | Arg | Val | Leu | Thr | Ser | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Glu | Arg | Leu | Ile | Asp | Ser | Val | Ala | Trp | Thr | Gly | Asn | Gln | Ser | Met |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Arg | Lys | Ser | Met | Ser | Thr | Gly | Trp | Lys | Leu | Ala | Glu | Leu | Tyr | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Ala | Ser | Ser | Pro | Gly | Gln | Pro | Glu | Glu | Asn | Leu | Asp | Arg | Tyr | Thr |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Arg | Leu | Pro | Gln | Glu | Ile | His | Asp | Gln | Leu | Val | Asn | Ser | Ser | Leu |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Gly | Lys | Gln | Gly | Ser | Lys | Gly | Gln | Leu | Ala | Leu | Pro | Gln | Glu | Arg | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Val | Arg | Gly | Phe | Arg | Thr | Gly | Ser | Leu | Gly | Thr | Glu | Lys | Asn | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Tyr | Phe | Glu | Arg | Phe | Asp | Gln | Asp | Gly | Arg | Leu | Asp | Arg | Arg | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Ser | Ile | Thr | Pro | Pro | Tyr | His | Thr | Arg | Ser | Ile | Gln | Ser | Pro | Asp |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Ile | Ile | Asn | Ala | Ser | Gly | Asn | Tyr | Gln | Asp | Arg | Ala | Gly | Ser | Pro |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Lys | Gly | Leu | Leu | Leu | Ala | Ile | Arg | Ser | Pro | Phe | Asp | Arg | Leu | Phe | Thr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Gly | Lys | Lys | Asn | Ala | Gly | Glu | Arg | Ser | Tyr | Leu | Gln | Ser | Gly | Asp | Ala |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |

Ser Pro Val

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 842 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1497997

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:110 |             |             |             |            |             |     |
|------------------------------------------|-------------|-------------|-------------|------------|-------------|-----|
| ctacgattag                               | ttaaattctct | cagtcaccgcg | gagagtgttaa | aaacagcgcg | aaaatcgcgcg | 60  |
| tcgttcgtag                               | gccgactgcg  | agcgaagaag  | aagatggctg  | aagaagaagt | tgactacgta  | 120 |
| ttcaagggtg                               | ttttgaacgcg | agattcagcg  | gttggaagt   | cacagctacg | ggctcggttc  | 180 |
| acaagagacg                               | aattcagtat  | ggattccaaa  | gccacaattc  | ggtgtcgatt | tcaatactcg  | 240 |
| aacgctcggt                               | attgacgata  | agaacatcaa  | agctcagatc  | tgggacatcg | caggccagaa  | 300 |
| acgacacaga                               | gctattacat  | aagccttacta | caaagggtgct | gttggtgcaa | tgttagttta  | 360 |
| cgatatgaca                               | atacgtgaaa  | gctttgagca  | cattcctcag  | tggttggaag | aactacgagt  | 420 |
| gcacgcggat                               | aagaacattg  | tcattcatctt | gattggtaac  | aagacggatt | tagagaacca  | 480 |
| gagatcggtt                               | cctgtggaag  | atgccaaagga | atttgcagag  | aaggaagggc | tttttttctt  | 540 |
| tgagacttcv                               | gcactaaact  | ccacaaatgt  | cgagaactct  | ttcaacactc | tcttgactga  | 600 |
| gatcttcaac                               | aaggtgaaca  | agaagaatct  | cgctaagacc  | accgtgtctt | gcagctcaca  | 660 |
| agtcagtctt                               | ctaagaccac  | cgtgtgttgc  | agctcamtaa  | gtcagtcctt | tcgattttggt | 720 |
| ccattacagt                               | ttagaatgaa  | ataaaccatt  | tcataatactt | caaaaatatt | gtttatatatt | 780 |
| ggtttttaga                               | tagtgagttt  | tgtgtagtgt  | acgttgattt  | ttgaacaaa  | atctttctatt | 840 |
| tt                                       |             |             |             |            |             |     |

[illegible]

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:117:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ile | Arg | Glu | Ser | Phe | Glu | His | Ile | Pro | Gln | Trp | Leu | Glu | Glu |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| Leu | Arg | Val | His | Ala | Asp | Lys | Asn | Ile | Val | Ile | Ile | Leu | Ile | Gly | Asn |



```

 20 25 30
Lys Thr Asp Leu Glu Asn Gln Arg Ser Val Pro Val Glu Asp Ala Lys
 35 40 45
Glu Phe Ala Glu Lys Glu Gly Leu Phe Phe Leu Glu Thr Xaa Ala Leu
 50 55 60
Asn Ser Thr Asn Val Glu Asn Ser Phe Asn Thr Leu Leu Thr Glu Ile
65 70 75 80
Phe Asn Lys Val Asn Lys Lys Asn Leu Ala Lys Thr Thr Val Ser Cys
 85 90 95
Ser Ser Gln Val Ser Leu Leu Arg Pro Pro Cys Val Ala Ala Xaa
 100 105 110
```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```

taaaaaaggg tacaaaagga gatgtcacag cactaaagcc cactataatg acagctgttc 60
cagccattct tgatcgtgtc agggatgggtg tccgcaaaaa ggttgatgca aagggcggat 120
tgtcaaagaa attgtttgac tttgcatatg ctcggcgatt atctgcaatc aatggaagt 180
ggtttgaggc ctggggattg gaaaagcttt tgtgggatgt gcttggtgtc aggaaaattc 240
gtgcagtggt gggagggtcaa attcgctatt tgctctctgg tggtgccctt ctttctgggtg 300
acactcagag attcattaac atctgcgttg gggctccaat cggtcaggga tatggggtca 360
cagagacttg tgctgggtga accttctctg agtttgagga cacatccgtt ggccgagttg 420
gtgctccact tccttgctcc tttgtaaagc tagtagactg ggcggaaggt gggatatctaa 480
ccagtgtataa gccaatgtcc cgtggtgaaa ttgtaattgg tggctcaa atcacgcttg 540
ggtatttcaa aaatgaggag aaaactaaa aagtgtacaa ggttgatgaa aagggaatga 600
ggtggttcta cacaggagac ataggacgat ttcaccctga tggctgcctc gagataatag 660
accgaaaaaa ggatatcggt aaacttcagc acggagaata tgtctccttg ggcaaagttg 720
aagctgctct aagtataagt ccctatgttg aaaacataat ggttcatgct gattcgttct 780
acagttactg tgtggctctt gtggtcgcgt cccaacatac agttgaaggt tgggcttcaa 840
agsaaggaat agastttgcc aacttcgaag aactgtgcac gaaagagcaa gccgtgaaag 900
aagtgtatgc ttatcttgtc aaggcggtca aacaatcacg attggagaag tttgagatac 960
cmgcaaagat caaattgttg gcatctccat ggacgccaga gtcaggatta gtcacagcag 1020
ctctaaagct taaaagagac gtaattagga gggaattctc tgaagatctc accaagttat 1080
atgcctaaac ttttcttctt cctttacttt gttttatctt ttacgtctcg atgcattcga 1140
aagacgcaac agctgcacaa aaacttaatt ctaagaatag tgtatctttt ctctctgtga 1200
tgtctgtctt ttcgtgcaaa tgtatggggg taactgtgac gagactgaaa gaaagaaagt 1260
tatgggtctt
```

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..361
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```

Lys Lys Gly Thr Lys Gly Asp Val Thr Ala Leu Lys Pro Thr Ile Met
1 5 10 15
Thr Ala Val Pro Ala Ile Leu Asp Arg Val Arg Asp Gly Val Arg Lys
 20 25 30
```

Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe Ala  
35 40 45  
Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala Trp  
50 55 60  
Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile Arg  
65 70 75 80  
Ala Val Leu Gly Gly Gln Ile Arg Tyr Leu Leu Ser Gly Gly Ala Pro  
85 90 95  
Leu Ser Gly Asp Thr Gln Arg Phe Ile Asn Ile Cys Val Gly Ala Pro  
100 105 110  
Ile Gly Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Gly Thr Phe  
115 120 125  
Ser Glu Phe Glu Asp Thr Ser Val Gly Arg Val Gly Ala Pro Leu Pro  
130 135 140  
Cys Ser Phe Val Lys Leu Val Asp Trp Ala Glu Gly Gly Tyr Leu Thr  
145 150 155 160  
Ser Asp Lys Pro Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser Asn  
165 170 175  
Ile Thr Leu Gly Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val Tyr  
180 185 190  
Lys Val Asp Glu Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile Gly  
195 200 205  
Arg Phe His Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp  
210 215 220  
Ile Val Lys Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu  
225 230 235 240  
Ala Ala Leu Ser Ile Ser Pro Tyr Val Glu Asn Ile Met Val His Ala  
245 250 255  
Asp Ser Phe Tyr Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His  
260 265 270  
Thr Val Glu Gly Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe  
275 280 285  
Glu Glu Leu Cys Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr  
290 295 300  
Leu Val Lys Ala Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa  
305 310 315 320  
Ala Lys Ile Lys Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu  
325 330 335  
Val Thr Ala Ala Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe  
340 345 350  
Ser Glu Asp Leu Thr Lys Leu Tyr Ala  
355 360

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..346
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met Thr Ala Val Pro Ala Ile Leu Asp Arg Val Arg Asp Gly Val Arg  
1 5 10 15  
Lys Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe  
20 25 30  
Ala Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala  
35 40 45  
Trp Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Arg Ala Val Leu Gly Gly Gln Ile Arg Tyr Leu Leu Ser Gly Gly Ala |     |     |
| 65                                                              | 70  | 75  |
| Pro Leu Ser Gly Asp Thr Gln Arg Phe Ile Asn Ile Cys Val Gly Ala |     | 80  |
|                                                                 | 85  | 90  |
| Pro Ile Gly Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Gly Thr |     | 95  |
|                                                                 | 100 | 105 |
| Phe Ser Glu Phe Glu Asp Thr Ser Val Gly Arg Val Gly Ala Pro Leu |     | 110 |
|                                                                 | 115 | 120 |
| Pro Cys Ser Phe Val Lys Leu Val Asp Trp Ala Glu Gly Gly Tyr Leu |     | 125 |
|                                                                 | 130 | 135 |
| Thr Ser Asp Lys Pro Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser |     | 140 |
| 145                                                             | 150 | 155 |
| Asn Ile Thr Leu Gly Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val |     | 160 |
|                                                                 | 165 | 170 |
| Tyr Lys Val Asp Glu Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile |     | 175 |
|                                                                 | 180 | 185 |
| Gly Arg Phe His Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys |     | 190 |
|                                                                 | 195 | 200 |
| Asp Ile Val Lys Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val |     | 205 |
|                                                                 | 210 | 215 |
| Glu Ala Ala Leu Ser Ile Ser Pro Tyr Val Glu Asn Ile Met Val His |     | 220 |
| 225                                                             | 230 | 235 |
| Ala Asp Ser Phe Tyr Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln |     | 240 |
|                                                                 | 245 | 250 |
| His Thr Val Glu Gly Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn |     | 255 |
|                                                                 | 260 | 265 |
| Phe Glu Glu Leu Cys Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala |     | 270 |
|                                                                 | 275 | 280 |
| Tyr Leu Val Lys Ala Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile |     | 285 |
|                                                                 | 290 | 295 |
| Xaa Ala Lys Ile Lys Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly     |     | 300 |
| 305                                                             | 310 | 315 |
| Leu Val Thr Ala Ala Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu |     | 320 |
|                                                                 | 325 | 330 |
| Phe Ser Glu Asp Leu Thr Lys Leu Tyr Ala                         |     | 335 |
|                                                                 | 340 | 345 |

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1498003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser Asn Ile Thr Leu Gly |    |    |
| 1                                                               | 5  | 10 |
| Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val Tyr Lys Val Asp Glu |    | 15 |
|                                                                 | 20 | 25 |
| Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile Gly Arg Phe His Pro |    | 30 |
|                                                                 | 35 | 40 |
| Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp Ile Val Lys Leu |    | 45 |
|                                                                 | 50 | 55 |
| Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu Ala Ala Leu Ser |    | 60 |
| 65                                                              | 70 | 75 |
| Ile Ser Pro Tyr Val Glu Asn Ile Met Val His Ala Asp Ser Phe Tyr |    | 80 |
|                                                                 | 85 | 90 |
|                                                                 |    | 95 |

Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His Thr Val Glu Gly  
100 105 110  
Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe Glu Leu Cys  
115 120 125  
Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr Leu Val Lys Ala  
130 135 140  
Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa Ala Lys Ile Lys  
145 150 155 160  
Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu Val Thr Ala Ala  
165 170 175  
Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe Ser Glu Asp Leu  
180 185 190  
Thr Lys Leu Tyr Ala  
195

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..764
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ctaatacgaaa aatcatcact ttcacaatct tcttcacgga tttctctctt ccaaactctcc | 60  |
| caaaagatgt cgaaccctag agttttcttc gacatgagtc tcagcggtag tcccatcgga   | 120 |
| cggatcgaga tggagctttt cgctgataca accccaaaca cggcggagaa tttccgtgct   | 180 |
| ctctgtaccg gcgagaaagg aatgggaaag ctaggtaagc cacttcactt caaaggatcg   | 240 |
| atcttccacc gtgtgattcc cggattcatg tgtcaaggag gtgatttcac cgccaagaac   | 300 |
| ggaaccggtg gtgaatcgat ctacggtgct aagttcaagg acgagaactt tatcaagaag   | 360 |
| catacaggag ctgggattct ctcaatggct aactctggtc ctaacactaa cggatctcag   | 420 |
| ttcttcactt gtaccgataa gacgtcgtgg ttagatggta agcacgttgt gtttgacaa    | 480 |
| gttgtaaaag gcttggaagt cgtgaaggcg attgagaaag ttggatctga ttctggaaag   | 540 |
| acttccaaag tcgttaccat cactgattgt ggtcagcttt cttagatcta agtgagaaag   | 600 |
| tgagagactt tgatctttat gagtaataat ggtgtctttt gctttcgggt gttcttcctc   | 660 |
| ttaccttaat ggattattct gtttaggggt tgagttttcg tttcagagtt tgtaacaaaa   | 720 |
| cccttttgtg ttttctgggg tttgaaataa ttatgagctt actc                    |     |

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Leu Ile Glu Lys Ser Ser Leu Ser Gln Ser Ser Ser Ser Ile Ser Leu |  |
| 1 5 10 15                                                       |  |
| Phe Gln Ile Ser Gln Lys Met Ser Asn Pro Arg Val Phe Phe Asp Met |  |
| 20 25 30                                                        |  |
| Ser Leu Ser Gly Thr Pro Ile Gly Arg Ile Glu Met Glu Leu Phe Ala |  |
| 35 40 45                                                        |  |
| Asp Thr Thr Pro Asn Thr Ala Glu Asn Phe Arg Ala Leu Cys Thr Gly |  |
| 50 55 60                                                        |  |
| Glu Lys Gly Met Gly Lys Leu Gly Lys Pro Leu His Phe Lys Gly Ser |  |
| 65 70 75 80                                                     |  |

(D) OTHER INFORMATION: / Ceres Seq. ID 1498009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Ser | Gly | Thr | Pro | Ile | Gly | Arg | Ile | Glu | Met | Glu | Leu | Phe |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Asp | Thr | Thr | Pro | Asn | Thr | Ala | Glu | Asn | Phe | Arg | Ala | Leu | Cys | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Glu | Lys | Gly | Met | Gly | Lys | Leu | Gly | Lys | Pro | Leu | His | Phe | Lys | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ile | Phe | His | Arg | Val | Ile | Pro | Gly | Phe | Met | Cys | Gln | Gly | Gly | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Phe | Thr | Ala | Lys | Asn | Gly | Thr | Gly | Gly | Glu | Ser | Ile | Tyr | Gly | Ala | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Lys | Asp | Glu | Asn | Phe | Ile | Lys | Lys | His | Thr | Gly | Ala | Gly | Ile | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Met | Ala | Asn | Ser | Gly | Pro | Asn | Thr | Asn | Gly | Ser | Gln | Phe | Phe | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Thr | Asp | Lys | Thr | Ser | Trp | Leu | Asp | Gly | Lys | His | Val | Val | Phe | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Val | Val | Lys | Gly | Leu | Asp | Val | Val | Lys | Ala | Ile | Glu | Lys | Val | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Asp | Ser | Gly | Lys | Thr | Ser | Lys | Val | Val | Thr | Ile | Thr | Asp | Cys | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Leu | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

|             |            |             |             |            |            |      |
|-------------|------------|-------------|-------------|------------|------------|------|
| aacccaaaaga | atcacgacat | tgaatcttct  | ttcattttctc | tcctcaagac | atagtagcat | 60   |
| aagamaatga  | agatatcatc | actaggatgg  | gtcttagtcc  | ttatcttcat | ctctattacc | 120  |
| attgtttcga  | gtgcaccagc | acctaaacct  | cctaaacct   | agcctgcacc | agcacctaca | 180  |
| cctcctaaac  | ctaagccac  | accagcacct  | acacctccta  | aacctagcc  | caaaccagca | 240  |
| cctacacctc  | ctaaacctaa | gcccacacca  | gcacctacac  | ctcctaaacc | taagcctgca | 300  |
| ccagcaccag  | caccagcacc | aaccaccagca | ccgaaacct   | aacctgcacc | taaaccagca | 360  |
| ccaggtggag  | aagttgagga | cgaaaccgag  | tttagctacg  | agacgaaagg | aaacaagggg | 420  |
| ccagcgaaat  | ggggaacact | acatgcagag  | tggaaaatgt  | gtggaatagg | caaatgcaa  | 480  |
| tctcctattg  | atcttcggga | caaaaatgtg  | gtagttagta  | ataaatttg  | attgcttcgt | 540  |
| agccagtatc  | tgccttctaa | taccaccatt  | agaacagag   | gtcatgat   | catgttgaaa | 600  |
| ttcaaaggag  | gcaataaagg | tattggtgtc  | actatccgtg  | gtactagata | tcaacttcaa | 660  |
| caacttcatt  | ggcactctcc | ttccgaacat  | acaatcaatg  | gcaaaagggt | tgcgctagag | 720  |
| gaacacttgg  | ttcatgagag | taaagatava  | cgctacgctg  | ttgtcgcttt | cttatacaat | 780  |
| ctcggagcat  | ctgacccttt | tctcttttctg | ttggaaaaac  | aattgaagaa | gataactgat | 840  |
| acacatgcgt  | ccgaggaaca | tgtcggaatc  | attgatccca  | aaaaactcag | ttttgaatca | 900  |
| aaacattatt  | atagatatct | cggatcactt  | actgctcctc  | catgttctga | aaatgttatt | 960  |
| tggtccggtt  | ccaaagagat | tgcgactgtg  | tcaagtaaac  | aagtgaagct | tctccgtgtg | 1020 |
| gctgtacacg  | atgcttcaga | ttcaaagtcc  | aggccgcttc  | aagcagtcaa | taagcgcaag | 1080 |
| gtatatattt  | acaaacccaa | ggttaaagta  | atgaagaaat  | actgtaatat | aagttcttac | 1140 |
| tagtaattct  | tattctttta | tatatgtaca  | ttatgaattg  | tacactaaaa | tgatgttttt | 1200 |
| agggataaac  | tgatgacttg | gttttgttat  | t           |            |            |      |

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..358  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Ser | Ser | Leu | Gly | Trp | Val | Leu | Val | Leu | Ile | Phe | Ile | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Thr | Ile | Val | Ser | Ser | Ala | Pro | Ala | Pro | Lys | Pro | Pro | Lys | Pro | Lys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Pro | Ala | Pro | Ala | Pro | Thr | Pro | Pro | Lys | Pro | Lys | Pro | Thr | Pro | Ala | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Pro | Pro | Lys | Pro | Lys | Pro | Lys | Pro | Ala | Pro | Thr | Pro | Pro | Lys | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Pro | Thr | Pro | Ala | Pro | Thr | Pro | Pro | Lys | Pro | Lys | Pro | Ala | Pro | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Pro | Ala | Pro | Ala | Pro | Thr | Pro | Ala | Pro | Lys | Pro | Lys | Pro | Ala | Pro | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Pro | Ala | Pro | Gly | Gly | Glu | Val | Glu | Asp | Glu | Thr | Glu | Phe | Ser | Tyr | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Lys | Gly | Asn | Lys | Gly | Pro | Ala | Lys | Trp | Gly | Thr | Leu | His | Ala | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Trp | Lys | Met | Cys | Gly | Ile | Gly | Lys | Met | Gln | Ser | Pro | Ile | Asp | Leu | Arg |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asp | Lys | Asn | Val | Val | Val | Ser | Asn | Lys | Phe | Gly | Leu | Leu | Arg | Ser | Gln |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Tyr | Leu | Pro | Ser | Asn | Thr | Thr | Ile | Lys | Asn | Arg | Gly | His | Asp | Ile | Met |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Lys | Phe | Lys | Gly | Gly | Asn | Lys | Gly | Ile | Gly | Val | Thr | Ile | Arg | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Arg | Tyr | Gln | Leu | Gln | Gln | Leu | His | Trp | His | Ser | Pro | Ser | Glu | His |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Ile | Asn | Gly | Lys | Arg | Phe | Ala | Leu | Glu | Glu | His | Leu | Val | His | Glu |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Ser | Lys | Asp | Xaa | Arg | Tyr | Ala | Val | Val | Ala | Phe | Leu | Tyr | Asn | Leu | Gly |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Ala | Ser | Asp | Pro | Phe | Leu | Phe | Ser | Leu | Glu | Lys | Gln | Leu | Lys | Lys | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Asp | Thr | His | Ala | Ser | Glu | Glu | His | Val | Gly | Ile | Ile | Asp | Pro | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Leu | Ser | Phe | Glu | Ser | Lys | His | Tyr | Tyr | Arg | Tyr | Ser | Gly | Ser | Leu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Ala | Pro | Pro | Cys | Ser | Glu | Asn | Val | Ile | Trp | Ser | Val | Ser | Lys | Glu |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Ile | Arg | Thr | Val | Ser | Ser | Lys | Gln | Val | Lys | Leu | Leu | Arg | Val | Ala | Val |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |
| His | Asp | Ala | Ser | Asp | Ser | Asn | Ala | Arg | Pro | Leu | Gln | Ala | Val | Asn | Lys |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Arg | Lys | Val | Tyr | Leu | Tyr | Lys | Pro | Lys | Val | Lys | Leu | Met | Lys | Lys | Tyr |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Cys | Asn | Ile | Ser | Ser | Tyr |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 355 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 228 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..228

(D) OTHER INFORMATION: / Ceres Seq. ID 1498012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Cys Gly Ile Gly Lys Met Gln Ser Pro Ile Asp Leu Arg Asp Lys  
1 5 10 15  
Asn Val Val Val Ser Asn Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu  
20 25 30  
Pro Ser Asn Thr Thr Ile Lys Asn Arg Gly His Asp Ile Met Leu Lys  
35 40 45  
Phe Lys Gly Gly Asn Lys Gly Ile Gly Val Thr Ile Arg Gly Thr Arg  
50 55 60  
Tyr Gln Leu Gln Gln Leu His Trp His Ser Pro Ser Glu His Thr Ile  
65 70 75 80  
Asn Gly Lys Arg Phe Ala Leu Glu Glu His Leu Val His Glu Ser Lys  
85 90 95  
Asp Xaa Arg Tyr Ala Val Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser  
100 105 110  
Asp Pro Phe Leu Phe Ser Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp  
115 120 125  
Thr His Ala Ser Glu Glu His Val Gly Ile Ile Asp Pro Lys Lys Leu  
130 135 140  
Ser Phe Glu Ser Lys His Tyr Tyr Arg Tyr Ser Gly Ser Leu Thr Ala  
145 150 155 160  
Pro Pro Cys Ser Glu Asn Val Ile Trp Ser Val Ser Lys Glu Ile Arg  
165 170 175  
Thr Val Ser Ser Lys Gln Val Lys Leu Leu Arg Val Ala Val His Asp  
180 185 190  
Ala Ser Asp Ser Asn Ala Arg Pro Leu Gln Ala Val Asn Lys Arg Lys  
195 200 205  
Val Tyr Leu Tyr Lys Pro Lys Val Lys Leu Met Lys Lys Tyr Cys Asn  
210 215 220  
Ile Ser Ser Tyr  
225

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1498013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Met Gln Ser Pro Ile Asp Leu Arg Asp Lys Asn Val Val Val Ser Asn  
1 5 10 15  
Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu Pro Ser Asn Thr Thr Ile  
20 25 30  
Lys Asn Arg Gly His Asp Ile Met Leu Lys Phe Lys Gly Gly Asn Lys  
35 40 45  
Gly Ile Gly Val Thr Ile Arg Gly Thr Arg Tyr Gln Leu Gln Gln Leu  
50 55 60  
His Trp His Ser Pro Ser Glu His Thr Ile Asn Gly Lys Arg Phe Ala  
65 70 75 80  
Leu Glu Glu His Leu Val His Glu Ser Lys Asp Xaa Arg Tyr Ala Val  
85 90 95  
Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser Asp Pro Phe Leu Phe Ser  
100 105 110  
Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp Thr His Ala Ser Glu Glu



|     |                     |                     |                     |  |     |
|-----|---------------------|---------------------|---------------------|--|-----|
|     | 115                 |                     | 120                 |  | 125 |
| His | Val Gly Ile Ile Asp | Pro Lys Lys Leu Ser | Phe Glu Ser Lys His |  |     |
|     | 130                 | 135                 | 140                 |  |     |
| Tyr | Tyr Arg Tyr Ser Gly | Ser Leu Thr Ala Pro | Pro Cys Ser Glu Asn |  |     |
| 145 |                     | 150                 | 155                 |  | 160 |
| Val | Ile Trp Ser Val Ser | Lys Glu Ile Arg Thr | Val Ser Ser Lys Gln |  |     |
|     | 165                 | 170                 | 175                 |  |     |
| Val | Lys Leu Leu Arg Val | Ala Val His Asp Ala | Ser Asp Ser Asn Ala |  |     |
|     | 180                 | 185                 | 190                 |  |     |
| Arg | Pro Leu Gln Ala Val | Asn Lys Arg Lys Val | Tyr Leu Tyr Lys Pro |  |     |
|     | 195                 | 200                 | 205                 |  |     |
| Lys | Val Lys Leu Met Lys | Lys Tyr Cys Asn Ile | Ser Ser Tyr         |  |     |
|     | 210                 | 215                 | 220                 |  |     |

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1084 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1084
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| aaatttcaac  | ccctggttgc | tttgtttgat | ccctagattt | tcgccgtggt | atagaagaat  | 60   |
| ctcatTTTTT  | gccgtctgaa | tcgaaatttc | gtgtcgagaa | ctcctccact | cctccacttc  | 120  |
| tcgtttttctc | tttttaattt | attttactct | attgtgacca | ttttgagcgt | tattgagaac  | 180  |
| tcaaagctca  | agaatgcgtg | caccatcttt | gcttgacaaa | tgcttgccgg | gtttgctgcc  | 240  |
| tcaagaccga  | ggsggtgtgt | ctgcrttatc | agagaaggat | ttgcagcttc | caacaccagc  | 300  |
| tgttgagatc  | ataccttcta | agacagtagc | tcatcacagg | tattcagggg | agaatctaga  | 360  |
| tgcgctcggg  | ttacaagttt | tcaagggaaa | agtaagtgtt | gctgatatca | ttgggctctc  | 420  |
| tgggtcagaa  | actgctcctt | taaaaaatga | aggttctttg | aaaagttggg | aaagctctgt  | 480  |
| tgttctttgt  | aatgtcctta | aaaacgagat | ccgtgatgga | cagcttagct | tcaggggcaa  | 540  |
| aagggctctc  | gagctaggct | gtccatcacg | gatctcgttt | ttaaggacnt | taaagagwac  | 600  |
| aagcaacttg  | atgctgaaat | ccacaggaac | tacatctacg | gtggccatct | ctcaaactac  | 660  |
| atgaagctgt  | tgggggaaga | tgagccggag | aagttgcaaa | ctcacttcag | tgcttacatt  | 720  |
| aagaaaggag  | ttgaagctga | gagcatcgag | gagatgtaca | agaaggttca | cgcagctatc  | 780  |
| cgagcagaac  | ccaaccataa | gaaaaccgag | aaatctgctc | ccamsgaaca | caagagggtac | 840  |
| aacttgaaga  | aactgactta | cgaagagagg | aagaacaagt | tgatcgagag | agtgaaggca  | 900  |
| ttaaaccggg  | caggtgggtg | tgatgatgat | gaggatgatg | aagagtaaat | caccaatcaa  | 960  |
| gccttctttg  | tctcatgcct | ctagtagctt | tttacttatt | tattttcaga | ctaaaacact  | 1020 |
| cagtttttgt  | tttcacattt | tagttgcgtt | tgaagatttt | gaattcgagg | atatgttttg  | 1080 |
| tttg        |            |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ala | Pro | Ser | Leu | Leu | Ala | Gln | Cys | Leu | Pro | Gly | Leu | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Asp | Arg | Xaa | Gly | Val | Ser | Xaa | Leu | Ser | Glu | Lys | Asp | Leu | Gln | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Thr | Pro | Ala | Val | Glu | Ile | Ile | Pro | Ser | Lys | Thr | Val | Ala | His | His |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Arg Tyr Ser Gly Glu Asn Leu Asp Ala Leu Gly Leu Gln Val Phe Lys |     |     |
| 50                                                              | 55  | 60  |
| Gly Lys Val Ser Val Ala Asp Ile Ile Gly Leu Ser Gly Ser Glu Thr |     |     |
| 65                                                              | 70  | 75  |
| Ala Pro Leu Lys Asn Glu Gly Ser Leu Lys Ser Trp Glu Ser Ser Val |     | 80  |
|                                                                 | 85  | 90  |
| Val Leu Val Asn Val Leu Lys Asn Glu Ile Arg Asp Gly Gln Leu Ser |     | 95  |
|                                                                 | 100 | 105 |
| Phe Arg Gly Lys Arg Val Leu Glu Gly Cys Pro Ser Arg Ile Ser     |     | 110 |
|                                                                 | 115 | 120 |
| Phe Leu Arg Xaa Leu Lys Xaa Thr Ser Asn Leu Met Leu Lys Ser Thr |     | 125 |
|                                                                 | 130 | 135 |
| Gly Thr Thr Ser Thr Val Ala Ile Ser Gln Thr Thr                 |     | 140 |
| 145                                                             | 150 | 155 |

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1498020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Lys Leu Leu Gly Glu Asp Glu Pro Glu Lys Leu Gln Thr His Phe |    |    |
| 1                                                               | 5  | 10 |
| Ser Ala Tyr Ile Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Met |    | 15 |
|                                                                 | 20 | 25 |
| Tyr Lys Lys Val His Ala Ala Ile Arg Ala Glu Pro Asn His Lys Lys |    | 30 |
|                                                                 | 35 | 40 |
| Thr Glu Lys Ser Ala Pro Xaa Glu His Lys Arg Tyr Asn Leu Lys Lys |    | 45 |
|                                                                 | 50 | 55 |
| Leu Thr Tyr Glu Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Lys Ala |    | 60 |
| 65                                                              | 70 | 75 |
| Leu Asn Gly Ala Gly Gly Asp Asp Asp Asp Glu Asp Asp Glu Glu     |    | 80 |
|                                                                 | 85 | 90 |

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 656 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..656

(D) OTHER INFORMATION: / Ceres Seq. ID 1498028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| attaaatcct | aaaatccatt | attgattgaa | tcttcgagtt | accaacaaaa | aaaaaactct | 60  |
| cctttatttc | agttttcttt | tacaaacat  | aatcttctct | ttgattccat | cttgtgaacc | 120 |
| accggcataa | gaaaatatga | caattgcttt | aacgatcgga | ggaaacgggt | tttcgggtct | 180 |
| accaggatcg | tcgttttcat | catcatcttc | gtcgtttcga | ttaaaaaaca | gcagaagaaa | 240 |
| gaacacgaag | atgctcaaca | gatcaaaagt | cgtttggtct | tcttcatctt | ctgtaatgga | 300 |
| tccgthtaag | actcttaaga | tccgaccoga | ttcatctgaa | tacgaggtca | agaaagcttt | 360 |
| cagacaactc | gctaaaaagg | tttgaccttt | tgtttagctc | aatcatctta | gatctgggtt | 420 |
| tttaaaattt | gacatctttc | tgatcgattt | tgttttgatt | gttgaggtat | catcctgatg | 480 |
| tttgtagagg | aagcaattgt | ggggtacagt | ttcagacaat | taacgaagct | tacgatgtaa | 540 |
| gcgtgtgttt | atgaaagcta | actatgcttt | ttggttaact | taaaacagat | tgaaattcgc | 600 |

ttttgtaatg aaaattgata tctttgtttt ttttcctttg aagattgtgt tgaagc

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1498029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ile | Ala | Leu | Thr | Ile | Gly | Gly | Asn | Gly | Phe | Ser | Gly | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Ser | Phe | Ser | Ser | Ser | Ser | Ser | Ser | Phe | Arg | Leu | Lys | Asn | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Lys | Asn | Thr | Lys | Met | Leu | Asn | Arg | Ser | Lys | Val | Val | Cys | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Ser | Ser | Ser | Val | Met | Asp | Pro | Xaa | Lys | Thr | Leu | Lys | Ile | Arg | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asp | Ser | Ser | Glu | Tyr | Glu | Val | Lys | Lys | Ala | Phe | Arg | Gln | Leu | Ala | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Lys | Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1498030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Arg | Ser | Lys | Val | Val | Cys | Ser | Ser | Ser | Ser | Ser | Val | Met |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | Pro | Xaa | Lys | Thr | Leu | Lys | Ile | Arg | Pro | Asp | Ser | Ser | Glu | Tyr | Glu |
|     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| Val | Lys | Lys | Ala | Phe | Arg | Gln | Leu | Ala | Lys | Lys | Val |     |     |     |     |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1135

(D) OTHER INFORMATION: / Ceres Seq. ID 1498033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| actcacaaa  | gcatacata  | acactcacac | acacacttc  | tcttctctta | ttttctcagt | 60  |
| tcttttaact | cttttctcta | cctatatcca | aatggccacc | gtcgagggtg | aacaagtgac | 120 |
| tccagtagca | gctgagaaca | tcgaggtgcc | accaccaaag | gctgtggagt | cggaggaagt | 180 |
| caccaccgtc | tccgagtctc | ttccagctcc | ggtaacagaa | tctcaagcgc | ctgtcgaagt | 240 |
| aacaactaaa | gatttggtcg | tggaagagac | agagaaacca | atcgaagaaa | cagaggaagc | 300 |
| tcaagttgaa | actccggagg | ttgtggagat | caagaaagat | gaagaagctc | cggttgaaac | 360 |

```
tccggtggtt gtggaggatg agagcaaaac agaggaagtt gtagaggcga agaaagagga 420
agaagtagaa gaaaagaaga cagaggaagc tccagtgggt gtggaggaag agaagaagcc 480
agaggcagag gaggagaaac ccgctgggtt tacctccccg gctcaagcca ccatggtcgc 540
tccattcacc ggcttgaagt catccgcttc tttcccggtc acccgcaagg ccaacaacga 600
cattacttcc atcacaagca acggaggaag agttagctgc atgaaggtgt ggccaccaat 660
cggaagaag aagtttagac tctatcttac ctccctgacc ttagtgacgt tgaattggct 720
aaggaagttg actaccttct ccgcaacaag tggattcctt gtgttgaatt cgagttggag 780
cacggatttg tgtaccgtga gcacggaaac actcccggat actatgatgg acggtactgg 840
acaatgtgga agcttccatt gttcggatgc accgactccg ctcaagtgtt gaaggaagtt 900
gaagaatgca agaaggagta ccctggcgcc ttcattagga tcacggatt cgacaacacc 960
cgtcaagtcc aatgcattcag ttctattgcc tacaagcccc caagcttcac cgaagcttaa 1020
tcccccttct ggaatattca gcgttgatta ttctggaacc catttctatg tggtaaatgc 1080
aaatttaaga aattatttgc cgacttaaaa gttgaggaac tattgtttga aagtc
```

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1498034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```
Leu Thr Lys Ala Ser His Asn Thr His Thr His Thr Phe Ser Ser Leu
1 5 10 15
Ile Phe Ser Val Leu Leu Thr Leu Phe Ser Thr Tyr Ile Gln Met Ala
20 25 30
Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Ala Glu Asn Ile Glu
35 40 45
Val Pro Pro Pro Lys Ala Val Glu Ser Glu Glu Val Thr Thr Val Ser
50 55 60
Glu Ser Leu Pro Ala Pro Val Thr Glu Ser Gln Ala Pro Val Glu Val
65 70 75 80
Thr Thr Lys Asp Leu Val Val Glu Glu Thr Glu Lys Pro Ile Glu Glu
85 90 95
Thr Glu Glu Ala Gln Val Glu Thr Pro Glu Val Val Glu Ile Lys Lys
100 105 110
Asp Glu Glu Ala Pro Val Glu Thr Pro Val Val Val Glu Asp Glu Ser
115 120 125
Lys Thr Glu Glu Val Val Glu Ala Lys Lys Glu Glu Glu Val Glu Glu
130 135 140
Lys Lys Thr Glu Glu Ala Pro Val Val Val Glu Glu Glu Lys Lys Pro
145 150 155 160
Glu Ala Glu Glu Glu Lys Pro Ala Val Val Thr Ser Pro Ala Gln Ala
165 170 175
Thr Met Val Ala Pro Phe Thr Gly Leu Lys Ser Ser Ala Ser Phe Pro
180 185 190
Val Thr Arg Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser Asn Gly
195 200 205
Gly Arg Val Ser Cys Met Lys Val Trp Pro Pro Ile Gly Lys Lys Lys
210 215 220
Phe Arg Leu Tyr Leu Thr Ser Leu Thr Leu Val Thr Leu Asn Trp Leu
225 230 235 240
Arg Lys Leu Thr Thr Phe Ser Ala Thr Ser Gly Phe Leu Val Leu Asn
245 250 255
Ser Ser Trp Ser Thr Asp Leu Cys Thr Val Ser Thr Glu Thr Leu Pro
260 265 270
Asp Thr Met Met Asp Gly Thr Gly Gln Cys Gly Ser Phe His Cys Ser
275 280 285
```

Asp Ala Pro Thr Pro Leu Lys Cys  
290 295

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```
Met Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Ala Glu Asn
1 5 10 15
Ile Glu Val Pro Pro Lys Ala Val Glu Ser Glu Glu Val Thr Thr
20 25 30
Val Ser Glu Ser Leu Pro Ala Pro Val Thr Glu Ser Gln Ala Pro Val
35 40 45
Glu Val Thr Thr Lys Asp Leu Val Val Glu Glu Thr Glu Lys Pro Ile
50 55 60
Glu Glu Thr Glu Glu Ala Gln Val Glu Thr Pro Glu Val Val Glu Ile
65 70 75 80
Lys Lys Asp Glu Glu Ala Pro Val Glu Thr Pro Val Val Val Glu Asp
85 90 95
Glu Ser Lys Thr Glu Glu Val Val Glu Ala Lys Lys Glu Glu Glu Val
100 105 110
Glu Glu Lys Lys Thr Glu Glu Ala Pro Val Val Val Glu Glu Glu Lys
115 120 125
Lys Pro Glu Ala Glu Glu Glu Lys Pro Ala Val Val Thr Ser Pro Ala
130 135 140
Gln Ala Thr Met Val Ala Pro Phe Thr Gly Leu Lys Ser Ser Ala Ser
145 150 155 160
Phe Pro Val Thr Arg Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser
165 170 175
Asn Gly Gly Arg Val Ser Cys Met Lys Val Trp Pro Pro Ile Gly Lys
180 185 190
Lys Lys Phe Arg Leu Tyr Leu Thr Ser Leu Thr Leu Val Thr Leu Asn
195 200 205
Trp Leu Arg Lys Leu Thr Thr Phe Ser Ala Thr Ser Gly Phe Leu Val
210 215 220
Leu Asn Ser Ser Trp Ser Thr Asp Leu Cys Thr Val Ser Thr Glu Thr
225 230 235 240
Leu Pro Asp Thr Met Met Asp Gly Thr Gly Gln Cys Gly Ser Phe His
245 250 255
Cys Ser Asp Ala Pro Thr Pro Leu Lys Cys
260 265
```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..427
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

gctcattagg gtttctcatc tacgacggcg tgggtgttcct ctttctgct ctgaaaaatg

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| gcgaagagaa | cgaagaaggt | tggaatcgtc | ggcaaatacg | gaacacgtta | tggtgcgagt  | 120 |
| atcaggaagc | agattaagaa | gatggaggtc | agccagcaca | gcaagtactt | ctgtgagttg  | 180 |
| tatctggggg | tgcaaggatt | gtggcaaggt | caaggcaggt | ggtgcttaca | caatgaacac  | 240 |
| cgccagtgcg | gtcactgtta | gaagcacgat | cagaagggtg | agggagcaga | tcgagggtta  | 300 |
| aaagtctgct | ggctttttat | atttggtttc | cttgttttga | caatttaagt | tttgcaaact  | 360 |
| ctatgcttgt | gattttgaat | caagacttat | acattgagca | gtttaagcag | gtttttatatt | 420 |
| tttggttg   |            |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ile | Arg | Val | Ser | His | Leu | Arg | Arg | Arg | Gly | Val | Pro | Pro | Ser | Cys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Glu | Lys | Trp | Arg | Arg | Glu | Arg | Arg | Arg | Leu | Glu | Ser | Ser | Ala | Asn |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Glu | His | Val | Met | Val | Arg | Val | Ser | Gly | Ser | Arg | Leu | Arg | Arg | Trp |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Ser | Ala | Ser | Thr | Ala | Ser | Thr | Ser | Val | Ser | Cys | Ile | Trp | Gly | Cys |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Lys | Asp | Cys | Gly | Lys | Val | Lys | Ala | Gly | Gly | Ala | Tyr | Thr | Met | Asn | Thr |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ala | Ser | Ala | Val | Thr | Val | Arg | Ser | Thr | Ile | Arg | Arg | Leu | Arg | Glu | Gln |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ile | Glu | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Lys | Arg | Thr | Lys | Lys | Val | Gly | Ile | Val | Gly | Lys | Tyr | Gly | Thr |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Arg | Tyr | Gly | Ala | Ser | Ile | Arg | Lys | Gln | Ile | Lys | Lys | Met | Glu | Val | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Gln | His | Ser | Lys | Tyr | Phe | Cys | Glu | Leu | Tyr | Leu | Gly | Leu | Gln | Gly | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Trp | Gln | Gly | Gln | Gly | Arg | Trp | Cys | Leu | His | Asn | Glu | His | Arg | Gln | Cys |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | His | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..63  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```
Met Val Arg Val Ser Gly Ser Arg Leu Arg Arg Trp Arg Ser Ala Ser
 1 5 10 15
Thr Ala Ser Thr Ser Val Ser Cys Ile Trp Gly Cys Lys Asp Cys Gly
 20 25 30
Lys Val Lys Ala Gly Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala Val
 35 40 45
Thr Val Arg Ser Thr Ile Arg Arg Leu Arg Glu Gln Ile Glu Gly
 50 55 60
```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..2253  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```
aaaaccacac acacagcttc ttcactgaga gcttttttct agggtttctc tctttgtttc 60
ttacaatgcg actcttcttc acaccgtcaa tgtccaatct ctccatattc ttctcgattc 120
ttctcctttc tcttctctct ccgtaaatcg gagatctcgc cgccgacaaa tccgctcttc 180
tctcttttgc ttccgccgct ggtggctcgt cattactctg ggacgtcaag caaacctcac 240
catgcaactg gaccggcgct ttatgcgacg gtggctcgtt tactgctctt cgtcttcccg 300
gtgaaacgct ctccggctcat ataccggagg gtatttttgg taatttaact cagctccgga 360
cgcttagtct ccgtctcaat ggtcttactg gttctcttcc tttggatctc ggaagatgct 420
ccgatcttcg gcgtttgtac ctgcagggtg acagattctc cggtgagatt ccggaggttt 480
tgtttagtct tagtaacctt gttaggttga atctagctga gaatgaattt agtggagaga 540
tctcgtcagg gtttaaaaac cttactaggc ttaagactct gtacctggag aataacaagc 600
tctctggctc tcttttagac ttggatttgt ctttggatca gttcaacggt tctaataact 660
tgttgaacgg atctatacct aagagtttgc agaagtttga ttctgattcg tttgtgggaa 720
cttctctctg cggcaaaccg cttgttgtct gctctaataga gggaactgtg ccaagccagc 780
caatttctgt tggcaatatt cccggaactg ttgaaggacg tgaggagaag aagaaaagga 840
agaagcttgc tgggtggagct atagctggaa tagtgattgg atgtgtggtt ggtttgctcc 900
tgattgttat gattttgatg gttctcttta ggaaaaaggg gaacgagaga acaagggcca 960
ttgaccttgc aaccatcaag caccatgaag ttgaaattcc tggcgagaaa gcggccgtgg 1020
aagcaccgga gaataggagc tatgtaaatg agtactctcc gtctgcagtg aaagctgtgg 1080
aagtgaacag ttcagggatg aagaagttag tgttttttgg gaatgcgaca aaggtcttcg 1140
atcttgagga tctgttgaga gcttcagcgg aggttctggg gaaaggaacg ttcgggacag 1200
cttataaagc ggtgcttgac gcggtgacat tgggtggctgt gaagagactg aaggatgtaa 1260
cgatggcgga cagagagttt aaggagaaga ttgaggttgt tggggcgatg gatcatgaga 1320
acttggtgcc cttgagagcg tactattaca gtggagacga gaagctgctt gtctatgact 1380
tcatgcctat gggaagctta tcagctctct tacacggaaa caaaggtgca ggccggcctc 1440
cattgaactg ggaagtcaga tcaggcatcg cccttgagac tgctcgtggc ttagactatc 1500
ttcactcaca agaccactg agctctcacg gaaacgtcaa gtcctccaat atcctcttaa 1560
caaactccca tgacgcacga gtgtctgatt tcggcctggc tcagcttgta agcgccctcat 1620
ccacaacccc aaaccggggc actgggtacc gtgcgccaga agtaactgac ccgaggcggtg 1680
tctcacgaa agcggagcgt tacagctttg gtgtgggtgt gctagagttg ctcaccggaa 1740
aagctccgct taactcgggt atgaacgagg aaggaatgga tttggcgagg tgggtgcatt 1800
cagtgccgag agaggatgg aggaatgagg tttttgactc ggagctgatg agtatcgaga 1860
cagttgtctc ggtggaagaa gagatggcgg aaatgctgca gctgggcatt gactgtacag 1920
agcagcacc agacaagcgg ccagttatgg tggaggtggg gagaaggatc caggagttgc 1980
gccaatcggg tgcagatcgg gtggggtaag accatcagat gaaaggagac ttgagacatg 2040
agtctgttcg atgatctgaa gcggcgacgt tttcagtggt tagttttaag aatatggcgg 2100
```

gaattagagt tggggtcgtt aattagatgt ttttaatttt ttttttttgt ttttttggtt 2160  
tctttcatgt gtgggcactg atgatgagga gtttcgtggt ggttgtaatt attagtgcct 2220  
ttaactttaa ctttattttc aatattgttt ttc

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..668
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | His | Thr | His | Ser | Phe | Phe | Thr | Glu | Ser | Phe | Phe | Leu | Gly | Phe | Leu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ser | Leu | Phe | Leu | Thr | Met | Arg | Leu | Phe | Thr | Pro | Ser | Met | Ser | Asn |     |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Leu | Ser | Ile | Phe | Phe | Ser | Ile | Leu | Leu | Ser | Leu | Pro | Leu | Pro | Ser |     |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Ile | Gly | Asp | Leu | Ala | Ala | Asp | Lys | Ser | Ala | Leu | Leu | Ser | Phe | Arg | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Ala | Val | Gly | Gly | Arg | Thr | Leu | Leu | Trp | Asp | Val | Lys | Gln | Thr | Ser | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Cys | Asn | Trp | Thr | Gly | Val | Leu | Cys | Asp | Gly | Arg | Val | Thr | Ala | Leu |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |  |
| Arg | Leu | Pro | Gly | Glu | Thr | Leu | Ser | Gly | His | Ile | Pro | Glu | Gly | Ile | Phe |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |  |
| Gly | Asn | Leu | Thr | Gln | Leu | Arg | Thr | Leu | Ser | Leu | Arg | Leu | Asn | Gly | Leu |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |  |
| Thr | Gly | Ser | Leu | Pro | Leu | Asp | Leu | Gly | Arg | Cys | Ser | Asp | Leu | Arg | Arg |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Tyr | Leu | Gln | Gly | Asn | Arg | Phe | Ser | Gly | Glu | Ile | Pro | Glu | Val | Leu |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Phe | Ser | Leu | Ser | Asn | Leu | Val | Arg | Leu | Asn | Leu | Ala | Glu | Asn | Glu | Phe |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Ser | Gly | Glu | Ile | Ser | Ser | Gly | Phe | Lys | Asn | Leu | Thr | Arg | Leu | Lys | Thr |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |  |
| Leu | Tyr | Leu | Glu | Asn | Asn | Lys | Leu | Ser | Gly | Ser | Leu | Leu | Asp | Leu | Asp |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |
| Leu | Ser | Leu | Asp | Gln | Phe | Asn | Val | Ser | Asn | Asn | Leu | Leu | Asn | Gly | Ser |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Ile | Pro | Lys | Ser | Leu | Gln | Lys | Phe | Asp | Ser | Asp | Ser | Phe | Val | Gly | Thr |  |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |  |
| Ser | Leu | Cys | Gly | Lys | Pro | Leu | Val | Val | Cys | Ser | Asn | Glu | Gly | Thr | Val |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |
| Pro | Ser | Gln | Pro | Ile | Ser | Val | Gly | Asn | Ile | Pro | Gly | Thr | Val | Glu | Gly |  |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |  |
| Arg | Glu | Glu | Lys | Lys | Lys | Arg | Lys | Lys | Leu | Ser | Gly | Gly | Ala | Ile | Ala |  |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |  |
| Gly | Ile | Val | Ile | Gly | Cys | Val | Val | Gly | Leu | Ser | Leu | Ile | Val | Met | Ile |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Leu | Met | Val | Leu | Phe | Arg | Lys | Lys | Gly | Asn | Glu | Arg | Thr | Arg | Ala | Ile |  |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |  |
| Asp | Leu | Ala | Thr | Ile | Lys | His | His | Glu | Val | Glu | Ile | Pro | Gly | Glu | Lys |  |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |  |
| Ala | Ala | Val | Glu | Ala | Pro | Glu | Asn | Arg | Ser | Tyr | Val | Asn | Glu | Tyr | Ser |  |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Pro | Ser | Ala | Val | Lys | Ala | Val | Glu | Val | Asn | Ser | Ser | Gly | Met | Lys | Lys |  |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |  |



Leu Val Phe Phe Gly Asn Ala Thr Lys Val Phe Asp Leu Glu Asp Leu  
370 375 380  
Leu Arg Ala Ser Ala Glu Val Leu Gly Lys Gly Thr Phe Gly Thr Ala  
385 390 395 400  
Tyr Lys Ala Val Leu Asp Ala Val Thr Leu Val Ala Val Lys Arg Leu  
405 410 415  
Lys Asp Val Thr Met Ala Asp Arg Glu Phe Lys Glu Lys Ile Glu Val  
420 425 430  
Val Gly Ala Met Asp His Glu Asn Leu Val Pro Leu Arg Ala Tyr Tyr  
435 440 445  
Tyr Ser Gly Asp Glu Lys Leu Leu Val Tyr Asp Phe Met Pro Met Gly  
450 455 460  
Ser Leu Ser Ala Leu Leu His Gly Asn Lys Gly Ala Gly Arg Pro Pro  
465 470 475 480  
Leu Asn Trp Glu Val Arg Ser Gly Ile Ala Leu Gly Ala Ala Arg Gly  
485 490 495  
Leu Asp Tyr Leu His Ser Gln Asp Pro Leu Ser Ser His Gly Asn Val  
500 505 510  
Lys Ser Ser Asn Ile Leu Leu Thr Asn Ser His Asp Ala Arg Val Ser  
515 520 525  
Asp Phe Gly Leu Ala Gln Leu Val Ser Ala Ser Ser Thr Thr Pro Asn  
530 535 540  
Arg Ala Thr Gly Tyr Arg Ala Pro Glu Val Thr Asp Pro Arg Arg Val  
545 550 555 560  
Ser Gln Lys Ala Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu Leu  
565 570 575  
Leu Thr Gly Lys Ala Pro Ser Asn Ser Val Met Asn Glu Glu Gly Met  
580 585 590  
Asp Leu Ala Arg Trp Val His Ser Val Ala Arg Glu Glu Trp Arg Asn  
595 600 605  
Glu Val Phe Asp Ser Glu Leu Met Ser Ile Glu Thr Val Val Ser Val  
610 615 620  
Glu Glu Glu Met Ala Glu Met Leu Gln Leu Gly Ile Asp Cys Thr Glu  
625 630 635 640  
Gln His Pro Asp Lys Arg Pro Val Met Val Glu Val Val Arg Arg Ile  
645 650 655  
Gln Glu Leu Arg Gln Ser Gly Ala Asp Arg Val Gly  
660 665

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 647 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..647

(D) OTHER INFORMATION: / Ceres Seq. ID 1498045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Met Arg Leu Phe Phe Thr Pro Ser Met Ser Asn Leu Ser Ile Phe Phe  
1 5 10 15  
Ser Ile Leu Leu Leu Ser Leu Pro Leu Pro Ser Ile Gly Asp Leu Ala  
20 25 30  
Ala Asp Lys Ser Ala Leu Leu Ser Phe Arg Ser Ala Val Gly Gly Arg  
35 40 45  
Thr Leu Leu Trp Asp Val Lys Gln Thr Ser Pro Cys Asn Trp Thr Gly  
50 55 60  
Val Leu Cys Asp Gly Gly Arg Val Thr Ala Leu Arg Leu Pro Gly Glu  
65 70 75 80  
Thr Leu Ser Gly His Ile Pro Glu Gly Ile Phe Gly Asn Leu Thr Gln

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |  |  |  |  |
| Leu | Arg | Thr | Leu | Ser | Leu | Arg | Leu | Asn | Gly | Leu | Thr | Gly | Ser | Leu | Pro |  |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |  |
| Leu | Asp | Leu | Gly | Arg | Cys | Ser | Asp | Leu | Arg | Arg | Leu | Tyr | Leu | Gln | Gly |  |  |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |
| Asn | Arg | Phe | Ser | Gly | Glu | Ile | Pro | Glu | Val | Leu | Phe | Ser | Leu | Ser | Asn |  |  |  |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |  |  |  |
| Leu | Val | Arg | Leu | Asn | Leu | Ala | Glu | Asn | Glu | Phe | Ser | Gly | Glu | Ile | Ser |  |  |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |
| Ser | Gly | Phe | Lys | Asn | Leu | Thr | Arg | Leu | Lys | Thr | Leu | Tyr | Leu | Glu | Asn |  |  |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |  |
| Asn | Lys | Leu | Ser | Gly | Ser | Leu | Leu | Asp | Leu | Asp | Leu | Ser | Leu | Asp | Gln |  |  |  |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |  |
| Phe | Asn | Val | Ser | Asn | Asn | Leu | Leu | Asn | Gly | Ser | Ile | Pro | Lys | Ser | Leu |  |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |
| Gln | Lys | Phe | Asp | Ser | Asp | Ser | Phe | Val | Gly | Thr | Ser | Leu | Cys | Gly | Lys |  |  |  |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |
| Pro | Leu | Val | Val | Cys | Ser | Asn | Glu | Gly | Thr | Val | Pro | Ser | Gln | Pro | Ile |  |  |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |  |
| Ser | Val | Gly | Asn | Ile | Pro | Gly | Thr | Val | Glu | Gly | Arg | Glu | Glu | Lys | Lys |  |  |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |  |  |
| Lys | Arg | Lys | Lys | Leu | Ser | Gly | Gly | Ala | Ile | Ala | Gly | Ile | Val | Ile | Gly |  |  |  |  |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |  |  |  |  |
| Cys | Val | Val | Gly | Leu | Ser | Leu | Ile | Val | Met | Ile | Leu | Met | Val | Leu | Phe |  |  |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |
| Arg | Lys | Lys | Gly | Asn | Glu | Arg | Thr | Arg | Ala | Ile | Asp | Leu | Ala | Thr | Ile |  |  |  |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |
| Lys | His | His | Glu | Val | Glu | Ile | Pro | Gly | Glu | Lys | Ala | Ala | Val | Glu | Ala |  |  |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |  |  |
| Pro | Glu | Asn | Arg | Ser | Tyr | Val | Asn | Glu | Tyr | Ser | Pro | Ser | Ala | Val | Lys |  |  |  |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |  |  |
| Ala | Val | Glu | Val | Asn | Ser | Ser | Gly | Met | Lys | Lys | Leu | Val | Phe | Phe | Gly |  |  |  |  |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |  |  |  |  |
| Asn | Ala | Thr | Lys | Val | Phe | Asp | Leu | Glu | Asp | Leu | Leu | Arg | Ala | Ser | Ala |  |  |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |  |  |
| Glu | Val | Leu | Gly | Lys | Gly | Thr | Phe | Gly | Thr | Ala | Tyr | Lys | Ala | Val | Leu |  |  |  |  |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |  |  |
| Asp | Ala | Val | Thr | Leu | Val | Ala | Val | Lys | Arg | Leu | Lys | Asp | Val | Thr | Met |  |  |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |  |  |
| Ala | Asp | Arg | Glu | Phe | Lys | Glu | Lys | Ile | Glu | Val | Val | Gly | Ala | Met | Asp |  |  |  |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |  |  |
| His | Glu | Asn | Leu | Val | Pro | Leu | Arg | Ala | Tyr | Tyr | Tyr | Ser | Gly | Asp | Glu |  |  |  |  |
|     |     | 420 |     |     |     |     | 425 |     |     |     |     |     | 430 |     |     |  |  |  |  |
| Lys | Leu | Leu | Val | Tyr | Asp | Phe | Met | Pro | Met | Gly | Ser | Leu | Ser | Ala | Leu |  |  |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |  |  |
| Leu | His | Gly | Asn | Lys | Gly | Ala | Gly | Arg | Pro | Pro | Leu | Asn | Trp | Glu | Val |  |  |  |  |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |  |  |
| Arg | Ser | Gly | Ile | Ala | Leu | Gly | Ala | Ala | Arg | Gly | Leu | Asp | Tyr | Leu | His |  |  |  |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |  |  |  |
| Ser | Gln | Asp | Pro | Leu | Ser | Ser | His | Gly | Asn | Val | Lys | Ser | Ser | Asn | Ile |  |  |  |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |  |  |  |
| Leu | Leu | Thr | Asn | Ser | His | Asp | Ala | Arg | Val | Ser | Asp | Phe | Gly | Leu | Ala |  |  |  |  |
|     |     |     | 500 |     |     |     | 505 |     |     |     |     |     | 510 |     |     |  |  |  |  |
| Gln | Leu | Val | Ser | Ala | Ser | Ser | Thr | Pro | Asn | Arg | Ala | Thr | Gly | Tyr |     |  |  |  |  |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |  |  |  |
| Arg | Ala | Pro | Glu | Val | Thr | Asp | Pro | Arg | Arg | Val | Ser | Gln | Lys | Ala | Asp |  |  |  |  |
|     |     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |  |  |  |
| Val | Tyr | Ser | Phe | Gly | Val | Val | Leu | Leu | Glu | Leu | Leu | Thr | Gly | Lys | Ala |  |  |  |  |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |  |  |  |
| Pro | Ser | Asn | Ser | Val | Met | Asn | Glu | Glu | Gly | Met | Asp | Leu | Ala | Arg | Trp |  |  |  |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |  |  |  |

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Val His Ser Val Ala Arg Glu Glu Trp Arg Asn Glu Val Phe Asp Ser  
580 585 590  
Glu Leu Met Ser Ile Glu Thr Val Val Ser Val Glu Glu Glu Met Ala  
595 600 605  
Glu Met Leu Gln Leu Gly Ile Asp Cys Thr Glu Gln His Pro Asp Lys  
610 615 620  
Arg Pro Val Met Val Glu Val Val Arg Arg Ile Gln Glu Leu Arg Gln  
625 630 635 640  
Ser Gly Ala Asp Arg Val Gly  
645

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 639 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..639

(D) OTHER INFORMATION: / Ceres Seq. ID 1498046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met Ser Asn Leu Ser Ile Phe Phe Ser Ile Leu Leu Leu Ser Leu Pro  
1 5 10 15  
Leu Pro Ser Ile Gly Asp Leu Ala Ala Asp Lys Ser Ala Leu Ser  
20 25 30  
Phe Arg Ser Ala Val Gly Gly Arg Thr Leu Leu Trp Asp Val Lys Gln  
35 40 45  
Thr Ser Pro Cys Asn Trp Thr Gly Val Leu Cys Asp Gly Gly Arg Val  
50 55 60  
Thr Ala Leu Arg Leu Pro Gly Glu Thr Leu Ser Gly His Ile Pro Glu  
65 70 75 80  
Gly Ile Phe Gly Asn Leu Thr Gln Leu Arg Thr Leu Ser Leu Arg Leu  
85 90 95  
Asn Gly Leu Thr Gly Ser Leu Pro Leu Asp Leu Gly Arg Cys Ser Asp  
100 105 110  
Leu Arg Arg Leu Tyr Leu Gln Gly Asn Arg Phe Ser Gly Glu Ile Pro  
115 120 125  
Glu Val Leu Phe Ser Leu Ser Asn Leu Val Arg Leu Asn Leu Ala Glu  
130 135 140  
Asn Glu Phe Ser Gly Glu Ile Ser Ser Gly Phe Lys Asn Leu Thr Arg  
145 150 155 160  
Leu Lys Thr Leu Tyr Leu Glu Asn Asn Lys Leu Ser Gly Ser Leu Leu  
165 170 175  
Asp Leu Asp Leu Ser Leu Asp Gln Phe Asn Val Ser Asn Asn Leu Leu  
180 185 190  
Asn Gly Ser Ile Pro Lys Ser Leu Gln Lys Phe Asp Ser Asp Ser Phe  
195 200 205  
Val Gly Thr Ser Leu Cys Gly Lys Pro Leu Val Val Cys Ser Asn Glu  
210 215 220  
Gly Thr Val Pro Ser Gln Pro Ile Ser Val Gly Asn Ile Pro Gly Thr  
225 230 235 240  
Val Glu Gly Arg Glu Lys Lys Lys Arg Lys Lys Leu Ser Gly Gly  
245 250 255  
Ala Ile Ala Gly Ile Val Ile Gly Cys Val Val Gly Leu Ser Leu Ile  
260 265 270  
Val Met Ile Leu Met Val Leu Phe Arg Lys Lys Gly Asn Glu Arg Thr  
275 280 285  
Arg Ala Ile Asp Leu Ala Thr Ile Lys His His Glu Val Glu Ile Pro  
290 295 300  
Gly Glu Lys Ala Ala Val Glu Ala Pro Glu Asn Arg Ser Tyr Val Asn

305 310 315 320  
Glu Tyr Ser Pro Ser Ala Val Lys Ala Val Glu Val Asn Ser Ser Gly  
325 330 335  
Met Lys Lys Leu Val Phe Phe Gly Asn Ala Thr Lys Val Phe Asp Leu  
340 345 350  
Glu Asp Leu Leu Arg Ala Ser Ala Glu Val Leu Gly Lys Gly Thr Phe  
355 360 365  
Gly Thr Ala Tyr Lys Ala Val Leu Asp Ala Val Thr Leu Val Ala Val  
370 375 380  
Lys Arg Leu Lys Asp Val Thr Met Ala Asp Arg Glu Phe Lys Glu Lys  
385 390 395 400  
Ile Glu Val Val Gly Ala Met Asp His Glu Asn Leu Val Pro Leu Arg  
405 410 415  
Ala Tyr Tyr Tyr Ser Gly Asp Glu Lys Leu Leu Val Tyr Asp Phe Met  
420 425 430  
Pro Met Gly Ser Leu Ser Ala Leu Leu His Gly Asn Lys Gly Ala Gly  
435 440 445  
Arg Pro Pro Leu Asn Trp Glu Val Arg Ser Gly Ile Ala Leu Gly Ala  
450 455 460  
Ala Arg Gly Leu Asp Tyr Leu His Ser Gln Asp Pro Leu Ser Ser His  
465 470 475 480  
Gly Asn Val Lys Ser Ser Asn Ile Leu Leu Thr Asn Ser His Asp Ala  
485 490 495  
Arg Val Ser Asp Phe Gly Leu Ala Gln Leu Val Ser Ala Ser Ser Thr  
500 505 510  
Thr Pro Asn Arg Ala Thr Gly Tyr Arg Ala Pro Glu Val Thr Asp Pro  
515 520 525  
Arg Arg Val Ser Gln Lys Ala Asp Val Tyr Ser Phe Gly Val Val Leu  
530 535 540  
Leu Glu Leu Leu Thr Gly Lys Ala Pro Ser Asn Ser Val Met Asn Glu  
545 550 555 560  
Glu Gly Met Asp Leu Ala Arg Trp Val His Ser Val Ala Arg Glu Glu  
565 570 575  
Trp Arg Asn Glu Val Phe Asp Ser Glu Leu Met Ser Ile Glu Thr Val  
580 585 590  
Val Ser Val Glu Glu Glu Met Ala Glu Met Leu Gln Leu Gly Ile Asp  
595 600 605  
Cys Thr Glu Gln His Pro Asp Lys Arg Pro Val Met Val Glu Val Val  
610 615 620  
Arg Arg Ile Gln Glu Leu Arg Gln Ser Gly Ala Asp Arg Val Gly  
625 630 635

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..852
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acaccatcca | ctctactcaa | catggactcc | tccaaactct | catctctctc | tctttgcctc | 60  |
| ttcctcattt | gcattatcta | tctcccccaa | cattctctcg | catgcggtc  | ttgcaaccca | 120 |
| cggaagggcg | gaaagcactc | ccctaaagcc | cctaagctac | cagttcctcc | ggtgaccgtc | 180 |
| cctaagctac | cagttcctcc | ggtgaccgtc | cctaagctac | cagtcctcc  | ggtgaccgtc | 240 |
| cctaagctac | ccgttcctcc | tgtgamcatc | cctaagctac | ccgttcacc  | agtgactgta | 300 |
| cctaagctac | ccgttcctcc | tgtgaccgtc | cccaagctac | ccgttcctcc | agtgaccgtc | 360 |
| cccaaggagg | aacgggtagc | ttaggtacag | tactggtg   | aacgggtagc | ttaggggtg  | 420 |
| tcacggagkg | ggaggaggcc | acggacatgg | aggacacaac | ggaggagggg | gccacggact | 480 |

tgacggatac ggaggaggtg gaggacacta tggaggaggt ggaggacact acggaggagg 540  
tggaggacac tacgaaggag gtgaggacac tacggaggag gtggtggagg acacggaggt 600  
ggaggacact acggaggtgg tggaggagga tacggaggtg gaggaggaca ccacggagga 660  
ggaggccacg ggctaaacga acctgttcag actaagccgg gtgtttaaaa ctatataata 720  
ycttcactac catgcatgat tgcataatata tatatacgct tatgtattat ctatatgcct 780  
ataaataaac catggtgagt ttgtaacgca gtgccttcag aaatgttcgg aataaatttc 840  
cataatatta gt

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1498048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Thr Pro Ser Thr Leu Asn Met Asp Ser Ser Lys Leu Ser Ser Leu  
1 5 10 15  
Ser Leu Cys Leu Phe Leu Ile Cys Ile Ile Tyr Leu Pro Gln His Ser  
20 25 30  
Leu Ala Cys Gly Ser Cys Asn Pro Arg Lys Gly Gly Lys His Ser Pro  
35 40 45  
Lys Ala Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro  
50 55 60  
Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr Val  
65 70 75 80  
Pro Lys Leu Pro Val Pro Pro Val Xaa Ile Pro Lys Leu Pro Val Pro  
85 90 95  
Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys  
100 105 110  
Leu Pro Val Pro Pro Val Thr Val Pro Lys Glu Glu Arg Val Ala  
115 120 125

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1498049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Met Asp Ser Ser Lys Leu Ser Ser Leu Ser Leu Cys Leu Phe Leu Ile  
1 5 10 15  
Cys Ile Ile Tyr Leu Pro Gln His Ser Leu Ala Cys Gly Ser Cys Asn  
20 25 30  
Pro Arg Lys Gly Gly Lys His Ser Pro Lys Ala Pro Lys Leu Pro Val  
35 40 45  
Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro  
50 55 60  
Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro  
65 70 75 80  
Val Xaa Ile Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu  
85 90 95  
Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr  
100 105 110

Val Pro Lys Glu Glu Arg Val Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu
1 5 10 15
Glu Val Glu Asp Thr Met Glu Glu Val Glu Asp Thr Thr Glu Glu Val
 20 25 30
Glu Asp Thr Thr Lys Glu Val Arg Thr Leu Arg Arg Arg Trp Trp Arg
 35 40 45
Thr Arg Arg Trp Arg Thr Leu Arg Arg Trp Trp Arg Arg Ile Arg Arg
 50 55 60
Trp Arg Arg Thr Pro Arg Arg Arg Arg Pro Arg Ala Lys Arg Thr Cys
65 70 75 80
Ser Asp
```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1095
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```
gtagatcttt ttctgctctt tctctctctc tctctctctc tctctctctc tctctcttgt 60
attatttcta tctccccgc cgtcgaaaga gaaacgtcga tcggagaacc tttgaaatgt 120
cgactggatt agatatgtct ctgcagcaca tgatcgccaa gaaccgtaag tctcgtggtg 180
gagccggccc cgctcgtgga accggtatcg gatccggacc ggggccgact cgccgcaaca 240
accctaatac gaaatcaacc cgatctgctc cataccaatc agccaaggcg ccggagtcca 300
cctgggggtca cgacatgttc tccgatagat ctgaagatca ccgatcggga cgttcctccg 360
ccggaatcga aactggaacc aagctctaca tttccaattt ggattacggt gtcataaacg 420
aagacatcaa ggaactgttt gctgaagtgt gagaacttaa acgctacaca gttcattttg 480
atagaagtgg aagatcaaag ggaactgctg aagtagtgta ttctcggcgt ggcgatgcac 540
tcgcagctgt gaagaagtat aatgatgttc agctggatgg aaaacccatg aagatagaga 600
ttgtgggcac taatcttcaa actgctgcag ccccgctctg tagacctgcg aatggaaact 660
ccaatggtgc tccatggaga ggaggacaag ggagaggagg tcaacgaggt ggtggacgag 720
gaggcgggtg ccgaggtggt ggtggctcgt gtaggcgtcc tggttaagggc cctgcagaga 780
agatttctgc ggaagatctt gatgcggatc ttgataagta ccattctgga gatattgaga 840
caaactaagg aacgtgactg atcttctcaa accggtaggg gttttaggag gaagagaatc 900
gagaaaatgt ttgccagagg ctttaccact tagcgccttt ttggctgtgt tgttcatttg 960
tttcattaga atgactttac agaattgaga atatgtgtta tttaaagtgt ttgtctatct 1020
taataccctc aagtgaagg cagaggaagg aataccaatt tcgtttacag atcatatgca 1080
ggcaaaagag ttttc
```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..281  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498052  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Phe | Ser | Ala | Leu | Ser | Leu | Ser | Leu | Ser | Leu | Ser | Leu | Ser | Leu |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| Ser | Leu | Leu | Tyr | Phe | Tyr | Leu | Pro | Arg | Arg | Arg | Lys | Arg | Asn | Val |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Asp | Arg | Arg | Thr | Phe | Glu | Met | Ser | Thr | Gly | Leu | Asp | Met | Ser | Leu | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Asp | Met | Ile | Ala | Lys | Asn | Arg | Lys | Ser | Arg | Gly | Gly | Ala | Gly | Pro | Ala |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Arg | Gly | Thr | Gly | Ser | Gly | Ser | Gly | Pro | Gly | Pro | Thr | Arg | Arg | Asn | Asn |
| 65  |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Pro | Asn | Arg | Lys | Ser | Thr | Arg | Ser | Ala | Pro | Tyr | Gln | Ser | Ala | Lys | Ala |
|     |     |     | 85  |     |     |     |     |     |     |     | 90  |     |     |     | 95  |
| Pro | Glu | Ser | Thr | Trp | Gly | His | Asp | Met | Phe | Ser | Asp | Arg | Ser | Glu | Asp |
|     |     |     | 100 |     |     |     |     |     |     |     | 105 |     |     |     | 110 |
| His | Arg | Ser | Gly | Arg | Ser | Ser | Ala | Gly | Ile | Glu | Thr | Gly | Thr | Lys | Leu |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     | 125 |
| Tyr | Ile | Ser | Asn | Leu | Asp | Tyr | Gly | Val | Met | Asn | Glu | Asp | Ile | Lys | Glu |
|     |     |     | 130 |     |     |     |     |     |     |     |     |     |     |     | 140 |
| Leu | Phe | Ala | Glu | Val | Gly | Glu | Leu | Lys | Arg | Tyr | Thr | Val | His | Phe | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 160 |
| Arg | Ser | Gly | Arg | Ser | Lys | Gly | Thr | Ala | Glu | Val | Val | Tyr | Ser | Arg | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 175 |
| Gly | Asp | Ala | Leu | Ala | Ala | Val | Lys | Lys | Tyr | Asn | Asp | Val | Gln | Leu | Asp |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     | 190 |
| Gly | Lys | Pro | Met | Lys | Ile | Glu | Ile | Val | Gly | Thr | Asn | Leu | Gln | Thr | Ala |
|     |     |     | 195 |     |     |     |     |     |     |     |     |     |     |     | 205 |
| Ala | Ala | Pro | Ser | Gly | Arg | Pro | Ala | Asn | Gly | Asn | Ser | Asn | Gly | Ala | Pro |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 220 |
| Trp | Arg | Gly | Gly | Gln | Gly | Arg | Gly | Gly | Gln | Arg | Gly | Gly | Gly | Arg | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 240 |
| Gly | Gly | Gly | Arg | Gly | Gly | Gly | Gly | Arg | Gly | Arg | Arg | Pro | Gly | Lys | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 255 |
| Pro | Ala | Glu | Lys | Ile | Ser | Ala | Glu | Asp | Leu | Asp | Ala | Asp | Leu | Asp | Lys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 270 |
| Tyr | His | Ser | Gly | Asp | Met | Glu | Thr | Asn |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 280 |

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 243 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..243  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498053  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Gly | Leu | Asp | Met | Ser | Leu | Asp | Asp | Met | Ile | Ala | Lys | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Lys | Ser | Arg | Gly | Gly | Ala | Gly | Pro | Ala | Arg | Gly | Thr | Gly | Ser | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Pro | Gly | Pro | Thr | Arg | Arg | Asn | Asn | Pro | Asn | Arg | Lys | Ser | Thr |

|                         |                         |                     |
|-------------------------|-------------------------|---------------------|
| 35                      | 40                      | 45                  |
| Arg Ser Ala Pro Tyr Gln | Ser Ala Lys Ala Pro Glu | Ser Thr Trp Gly     |
| 50                      | 55                      | 60                  |
| His Asp Met Phe Ser Asp | Arg Ser Glu Asp His Arg | Ser Gly Arg Ser     |
| 65                      | 70                      | 75                  |
| Ser Ala Gly Ile Glu Thr | Gly Thr Lys Leu Tyr Ile | Ser Asn Leu Asp     |
| 85                      | 90                      | 95                  |
| Tyr Gly Val Met Asn Glu | Asp Ile Lys Glu Leu Phe | Ala Glu Val Gly     |
| 100                     | 105                     | 110                 |
| Glu Leu Lys Arg Tyr Thr | Val His Phe Asp Arg Ser | Gly Arg Ser Lys     |
| 115                     | 120                     | 125                 |
| Gly Thr Ala Glu Val Val | Tyr Ser Arg Arg Gly Asp | Ala Leu Ala Ala     |
| 130                     | 135                     | 140                 |
| Val Lys Lys Tyr Asn Asp | Val Gln Leu Asp Gly Lys | Pro Met Lys Ile     |
| 145                     | 150                     | 155                 |
| Glu Ile Val Gly Thr Asn | Leu Gln Thr Ala Ala     | Pro Ser Gly Arg     |
| 165                     | 170                     | 175                 |
| Pro Ala Asn Gly Asn Ser | Asn Gly Ala Pro Trp     | Arg Gly Gly Gln Gly |
| 180                     | 185                     | 190                 |
| Arg Gly Gly Gln Arg Gly | Gly Gly Arg Gly Gly Gly | Gly Arg Gly Gly     |
| 195                     | 200                     | 205                 |
| Gly Gly Arg Gly Arg Arg | Pro Gly Lys Gly Pro     | Ala Glu Lys Ile Ser |
| 210                     | 215                     | 220                 |
| Ala Glu Asp Leu Asp Ala | Asp Leu Asp Lys Tyr     | His Ser Gly Asp Met |
| 225                     | 230                     | 235                 |
| Glu Thr Asn             |                         |                     |

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..237
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Met Ser Leu Asp Asp Met Ile Ala Lys Asn Arg Lys Ser Arg Gly Gly |             |
| 1                                                               | 5 10 15     |
| Ala Gly Pro Ala Arg Gly Thr Gly Ser Gly Ser Gly Pro Gly Pro Thr |             |
|                                                                 | 20 25 30    |
| Arg Arg Asn Asn Pro Asn Arg Lys Ser Thr Arg Ser Ala Pro Tyr Gln |             |
|                                                                 | 35 40 45    |
| Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly His Asp Met Phe Ser Asp |             |
| 50                                                              | 55 60       |
| Arg Ser Glu Asp His Arg Ser Gly Arg Ser Ser Ala Gly Ile Glu Thr |             |
| 65                                                              | 70 75 80    |
| Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Tyr Gly Val Met Asn Glu |             |
|                                                                 | 85 90 95    |
| Asp Ile Lys Glu Leu Phe Ala Glu Val Gly Glu Leu Lys Arg Tyr Thr |             |
|                                                                 | 100 105 110 |
| Val His Phe Asp Arg Ser Gly Arg Ser Lys Gly Thr Ala Glu Val Val |             |
|                                                                 | 115 120 125 |
| Tyr Ser Arg Arg Gly Asp Ala Leu Ala Ala Val Lys Lys Tyr Asn Asp |             |
|                                                                 | 130 135 140 |
| Val Gln Leu Asp Gly Lys Pro Met Lys Ile Glu Ile Val Gly Thr Asn |             |
| 145                                                             | 150 155 160 |
| Leu Gln Thr Ala Ala Ala Pro Ser Gly Arg Pro Ala Asn Gly Asn Ser |             |
|                                                                 | 165 170 175 |



Asn Gly Ala Pro Trp Arg Gly Gly Gln Gly Arg Gly Gly Gln Arg Gly  
180 185 190  
Gly Gly Arg Gly Gly Gly Gly Arg Gly Gly Gly Arg Gly Arg Arg  
195 200 205  
Pro Gly Lys Gly Pro Ala Glu Lys Ile Ser Ala Glu Asp Leu Asp Ala  
210 215 220  
Asp Leu Asp Lys Tyr His Ser Gly Asp Met Glu Thr Asn  
225 230 235

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..539
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| scagcggttc cyggtcaagc acctcctttt aacaacaagc tttgcgacat aagacacgtg  | 60  |
| tcaagcaggg acgagaacgt taagagacgg agccgtggtg catgcaagga agagagaaac  | 120 |
| gtgaggtctt tgagtcatga gtcgtcactg agtcacgagt caccggtgtc ttctgaggag  | 180 |
| acgacgacgg aggaaccaa gacttggatc gggcttgagc tgactttggg gttggagcct   | 240 |
| ttagcacgtg gaaatcacgt ggtggtaccg atgaagaaaa gaaagttaga gaggtgtggc  | 300 |
| acgtctgagg atgaggacac gtgtaagatt gagcttggac tgggtgtgcag tgagtgaatg | 360 |
| gttctttttt tgtggctggt ctttaattaca agttttggtg ttgagtttta ggtgtacaaa | 420 |
| tagagattaa cgaatctctc ttttttctct ttttgagttt tatgttttgk tttgktttct  | 480 |
| tttgcattgt cggtgttctt cataaatatg tatgatgaat gataaagagg tcttaactt   |     |

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Xaa Ala Val Xaa Gly Gln Ala Pro Pro Phe Asn Asn Lys Leu Cys Asp |  |
| 1 5 10 15                                                       |  |
| Ile Arg His Val Ser Ser Arg Asp Glu Asn Val Lys Arg Arg Ser Arg |  |
| 20 25 30                                                        |  |
| Gly Ala Cys Lys Glu Glu Arg Asn Val Arg Ser Leu Ser His Glu Ser |  |
| 35 40 45                                                        |  |
| Ser Leu Ser His Glu Ser Pro Val Ser Ser Glu Glu Thr Thr Thr Glu |  |
| 50 55 60                                                        |  |
| Glu Pro Lys Thr Trp Ile Gly Leu Glu Leu Thr Leu Gly Leu Glu Pro |  |
| 65 70 75 80                                                     |  |
| Leu Ala Arg Gly Asn His Val Val Val Pro Met Lys Lys Arg Lys Leu |  |
| 85 90 95                                                        |  |
| Glu Arg Cys Gly Thr Ser Glu Asp Glu Asp Thr Cys Lys Ile Glu Leu |  |
| 100 105 110                                                     |  |
| Gly Leu Val Cys Ser Glu                                         |  |
| 115                                                             |  |

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..676
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaaaaaaaca aaaagatctg aaacaaaaat ggtgaatcaa agaaagctac aagaagaaga | 60  |
| agagcgaaaaa ggagaattat cctctcatta caaccaaagt agttgagtat ttgcagccag | 120 |
| taatgtgtcg agagcttctc tgcaaatttc cagataactc tgcttttgga ttcgactact  | 180 |
| cacagagctc tctttggtct cctctcttgc ctcgaaatta cgccagtcct tcagatctag  | 240 |
| actccgacag ttgcgtttgt cggaatctta agctagggga gtttcaagta ggcaagaaga  | 300 |
| agaagatgaa gatgatgtca atgaagaaga acaagaagaa gagtaaatta ctgaaactag  | 360 |
| acataccttc aatgaagaat gatgattctt ctctctaaaat tggctgtttt cctcttccta | 420 |
| ccaagggatg gaatgggtgtg ttaaaggcag cttcaaaaca tttcaagaaa tcgaaaaaga | 480 |
| agagagattc attcgctgat gccaaagcttc tcgacttcaa atactaagat tatagcaact | 540 |
| tcaattgctt ttcattgtat tcaataatta ctagaccttt gatgaattgt gaagttgagc  | 600 |
| tgtttctatt atggtcattca tgtaatcatt tggagtgttt gatcatagat atatccatga | 660 |
| ctgcttttga tttctg                                                  |     |

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 134 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..134
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Cys Arg Glu Leu Cys Lys Phe Pro Asp Asn Ser Ala Phe Gly     |  |
| 1 5 10 15                                                       |  |
| Phe Asp Tyr Ser Gln Ser Ser Leu Trp Ser Pro Leu Leu Pro Arg Asn |  |
| 20 25 30                                                        |  |
| Tyr Ala Ser Pro Ser Asp Leu Asp Ser Asp Ser Cys Val Cys Arg Asn |  |
| 35 40 45                                                        |  |
| Leu Lys Leu Gly Glu Phe Gln Val Gly Lys Lys Lys Lys Met Lys Met |  |
| 50 55 60                                                        |  |
| Met Ser Met Lys Lys Asn Lys Lys Lys Ser Lys Leu Leu Lys Leu Asp |  |
| 65 70 75 80                                                     |  |
| Ile Pro Ser Met Lys Asn Asp Asp Ser Ser Pro Lys Ile Gly Cys Phe |  |
| 85 90 95                                                        |  |
| Pro Leu Pro Thr Lys Gly Trp Asn Gly Val Leu Lys Ala Ala Ser Lys |  |
| 100 105 110                                                     |  |
| His Phe Lys Lys Ser Lys Lys Lys Arg Asp Ser Phe Ala Asp Ala Lys |  |
| 115 120 125                                                     |  |
| Leu Leu Asp Phe Lys Tyr                                         |  |
| 130                                                             |  |

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 73 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..73
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Met Lys Met Met Ser Met Lys Lys Asn Lys Lys Lys Ser Lys Leu Leu  
1 5 10 15  
Lys Leu Asp Ile Pro Ser Met Lys Asn Asp Asp Ser Ser Pro Lys Ile  
20 25 30  
Gly Cys Phe Pro Leu Pro Thr Lys Gly Trp Asn Gly Val Leu Lys Ala  
35 40 45  
Ala Ser Lys His Phe Lys Lys Ser Lys Lys Lys Arg Asp Ser Phe Ala  
50 55 60  
Asp Ala Lys Leu Leu Asp Phe Lys Tyr  
65 70

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1498066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Met Met Ser Met Lys Lys Asn Lys Lys Lys Ser Lys Lys Leu Leu Lys Leu  
1 5 10 15  
Asp Ile Pro Ser Met Lys Asn Asp Asp Ser Ser Pro Lys Ile Gly Cys  
20 25 30  
Phe Pro Leu Pro Thr Lys Gly Trp Asn Gly Val Leu Lys Ala Ala Ser  
35 40 45  
Lys His Phe Lys Lys Ser Lys Lys Lys Arg Asp Ser Phe Ala Asp Ala  
50 55 60  
Lys Leu Leu Asp Phe Lys Tyr  
65 70

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..869

(D) OTHER INFORMATION: / Ceres Seq. ID 1498067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aacattctca gagaagccgt cttcttcctc cttcaatctc tctcggttcgt atcatctgct | 60  |
| ctgcgatttc aatggcgagc cgttggttga gacctgaggt gtatcctttg ttcgctgcta  | 120 |
| ccggagttgc cgttgggagc tgtgcgtttt ccttgatcag aaacatcacc ggaaaccctg  | 180 |
| aagtcagatg caccaaggag aacagggctg ctggaatttt ggataaccat gcagagggag  | 240 |
| agaagtataa ggaaaatttc ctgaggaaga ggaattaggt ttatccgacg tgattctcag  | 300 |
| gttttcttgt ttcttaactc aaaatgtaag aggtacttcc ataacaagtt gaagccatcc  | 360 |
| aagcttgcat ggactgccat gtacagaaag caacacaaga aggatgcagc acaagaggct  | 420 |
| gtgaagagaa ggagacgtgc caccaagaag ccatactcaa ggtccattgt tgggtgctacc | 480 |
| ttggaagtaa ttcagaagaa gagagctgag aagcctgaag ttcgtgatgc agccagggaa  | 540 |
| gctgctctgc gtgagatcaa ggaaagaatc aaaaagacca aagatgaaaa gaaggctaag  | 600 |
| aagtggaat ttgcttctaa gcaacagaag gtcaggcta atttcccaa agctgctgct     | 660 |
| gcatccaagg gtcctaagggt gggagggtgt ggtggcaaac gctgaagagc ttaaagccat | 720 |
| cttttctcac tctgcgtctt ttctgctagt agctactttt agtagttgat gttcatttct  | 780 |
| gaatatttgc aaaacataaa ccttgttatt ttcgtttttg tctctcactt ttgctactct  | 840 |
| tataatatca gacttgagaa ttttgctgc                                    |     |

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 91 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..91  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498068  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

His Ser Gln Arg Ser Arg Leu Leu Pro Pro Ser Ile Ser Leu Val Arg  
1                  5                  10                  15  
Ile Ile Cys Ser Ala Ile Ser Met Ala Ser Arg Trp Leu Arg Pro Glu  
                  20                  25                  30  
Val Tyr Pro Leu Phe Ala Ala Thr Gly Val Ala Val Gly Ile Cys Ala  
                  35                  40                  45  
Phe Ser Leu Ile Arg Asn Ile Thr Gly Asn Pro Glu Val Arg Cys Thr  
                  50                  55                  60  
Lys Glu Asn Arg Ala Ala Gly Ile Leu Asp Asn His Ala Glu Gly Glu  
65                  70                  75                  80  
Lys Tyr Lys Glu Asn Phe Leu Arg Lys Arg Asn  
                  85                  90

- (2) INFORMATION FOR SEQ ID NO:163:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 108 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..108  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498069  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Met Tyr Arg Lys Gln His Lys Lys Asp Ala Ala Gln Glu Ala Val Lys  
1                  5                  10                  15  
Arg Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly  
                  20                  25                  30  
Ala Thr Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val  
                  35                  40                  45  
Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile  
                  50                  55                  60  
Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Val Glu Phe Ala Ser  
65                  70                  75                  80  
Lys Gln Gln Lys Val Lys Ala Asn Phe Pro Lys Ala Ala Ala Ala Ser  
                  85                  90                  95  
Lys Gly Pro Lys Val Gly Gly Gly Gly Gly Lys Arg  
                  100                  105

- (2) INFORMATION FOR SEQ ID NO:164:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 80 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..80  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498070  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met Gln Pro Gly Lys Leu Leu Cys Val Arg Ser Arg Lys Glu Ser Lys  
1 5 10 15  
Arg Pro Lys Met Lys Arg Arg Leu Arg Arg Trp Asn Leu Leu Leu Ser  
20 25 30  
Asn Arg Arg Ser Arg Leu Ile Ser Pro Lys Leu Leu Leu His Pro Arg  
35 40 45  
Val Leu Arg Trp Glu Val Val Val Ala Asn Ala Glu Glu Leu Lys Ala  
50 55 60  
Ile Phe Ser His Ser Ala Ser Phe Leu Leu Val Ala Thr Phe Ser Ser  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

accaccgaaa cccactaaga atacagcaaa tcgtctcttc gccattaaaa caccttcctt 60  
tgcaaacaaa gcttcaaact ttctcttaaa acacccccaa atcagcaaag ataggggttaa 120  
tcgaagaacc tcaccgtaag tccactgagg attcaagttc ttgctttggt ttaaggaaga 180  
agaacagcaa aaacctcaag gagaagaaga agtcaaagat gactcagagt caaaccaacg 240  
acggagctgg agctggagct gttacgacgg tagaatctgt tcctcctcag cctcaatctc 300  
agcctcagcc tcagccgcag cagcagacga acgagatggt tctgcatacg ggaagcttga 360  
gttttagtag tcatatgtcg agagaagacg aagagatgac tcgttctgct ctttcggcgt 420  
ttagagctaa agaagatgag attgagaaga ggaggatgga agttcgtgaa cggatccaag 480  
ctcaattggg tcgggtcgaa caagaaacca aacgtctctc tactattcgt gaggagcttg 540  
agtctatggc agatcctatg aggaaggaag tttctgtggt tcgtaagaag attgatagtg 600  
ttaacaaaga actcaaacct ctagggttcca ctgttcaaaa gaaggaaagg gaatacaaaag 660  
aagcacttga tgayattcaa cgagaagaac agggagaaaag tacagctgat cacaaaactc 720  
atggagatgg aacagttggt tggagaaagc gagaagtga ggatgattaa gctggaggag 780  
ctgagcaaga gcatagaaac cgtgtgaaaa aggttggttca agaagaacta attgggttct 840  
tttgtgtgat gtacctacct agtttaaaat tttcatcatg taagatgtgt ggggttgctt 900  
tttttttatt gbtatagttt ttttaaagtc tttgggggtt tgatttgtaa aatttgkggg 960  
ttctctcttw tttttgatta accaaattta gggatatggg aaaatgggag attcttagga 1020  
tactgaaact catcacagtg attattcttt ctttctctgt attatgtttt gtatctgtct 1080  
tttgaagaat ttattatttt tttt

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..183  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met Thr Gln Ser Gln Thr Asn Asp Gly Ala Gly Ala Val Thr  
1 5 10 15  
Thr Val Glu Ser Val Pro Pro Gln Pro Gln Ser Gln Pro Gln Pro Gln  
20 25 30  
Pro Gln Gln Gln Ser Asn Glu Met Val Leu His Thr Gly Ser Leu Ser  
35 40 45

Phe Ser Ser His Met Ser Arg Glu Asp Glu Glu Met Thr Arg Ser Ala  
50 55 60  
Leu Ser Ala Phe Arg Ala Lys Glu Asp Glu Ile Glu Lys Arg Arg Met  
65 70 75 80  
Glu Val Arg Glu Arg Ile Gln Ala Gln Leu Gly Arg Val Glu Gln Glu  
85 90 95  
Thr Lys Arg Leu Ser Thr Ile Arg Glu Leu Glu Ser Met Ala Asp  
100 105 110  
Pro Met Arg Lys Glu Val Ser Val Val Arg Lys Lys Ile Asp Ser Val  
115 120 125  
Asn Lys Glu Leu Lys Pro Leu Gly Ser Thr Val Gln Lys Lys Glu Arg  
130 135 140  
Glu Tyr Lys Glu Ala Leu Asp Xaa Ile Gln Arg Glu Glu Gln Gly Glu  
145 150 155 160  
Ser Thr Ala Asp His Lys Thr His Gly Asp Gly Thr Val Gly Trp Arg  
165 170 175  
Lys Arg Glu Val Glu Asp Asp  
180

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Met Val Leu His Thr Gly Ser Leu Ser Phe Ser Ser His Met Ser Arg  
1 5 10 15  
Glu Asp Glu Glu Met Thr Arg Ser Ala Leu Ser Ala Phe Arg Ala Lys  
20 25 30  
Glu Asp Glu Ile Glu Lys Arg Arg Met Glu Val Arg Glu Arg Ile Gln  
35 40 45  
Ala Gln Leu Gly Arg Val Glu Gln Glu Thr Lys Arg Leu Ser Thr Ile  
50 55 60  
Arg Glu Glu Leu Glu Ser Met Ala Asp Pro Met Arg Lys Glu Val Ser  
65 70 75 80  
Val Val Arg Lys Lys Ile Asp Ser Val Asn Lys Glu Leu Lys Pro Leu  
85 90 95  
Gly Ser Thr Val Gln Lys Lys Glu Arg Glu Tyr Lys Glu Ala Leu Asp  
100 105 110  
Xaa Ile Gln Arg Glu Glu Gln Gly Glu Ser Thr Ala Asp His Lys Thr  
115 120 125  
His Gly Asp Gly Thr Val Gly Trp Arg Lys Arg Glu Val Glu Asp Asp  
130 135 140

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ser Arg Glu Asp Glu Glu Met Thr Arg Ser Ala Leu Ser Ala Phe  
1 5 10 15  
Arg Ala Lys Glu Asp Glu Ile Glu Lys Arg Arg Met Glu Val Arg Glu  
20 25 30  
Arg Ile Gln Ala Gln Leu Gly Arg Val Glu Gln Glu Thr Lys Arg Leu  
35 40 45  
Ser Thr Ile Arg Glu Glu Leu Glu Ser Met Ala Asp Pro Met Arg Lys  
50 55 60  
Glu Val Ser Val Val Arg Lys Lys Ile Asp Ser Val Asn Lys Glu Leu  
65 70 75 80  
Lys Pro Leu Gly Ser Thr Val Gln Lys Lys Glu Arg Glu Tyr Lys Glu  
85 90 95  
Ala Leu Asp Xaa Ile Gln Arg Glu Glu Gln Gly Glu Ser Thr Ala Asp  
100 105 110  
His Lys Thr His Gly Asp Gly Thr Val Gly Trp Arg Lys Arg Glu Val  
115 120 125  
Glu Asp Asp  
130

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..757
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| aaccaaaaaca | aaacataaaaa | aaacaagtgg | aagcttttaa | acgagagggga | gagagcaaaa | 60  |
| atggcgacgt  | cgggaacgta  | cgtgacggaa | gttccgctaa | aaggatcggc  | cgagaaatac | 120 |
| tacaagaggt  | ggaagaacga  | gaaccatgtc | ttccctgatg | ctatcggcca  | ccacatccaa | 180 |
| aatgttaccg  | ttcacgaagg  | cgaacatgac | tctcacgggt | ctatcaggag  | ttggaactac | 240 |
| acatgggatg  | gaaaggagga  | ggtgttcaag | gagagaagag | agatagacga  | tgagaccaaa | 300 |
| acgttgacgt  | taagaggact  | tgagggtcac | gtgatggagc | agctcaaagt  | gtacgacgtc | 360 |
| gtctaccaat  | tcattcccaa  | atctgaggat | acctgcacgc | gcaaaatcac  | tttaatatgg | 420 |
| gagaagcgca  | acgatgattc  | cccagaacca | agcggctaca | tgaaattcgt  | caagagcttg | 480 |
| gttgctgaca  | tgggaaacca  | cgttagcaaa | acttaatcat | cattcccaca  | gtcgtcgtcg | 540 |
| tcgtcatcat  | catcatcatc  | atcatcatca | tcacatcatc | catcatcatc  | atcatcrtca | 600 |
| tcactatctc  | gatttataag  | ttaagatggt | ttcagtataa | taaatggggg  | cttgtggatc | 660 |
| gttcatttct  | atgtgtaaac  | cgtttggttc | tgtatgatgc | ttcgatatat  | tgttatgttc | 720 |
| atgatcatat  | gtcgggttcg  | atataatgat | tcttaag    |             |            |     |

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser  
1 5 10 15  
Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro  
20 25 30  
Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| His Asp Ser His Gly Ser Ile Arg Ser Trp Asn Tyr Thr Trp Asp Gly |     |     |
| 50                                                              | 55  | 60  |
| Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Glu Thr Lys |     |     |
| 65                                                              | 70  | 75  |
| Thr Leu Thr Leu Arg Gly Leu Glu Gly His Val Met Glu Gln Leu Lys |     |     |
| 85                                                              | 90  | 95  |
| Val Tyr Asp Val Val Tyr Gln Phe Ile Pro Lys Ser Glu Asp Thr Cys |     |     |
| 100                                                             | 105 | 110 |
| Ile Gly Lys Ile Thr Leu Ile Trp Glu Lys Arg Asn Asp Asp Ser Pro |     |     |
| 115                                                             | 120 | 125 |
| Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Ser Leu Val Ala Asp Met |     |     |
| 130                                                             | 135 | 140 |
| Gly Asn His Val Ser Lys Thr                                     |     |     |
| 145                                                             | 150 |     |

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1944 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1944
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

|            |             |             |            |            |             |      |
|------------|-------------|-------------|------------|------------|-------------|------|
| atcccaaaag | gagaaaaaca  | aacmaaaaaa  | caagaacaaa | acaaaaacca | aaaaaacaaa  | 60   |
| aaaataaatg | gcaagaattt  | cactagggat  | atgtctgatg | ttagtagtag | catcaagtgt  | 120  |
| gatctatgaa | gcgcaaggaa  | cgttcttact  | aaaccattac | ttgaagaaga | attttccaaa  | 180  |
| aaaatgcaac | gagtttacgc  | cttacgctaa  | caaggggatg | ataacgttgg | tgaccgatct  | 240  |
| cgaaggtagc | agtcgggcca  | ctacagagtt  | caagactttc | tttacacagt | tcaagtctta  | 300  |
| catgtctttc | atcgagacaa  | catcggcctc  | aacaaaaaat | gttgatgccg | agatgacagc  | 360  |
| taaatgtgac | ggtcttttca  | aggccatgtc  | tgcattgagt | gctagtaaag | gcgtcaaadc  | 420  |
| agcggatgct | gggagtatga  | agatgaccat  | gttgctgatg | ggaaagactt | tgggtgagca  | 480  |
| gaagaagaat | acaaagataa  | tgacattgaa  | ggaaaagaaa | gagttggtca | tagatatggt  | 540  |
| gaaatggact | aaaatggtcg  | ctacatttgt  | gaagtcggcc | tccgagcaga | aaggaaagtc  | 600  |
| tatcaatata | gcatcttatg  | gtcttgatgt  | cgatgttaac | gatagtctta | ttgtcgggtg  | 660  |
| agctgcaagt | agtgaatcat  | cctccactaa  | atctggatct | gtttccagta | gcggaagtgt  | 720  |
| ttctaccaag | tcgaaagaat  | cgagtagtag  | tggaagtgtt | gccagtggaa | gtgttgctac  | 780  |
| caaattccaa | gaattccagc  | gtggaagtgc  | tgctacccaa | tccaaagaat | ctagcgggtg  | 840  |
| aagtgtctgt | accaaatcca  | aagaatctag  | tgggtggaag | gctactacag | gtaaaacttc  | 900  |
| gggcagtccg | agcggaaagtc | ctaaggccag  | cccatctggt | tcagttagtg | gcaaatcatc  | 960  |
| ttcaaaagga | agcgcgaagt  | ctcaagggaag | cgcaagtgtc | caaggaagtg | caagtgtctc  | 1020 |
| aggaagcgca | agtgtctcaag | gaagtgcgaag | tgctcaaaga | agagaaagtg | gggcaatggc  | 1080 |
| tatgtccaag | agcagagaaa  | caaagacatc  | gagccaaaga | caatccaaat | catcgagtga  | 1140 |
| aagttcatct | tctagcacaa  | ccaccacaac  | agtgaacaaa | gtcgagagtg | agacttccaa  | 1200 |
| agaagtaaat | tcattcataa  | tgcaactcga  | gaagaagtat | gcagcaaagg | cggaactcaa  | 1260 |
| ggtcttcttc | gagttcttaa  | agtcttccat  | gcaagcttcc | gcaagcgttg | gttccaaaac  | 1320 |
| cgcgaaagac | tatgtttctg  | cctcaaaaagc | agccactggt | aaactctccg | aagccatggc  | 1380 |
| ttcagtgagt | tccaaaaaat  | tcaaataaagc | aaagatgaag | agcaacttgg | acactagcaa  | 1440 |
| agatgaaatg | ctgaggtgtg  | tcaaacaaat  | tcaagatatc | aacgataaaa | tgggtgagtgg | 1500 |
| caagaccgtg | tcatcaaacac | aacagtcaga  | gctcaagcag | acaatcacca | agtgggaaaa  | 1560 |
| ggtcaccacc | caattttgtt  | agaccgctgc  | ttcttcaagt | tcctcgtcat | cctcatcctc  | 1620 |
| atcctcatcc | tcattctctg  | ctgcttctca  | gcagcagggc | aatgcagcaa | tgggtcaagac | 1680 |
| taatttagtt | taaaggtgaa  | gttactttat  | tgcgcaaaag | atcaccaaga | aagacacaac  | 1740 |
| cagtaatgcc | aaatagtata  | ataagtagtt  | aactattaga | tcattyttct | tgtaaataaa  | 1800 |
| actaagatcg | gtataggtaa  | gcattgcatg  | cttataaacc | gatgtatgca | agtaataact  | 1860 |
| ctgtaaaaaa | acgttacaga  | tagattgtaa  | ccgctttgta | tgtaaacata | caaaagttag  | 1920 |
| tgatacctat | gaaagggatt  | tttg        |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:172:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 446 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..446  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498078  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Arg | Ile | Ser | Leu | Gly | Ile | Cys | Leu | Met | Leu | Val | Val | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Val | Ile | Tyr | Glu | Ala | Gln | Gly | Thr | Phe | Leu | Leu | Asn | His | Tyr | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Lys | Lys | Asn | Phe | Pro | Lys | Lys | Cys | Asn | Glu | Phe | Thr | Pro | Tyr | Ala | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Gly | Met | Ile | Thr | Leu | Val | Thr | Asp | Leu | Glu | Gly | Ser | Ser | Pro | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Thr | Glu | Phe | Lys | Thr | Phe | Phe | Thr | Gln | Phe | Lys | Ser | Tyr | Met | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Ile | Glu | Thr | Thr | Ser | Ala | Ser | Thr | Lys | Asn | Val | Asp | Ala | Glu | Met |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Ala | Lys | Cys | Asp | Gly | Leu | Phe | Lys | Ala | Met | Ser | Ala | Leu | Ser | Ala |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ser | Lys | Gly | Val | Lys | Ser | Ala | Asp | Ala | Gly | Ser | Met | Lys | Met | Thr | Met |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Leu | Ser | Met | Gly | Lys | Thr | Leu | Val | Glu | Gln | Lys | Lys | Asn | Thr | Lys | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Thr | Leu | Lys | Glu | Lys | Lys | Glu | Leu | Val | Ile | Asp | Met | Val | Lys | Trp |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Thr | Lys | Met | Val | Ala | Thr | Phe | Val | Lys | Ser | Ala | Ser | Glu | Gln | Lys | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Ser | Ile | Asn | Ile | Ala | Ser | Tyr | Gly | Leu | Asp | Val | Asp | Val | Asn | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ser | Ile | Val | Gly | Gly | Ala | Ala | Ser | Ser | Glu | Ser | Ser | Ser | Thr | Lys |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ser | Gly | Ser | Val | Ser | Ser | Ser | Gly | Ser | Val | Ser | Thr | Lys | Ser | Lys | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Ser | Ser | Ser | Gly | Ser | Ser | Ala | Ser | Gly | Ser | Val | Ala | Thr | Lys | Ser |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Lys | Glu | Ser | Ser | Gly | Gly | Ser | Ala | Ala | Thr | Lys | Ser | Lys | Glu | Ser | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Gly | Ser | Ala | Ala | Thr | Lys | Ser | Lys | Glu | Ser | Ser | Gly | Gly | Ser | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Thr | Gly | Lys | Thr | Ser | Gly | Ser | Pro | Ser | Gly | Ser | Pro | Lys | Ala | Ser |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Pro | Ser | Gly | Ser | Val | Ser | Gly | Lys | Ser | Ser | Ser | Ser | Lys | Gly | Ser | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Ala | Gln | Gly | Ser | Ala | Ser | Ala | Gln | Gly | Ser | Ala | Ser | Ala | Gln | Gly | Ser |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Ala | Ser | Ala | Gln | Gly | Ser | Ala | Ser | Ala | Gln | Arg | Arg | Glu | Ser | Gly | Ala |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Met | Ala | Met | Ser | Lys | Ser | Arg | Glu | Thr | Lys | Thr | Ser | Ser | Gln | Arg | Gln |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ser | Lys | Ser | Ser | Ser | Glu | Ser | Ser | Ser | Ser | Ser | Thr | Thr | Thr | Thr | Thr |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Val | Lys | Gln | Val | Glu | Ser | Glu | Thr | Ser | Lys | Glu | Val | Met | Ser | Phe | Ile |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Met | Gln | Leu | Glu | Lys | Lys | Tyr | Ala | Ala | Lys | Ala | Glu | Leu | Lys | Val | Phe |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     |     | 400 |

Phe Glu Ser Leu Lys Ser Ser Met Gln Ala Ser Ala Ser Val Gly Ser  
405 410 415  
Lys Thr Ala Lys Asp Tyr Val Ser Ala Ser Lys Ala Ala Thr Gly Lys  
420 425 430  
Leu Ser Glu Ala Met Ala Ser Val Ser Ser Lys Asn Val Lys  
435 440 445

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..436
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Met Leu Val Val Ala Ser Ser Val Ile Tyr Glu Ala Gln Gly Thr Phe  
1 5 10 15  
Leu Leu Asn His Tyr Leu Lys Lys Asn Phe Pro Lys Lys Cys Asn Glu  
20 25 30  
Phe Thr Pro Tyr Ala Asn Lys Gly Met Ile Thr Leu Val Thr Asp Leu  
35 40 45  
Glu Gly Ser Ser Pro Ala Thr Thr Glu Phe Lys Thr Phe Phe Thr Gln  
50 55 60  
Phe Lys Ser Tyr Met Ser Phe Ile Glu Thr Thr Ser Ala Ser Thr Lys  
65 70 75 80  
Asn Val Asp Ala Glu Met Thr Ala Lys Cys Asp Gly Leu Phe Lys Ala  
85 90 95  
Met Ser Ala Leu Ser Ala Ser Lys Gly Val Lys Ser Ala Asp Ala Gly  
100 105 110  
Ser Met Lys Met Thr Met Leu Ser Met Gly Lys Thr Leu Val Glu Gln  
115 120 125  
Lys Lys Asn Thr Lys Ile Met Thr Leu Lys Glu Lys Lys Glu Leu Val  
130 135 140  
Ile Asp Met Val Lys Trp Thr Lys Met Val Ala Thr Phe Val Lys Ser  
145 150 155 160  
Ala Ser Glu Gln Lys Gly Lys Ser Ile Asn Ile Ala Ser Tyr Gly Leu  
165 170 175  
Asp Val Asp Val Asn Asp Ser Ser Ile Val Gly Gly Ala Ala Ser Ser  
180 185 190  
Glu Ser Ser Ser Thr Lys Ser Gly Ser Val Ser Ser Ser Gly Ser Val  
195 200 205  
Ser Thr Lys Ser Lys Glu Ser Ser Ser Ser Gly Ser Ser Ala Ser Gly  
210 215 220  
Ser Val Ala Thr Lys Ser Lys Glu Ser Ser Gly Gly Ser Ala Ala Thr  
225 230 235 240  
Lys Ser Lys Glu Ser Ser Gly Gly Ser Ala Ala Thr Lys Ser Lys Glu  
245 250 255  
Ser Ser Gly Gly Ser Ala Thr Thr Gly Lys Thr Ser Gly Ser Pro Ser  
260 265 270  
Gly Ser Pro Lys Ala Ser Pro Ser Gly Ser Val Ser Gly Lys Ser Ser  
275 280 285  
Ser Lys Gly Ser Ala Ser Ala Gln Gly Ser Ala Ser Ala Gln Gly Ser  
290 295 300  
Ala Ser Ala Gln Gly Ser Ala Ser Ala Gln Gly Ser Ala Ser Ala Gln  
305 310 315 320  
Arg Arg Glu Ser Gly Ala Met Ala Met Ser Lys Ser Arg Glu Thr Lys  
325 330 335  
Thr Ser Ser Gln Arg Gln Ser Lys Ser Ser Ser Glu Ser Ser Ser Ser

(2) INFORMATION FOR SEQ ID NO:174:

(A) LENGTH: 396 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptide

(A) NAME

(B) LOCATION: 1..396

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ile Thr Leu Val Thr Asp Leu Glu Gly Ser S

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Glu | Phe | Lys | Thr | Phe | Phe | Thr | Gln | Phe | Lys | Ser | Tyr | Met | Ser | Phe | Ile |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Glu | Thr | Thr | Ser | Ala | Ser | Thr | Lys | Asn | Val | Asp | Ala | Glu | Met | Thr | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Lys | Cys | Asp | Gly | Leu | Phe | Lys | Ala | Met | Ser | Ala | Leu | Ser | Ala | Ser | Lys |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Val | Lys | Ser | Ala | Asp | Ala | Gly | Ser | Met | Lys | Met | Thr | Met | Leu | Ser |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |
| Met | Gly | Lys | Thr | Leu | Val | Glu | Gln | Lys | Lys | Asn | Thr | Lys | Ile | Met | Thr |
|     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |     |
| Leu | Lys | Glu | Lys | Lys | Glu | Leu | Val | Ile | Asp | Met | Val | Lys | Trp | Thr | Lys |
|     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |     |
| Met | Val | Ala | Thr | Phe | Val | Lys | Ser | Ala | Ser | Glu | Gln | Lys | Gly | Lys | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Ile | Asn | Ile | Ala | Ser | Tyr | Gly | Leu | Asp | Val | Asp | Val | Asn | Asp | Ser | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ile | Val | Gly | Gly | Ala | Ala | Ser | Ser | Glu | Ser | Ser | Ser | Thr | Lys | Ser | Gly |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |     |     |
| Ser | Val | Ser | Ser | Ser | Gly | Ser | Val | Ser | Thr | Lys | Ser | Lys | Glu | Ser | Ser |
|     |     |     | 165 |     |     |     | 170 |     |     |     | 175 |     |     |     |     |
| Ser | Ser | Gly | Ser | Ser | Ala | Ser | Gly | Ser | Val | Ala | Thr | Lys | Ser | Lys | Glu |
|     |     |     | 180 |     |     |     | 185 |     |     |     | 190 |     |     |     |     |
| Ser | Ser | Gly | Gly | Ser | Ala | Ala | Thr | Lys | Ser | Lys | Glu | Ser | Ser | Gly | Gly |
|     |     |     | 195 |     |     |     | 200 |     |     |     | 205 |     |     |     |     |
| Ser | Ala | Ala | Thr | Lys | Ser | Lys | Glu | Ser | Ser | Gly | Gly | Ser | Ala | Thr | Thr |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Gly | Lys | Thr | Ser | Gly | Ser | Pro | Ser | Gly | Ser | Pro | Lys | Ala | Ser | Pro | Ser |
| 225 |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |     |     |
| Gly | Ser | Val | Ser | Gly | Lys | Ser | Ser | Ser | Lys | Gly | Ser | Ala | Ser | Ala | Gln |
|     |     |     | 245 |     |     |     | 250 |     |     |     | 255 |     |     |     |     |
| Gly | Ser | Ala | Ser | Ala | Gln | Gly | Ser | Ala | Ser | Ala | Gln | Gly | Ser | Ala | Ser |
|     |     |     | 260 |     |     |     | 265 |     |     |     | 270 |     |     |     |     |
| Ala | Gln | Gly | Ser | Ala | Ser | Ala | Gln | Arg | Arg | Glu | Ser | Gly | Ala | Met | Ala |
|     |     |     | 275 |     |     |     | 280 |     |     |     | 285 |     |     |     |     |

Met Ser Lys Ser Arg Glu Thr Lys Thr Ser Ser Gln Arg Gln Ser Lys  
290 295 300  
Ser Ser Ser Glu Ser Ser Ser Ser Thr Thr Thr Thr Val Lys  
305 310 315 320  
Gln Val Glu Ser Glu Thr Ser Lys Glu Val Met Ser Phe Ile Met Gln  
325 330 335  
Leu Glu Lys Lys Tyr Ala Ala Lys Ala Glu Leu Lys Val Phe Phe Glu  
340 345 350  
Ser Leu Lys Ser Ser Met Gln Ala Ser Ala Ser Val Gly Ser Lys Thr  
355 360 365  
Ala Lys Asp Tyr Val Ser Ala Ser Lys Ala Ala Thr Gly Lys Leu Ser  
370 375 380  
Glu Ala Met Ala Ser Val Ser Ser Lys Asn Val Lys  
385 390 395

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..760
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

|            |             |             |             |             |            |     |
|------------|-------------|-------------|-------------|-------------|------------|-----|
| attaacaaat | ttgttctgat  | ctatttttatt | ttatttttgg  | tatcaggaag  | agaagaaacc | 60  |
| agaagcagca | gaggaaaaga  | aaatggaaga  | gaagaaacca  | gaagagaaaa  | aagaaggaga | 120 |
| agacaagaaa | gtggatgctg  | agaaaaaagg  | agaagattct  | gacaagaagc  | ctcaagaagg | 180 |
| agaaactaac | aaagattcca  | aagaagattc  | tgctccggcg  | gcgctgagg   | ctccagcacc | 240 |
| gcctcctccg | ccgcaagagg  | ttgttcttaa  | ggtttacatg  | cactgtgaag  | gatgtgctag | 300 |
| aaaagtccgc | cgttgtctca  | aaggcttcga  | aggagtggaa  | gatgtgatga  | ctgattgtaa | 360 |
| aacggggaaa | gtggtggtga  | aaggtgagaa  | agctgatcca  | ttgaaagtat  | tagctagagt | 420 |
| tcagaggaag | acccaccgct  | aagttcaggc  | tagtgtttgt  | ggactttgaa  | gatggacgta | 480 |
| agaggtatct | gaagaaatca  | gctaagtggg  | ttaggagatt  | gttgaaggga  | gcratgggtg | 540 |
| ggacgaatga | gcagggtggct | gttattttaat | aaaccacgag  | tcattgggtca | atttagtcta | 600 |
| ctgtttcttt | tgctctatgt  | acagaaagaa  | aataaaacttt | ccaaaataag  | aggtggcttt | 660 |
| gtttggactt | tggatgttac  | tatatatatt  | ggtaattctt  | ggcgtttggt  | agtttccaaa | 720 |
| ccaaacatta | ataaataaat  | aaataaaaga  | gtttgaggtt  |             |            |     |

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Glu | Lys | Lys | Pro | Glu | Glu | Lys | Lys | Glu | Gly | Glu | Asp | Lys | Lys |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Val | Asp | Ala | Glu | Lys | Lys | Gly | Glu | Asp | Ser | Asp | Lys | Lys | Pro | Gln | Glu |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Glu | Thr | Asn | Lys | Asp | Ser | Lys | Glu | Asp | Ser | Ala | Pro | Ala | Ala | Pro |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Glu | Ala | Pro | Ala | Pro | Pro | Pro | Pro | Gln | Glu | Val | Val | Leu | Lys | Val |     |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Tyr | Met | His | Cys | Glu | Gly | Cys | Ala | Arg | Lys | Val | Arg | Arg | Cys | Leu | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Phe | Glu | Gly | Val | Glu | Asp | Val | Met | Thr | Asp | Cys | Lys | Thr | Gly | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Val | Val | Val | Lys | Gly | Glu | Lys | Ala | Asp | Pro | Leu | Lys | Val | Leu | Ala | Arg |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Gln | Arg | Lys | Thr | His | Arg | Gln | Val | Gln | Ala | Ser | Val | Cys | Gly | Leu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1498085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Arg | Lys | Lys | Glu | Lys | Ile | Leu | Thr | Arg | Ser | Leu | Lys | Lys | Glu |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Lys | Leu | Thr | Lys | Ile | Pro | Lys | Lys | Ile | Leu | Leu | Arg | Arg | Arg | Leu | Arg |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Leu | Gln | His | Arg | Leu | Leu | Arg | Arg | Lys | Arg | Leu | Phe | Leu | Arg | Phe | Thr |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Cys | Thr | Val | Lys | Asp | Val | Leu | Glu | Lys | Ser | Ala | Val | Val | Ser | Lys | Ala |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Lys | Glu | Trp | Lys | Met |     |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1498086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Gly | Arg | Met | Ser | Arg | Trp | Leu | Leu | Phe | Asn | Lys | Pro | Arg | Val |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ile | Gly | Gln | Phe | Ser | Leu | Leu | Phe | Leu | Leu | Leu | Tyr | Val | Gln | Lys | Glu |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Asn | Lys | Leu | Ser | Lys | Ile | Arg | Gly | Gly | Phe | Val | Trp | Thr | Leu | Asp | Val |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Thr | Ile | Tyr | Ile | Gly | Asn | Ser | Trp | Arg | Leu | Leu | Val | Ser | Lys | Pro | Asn |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Asn | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..748

(D) OTHER INFORMATION: / Ceres Seq. ID 1498090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| aaatcactta | cttaacatac  | taagagagtt | attagaactt | gcaaaaaatg | gcttccaagg | 60  |
| ctttgattct | gttaggtctc  | ttctcagttc | ttctcgtcgt | ctccgaagtg | tctgccgcaa | 120 |
| ggaatcgggc | atgggtgaagc | cagagagtga | ggaaactgtg | caacctgaag | gttatrgcgg | 180 |
| tggccacgga | ggacatggtg  | gtcacggagg | gggaggagga | cacggacatg | gaggacacaa | 240 |
| cggaggaggg | ggccacggac  | ttgacggata | cggaggaggt | ggaggacact | atggaggarg | 300 |
| tggaggacac | tacggaggag  | gtggaggaca | ctacggagga | ggtggaggac | actacggagg | 360 |
| aggtggtgga | gaggattaaa  | gctactgttt | cttgtgatgt | tggaggagga | gcgtagtttt | 420 |
| ttttcagaag | aagtaagaat  | aagagaaaag | gaaggattaa | gagcggttat | ggtttctcat | 480 |
| tttgtgtttt | ttgaaatcca  | aaggaagtca | agaacgcacc | ttttgcgttt | aatttcatct | 540 |
| caagctgatg | aaaaaaggta  | aagtggttcg | ggtattgact | tctgctggaa | accacggttt | 600 |
| taaatgtgtc | attttgcgtt  | tcgttgacag | ttttttgaac | accttttggg | tttccccttt | 660 |
| ttgcgttttc | cgacccaagt  | tgtcarwttc | tttgttgttt | tgtattgtaa | gcccttttgt | 720 |
| tgcacttgac | agatatggag  | ttaaaatc   |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1498091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | His | Leu | Leu | Asn | Ile | Leu | Arg | Glu | Leu | Leu | Glu | Leu | Ala | Lys | Asn |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gly | Phe | Gln | Gly | Phe | Asp | Ser | Val | Arg | Ser | Leu | Leu | Ser | Ser | Ser | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Arg | Leu | Arg | Ser | Val | Cys | Arg | Lys | Glu | Ser | Gly | Met | Val | Lys | Pro | Glu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Glu | Glu | Thr | Val | Gln | Pro | Glu | Gly | Tyr | Xaa | Gly | Gly | His | Gly | Gly |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| His | Gly | Gly | His | Gly | Gly | Gly | Gly | Gly | His | Gly | His | Gly | Gly | His | Asn |  |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |  |
| Gly | Gly | Gly | Gly | His | Gly | Leu | Asp | Gly | Tyr | Gly | Gly | Gly | Gly | Gly | His |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Tyr | Gly | Gly | Xaa | Gly | Gly | His | Tyr | Gly | Gly | Gly | Gly | Gly | His | Tyr | Gly |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Gly | Gly | Gly | Gly | His | Tyr | Gly | Gly | Gly | Gly | Gly | Glu | Asp |     |     |     |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1498092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Lys | Pro | Glu | Ser | Glu | Glu | Thr | Val | Gln | Pro | Glu | Gly | Tyr | Xaa |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gly | Gly | His | Gly | Gly | His | Gly | Gly | His | Gly | Gly | Gly | Gly | Gly | His | Gly |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| His | Gly | Gly | His | Asn | Gly | Gly | Gly | Gly | His | Gly | Leu | Asp | Gly | Tyr | Gly |  |

35 40 45  
Gly Gly Gly Gly His Tyr Gly Gly Xaa Gly Gly His Tyr Gly Gly Gly  
50 55 60  
Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly  
65 70 75 80  
Glu Asp

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..73  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Met Val Val Thr Glu Gly Glu Glu Ala Thr Asp Met Glu Asp Thr Thr  
1 5 10 15  
Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu Glu Val Glu Asp Thr  
20 25 30  
Met Glu Xaa Val Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu  
35 40 45  
Glu Val Glu Asp Thr Thr Glu Glu Val Val Glu Arg Ile Lys Ala Thr  
50 55 60  
Val Ser Cys Asp Val Gly Gly Ala  
65 70

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1526 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1526  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

aaaaattaaa agtggttcttg ttgctgtaga acacaaacag aacaaacaaa aaatcaattg 60  
aagagtctct cagtcggttag gggaagcaaa tagagaaatg gctagcttta ctgcctccgc 120  
ttccaccgtc tccgcgcgtc gtcaggctct ccttctcaag cctaccgtcg ccatctctgc 180  
tcctgttctt gggttgccct caatgggtaa gaagaaggga ggagtgaat gttcaatgga 240  
gacaaagcag gaaacgtctc agtcatgggg gctggagttt cagctgcagc aacagctgct 300  
ttgacggcgg tgatgagcaa tcccgcgatg gctttgggtg atgagaggat gtcaacagaa 360  
ggaacaggat tacccttttg tctaagcaac aacctcttgg gttggattct gtttgaggtc 420  
tttggtttga wctggacttt cttcttcgtc tacacttcat ctctcgagga ggatgaagaa 480  
tctggtcttt cactctgaag gaagaatcaa tctttcgtct tctcatttcc attttcatgt 540  
gagaacatga atcaaaagtg ttcacccttc tagtttcttg taattgttaa gtaaagacta 600  
aaaactagaa gggtgaacac tattcattca ttctcatcat gtcacgga tctgaaatcc 660  
cgccgttggt gtcacaaacc gccgcagcgg aggaatctgg agagaagacc agcaagaaag 720  
cggctaagaa ggaagctgcc aagctagaga agttaagacg tcgtcaagaa caagaggaag 780  
caacgcgtcg aacagcttgc atctctcttg aagagaatga cgagttttcc aataactacg 840  
gcgacgtgac tcttaccgag ttgcaatcgt cggcggatcc gaaagccggg aagtggatag 900  
aggctgttga gggaaaggag tggaccgatg tgagcgattt ggtggaagag atgttggaat 960  
cagaggttct gatcagagcg cgagtgcaca cgaatcgtcc aacgtctaac aaattggggg 1020  
ttgtggtctt gagggagagc ggatcaactg ttcatgctg ggtagccaa tcagagaaga 1080  
ccaaactagg tgccaacatg gttaaataatc tcaagcagct gagtcgcaaa tcctttgtcg 1140  
atgttatcgg tgtcgtcact ctccccaaag agccgctgac gggaactacg cagcaggttg 1200

aaattcaagt gagaaaagtg tactgcatca acaaatcctt ggccaaatta ccacttagtg 1260  
tgaggatgc tgctcggagt gaagcagata tcgaagcatc tcttcagact ccacttccag 1320  
ctgctcgtgt caatcaggat acacgtttga actatagggg gctcgacctc agaacaccgg 1380  
ctaataaagc catcttccag cttcagtacg aagtcgaata tgccttcaga gaaaaattac 1440  
gatttaagaa ttttggttga atccacacac caaaactgat ggctggtagt agtgaaggag 1500  
gttctgctgt atttaggttg gaatac

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1498098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met Ser Ser Glu Ser Glu Ile Pro Pro Leu Ser Ser Ser Thr Ala Ala  
1 5 10 15  
Ala Glu Glu Ser Gly Glu Lys Thr Ser Lys Lys Ala Ala Lys Lys Glu  
20 25 30  
Ala Ala Lys Leu Glu Lys Leu Arg Arg Arg Gln Glu Gln Glu Glu Ala  
35 40 45  
Thr Arg Arg Thr Ala Ser Ile Ser Leu Glu Glu Asn Asp Glu Phe Ser  
50 55 60  
Asn Asn Tyr Gly Asp Val Thr Leu Thr Glu Leu Gln Ser Ser Ala Asp  
65 70 75 80  
Pro Lys Ala Gly Lys Trp Ile Glu Ala Val Glu Gly Lys Glu Trp Thr  
85 90 95  
Asp Val Ser Asp Leu Val Glu Glu Met Leu Glu Ser Glu Val Leu Ile  
100 105 110  
Arg Gly Arg Val His Thr Asn Arg Pro Thr Ser Asn Lys Leu Gly Phe  
115 120 125  
Val Val Leu Arg Glu Ser Gly Ser Thr Val Gln Cys Val Val Ser Gln  
130 135 140  
Ser Glu Lys Thr Lys Leu Gly Ala Asn Met Val Lys Tyr Leu Lys Gln  
145 150 155 160  
Leu Ser Arg Glu Ser Phe Val Asp Val Ile Gly Val Val Thr Leu Pro  
165 170 175  
Lys Glu Pro Leu Thr Gly Thr Thr Gln Val Glu Ile Gln Val Arg  
180 185 190  
Lys Val Tyr Cys Ile Asn Lys Ser Leu Ala Lys Leu Pro Leu Ser Val  
195 200 205  
Glu Asp Ala Ala Arg Ser Glu Ala Asp Ile Glu Ala Ser Leu Gln Thr  
210 215 220  
Pro Ser Pro Ala Ala Arg Val Asn Gln Asp Thr Arg Leu Asn Tyr Arg  
225 230 235 240  
Val Leu Asp Leu Arg Thr Pro Ala Asn Gln Ala Ile Phe Gln Leu Gln  
245 250 255  
Tyr Glu Val Glu Tyr Ala Phe Arg Glu Lys Leu Arg Phe Lys Asn Phe  
260 265 270  
Val Gly Ile His Thr Pro Lys Leu Met Ala Gly Ser Ser Glu Gly Gly  
275 280 285  
Ser Ala Val Phe Arg Leu Glu Tyr  
290 295

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..192  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Glu | Ser | Glu | Val | Leu | Ile | Arg | Gly | Arg | Val | His | Thr | Asn | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Thr | Ser | Asn | Lys | Leu | Gly | Phe | Val | Val | Leu | Arg | Glu | Ser | Gly | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Thr | Val | Gln | Cys | Val | Val | Ser | Gln | Ser | Glu | Lys | Thr | Lys | Leu | Gly | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asn | Met | Val | Lys | Tyr | Leu | Lys | Gln | Leu | Ser | Arg | Glu | Ser | Phe | Val | Asp |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Val | Ile | Gly | Val | Val | Thr | Leu | Pro | Lys | Glu | Pro | Leu | Thr | Gly | Thr | Thr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Gln | Val | Glu | Ile | Gln | Val | Arg | Lys | Val | Tyr | Cys | Ile | Asn | Lys | Ser |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Leu | Ala | Lys | Leu | Pro | Leu | Ser | Val | Glu | Asp | Ala | Ala | Arg | Ser | Glu | Ala |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asp | Ile | Glu | Ala | Ser | Leu | Gln | Thr | Pro | Ser | Pro | Ala | Ala | Arg | Val | Asn |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Gln | Asp | Thr | Arg | Leu | Asn | Tyr | Arg | Val | Leu | Asp | Leu | Arg | Thr | Pro | Ala |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Asn | Gln | Ala | Ile | Phe | Gln | Leu | Gln | Tyr | Glu | Val | Glu | Tyr | Ala | Phe | Arg |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Glu | Lys | Leu | Arg | Phe | Lys | Asn | Phe | Val | Gly | Ile | His | Thr | Pro | Lys | Leu |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Met | Ala | Gly | Ser | Ser | Glu | Gly | Gly | Ser | Ala | Val | Phe | Arg | Leu | Glu | Tyr |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..697

(D) OTHER INFORMATION: / Ceres Seq. ID 1498100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

|            |             |             |             |            |             |     |
|------------|-------------|-------------|-------------|------------|-------------|-----|
| aacaccttct | ttaatccaga  | acaacaaaaa  | aaccaaacag  | aagaagaaaa | aagaaaaaaa  | 60  |
| actacaaaaa | aaaaaaatct  | ctgcccgctt  | ctccgttctc  | ggggttgctg | cgaaattgga  | 120 |
| ccaaattgat | caaaacctac  | ccagaaatca  | tttttgggtca | caggggatag | gcgggcagat  | 180 |
| ttaaaaaatt | tcttcttttt  | ttcttctgtt  | tgaatttgta  | ttgattcgtg | aaattgtgtg  | 240 |
| tgtttgatgg | gttttttggg  | ggatacgcaa  | aaggaaggag  | gtggacattc | atggggttac  | 300 |
| gttagaagtt | tggttagaag  | gaaacaagtc  | gactctgcta  | atggccaatc | tcattggtcac | 360 |
| caacttgcta | gagccctcac  | tgttcctcat  | ctcgttgcaa  | ttggtggttg | agcaacaata  | 420 |
| ggagctggag | tttatattct  | tgtaggaaca  | gttgcgagag  | agcattcagg | accttctctt  | 480 |
| gctttgtctt | ttcttattgc  | tgggaattgct | gctggtcttt  | ctgcgttttg | ttatgctgaa  | 540 |
| ctctctagtc | gttgctcnttc | agctgggagt  | gcgtatcact  | attcttacat | ttgtgttggt  | 600 |
| gaaggtggtg | cgtggataat  | cggttgggag  | ttgattctca  | agtgtgaagt | tgtacttgta  | 660 |
| aacaaaaaat | gtattatata  | aaagtgttat  | ttgttcc     |            |             |     |

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..144  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498101  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Phe | Leu | Val | Asp | Thr | Gln | Lys | Glu | Gly | Gly | Gly | His | Ser | Trp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly | Tyr | Val | Arg | Ser | Leu | Val | Arg | Arg | Lys | Gln | Val | Asp | Ser | Ala | Asn |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Gln | Ser | His | Gly | His | Gln | Leu | Ala | Arg | Ala | Leu | Thr | Val | Pro | His |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Val | Ala | Ile | Gly | Val | Gly | Ala | Thr | Ile | Gly | Ala | Gly | Val | Tyr | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Val | Gly | Thr | Val | Ala | Arg | Glu | His | Ser | Gly | Pro | Ser | Leu | Ala | Leu |
| 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Ser | Phe | Leu | Ile | Ala | Gly | Ile | Ala | Ala | Gly | Leu | Ser | Ala | Phe | Cys | Tyr |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Ala | Glu | Leu | Ser | Ser | Arg | Cys | Xaa | Ser | Ala | Gly | Ser | Ala | Tyr | His | Tyr |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ser | Tyr | Ile | Cys | Val | Gly | Glu | Gly | Val | Ala | Trp | Ile | Ile | Gly | Trp | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | Ile | Leu | Lys | Cys | Lys | Ile | Val | Leu | Val | Asn | Lys | Lys | Cys | Ile | Ile |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 771 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..771  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498102  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| acaatccaat | caaaacacac | agagagaaga | aaaactcaga | agaaaagcca  | aagagtga    | 60  |
| caaaaatggc | gtcgacgact | ctctcaatcg | caacaacaat | ccgttcctca  | tcttataccta | 120 |
| ctctcgcttc | catcaatcac | ttcccttccc | gaaccamcac | catcgaattc  | ccctctcgct  | 180 |
| tcggtgggtg | ttcatcatcc | acattgaccc | accgtgcaac | ccatctccgt  | ccaatcgccg  | 240 |
| ccgtcgaagc | tccggagaaa | atcgagaaga | tcggatccga | aatctcatcc  | ctaaccctcg  | 300 |
| aagaagctcg | tatcctcgtc | gactatctcc | aagacaaatt | cgggtgtctcc | ccactctctt  | 360 |
| tagccccgcg | agcagcggcg | gttgctgctc | cagccgacgg | tggcgcgggc  | gctgtagtgg  | 420 |
| aagagcaaac | agagttcgat | gtggttatca | atgaagttcc | cagcagttcc  | cgtattgcag  | 480 |
| tgattaaagc | tgttagggtc | ttaactagct | tggcgttgaa | ggaagctaag  | gagctaatac  | 540 |
| aaggattacc | aaagaagttt | aaagaaggta | tcactaaaga | tgaagctgaa  | gaagctaaga  | 600 |
| agactcttga | agaagctggg | gctaaagtct | ccattgctta | aggtttttat  | taaaaaaaaa  | 660 |
| aaagaagttg | ttatcttttc | tggaatttga | ttggtctttt | gtgttggtta  | gtatagtttg  | 720 |
| cgtctggaat | tgttgagaaa | ttgttgtaat | ttgaatcaca | tttggtttcc  | c           |     |

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 212 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1498103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Asn Pro Ile Lys Thr His Arg Glu Lys Lys Asn Ser Glu Glu Lys Pro  
1 5 10 15  
Lys Ser Glu Thr Lys Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr  
20 25 30  
Ile Arg Ser Ser Ser Tyr Pro Thr Leu Ala Ser Ile Asn His Phe Pro  
35 40 45  
Ser Arg Thr Xaa Thr Ile Glu Phe Pro Ser Arg Phe Gly Gly Gly Ser  
50 55 60  
Ser Ser Thr Leu Thr His Arg Ala Thr His Leu Arg Pro Ile Ala Ala  
65 70 75 80  
Val Glu Ala Pro Glu Lys Ile Glu Lys Ile Gly Ser Glu Ile Ser Ser  
85 90 95  
Leu Thr Leu Glu Glu Ala Arg Ile Leu Val Asp Tyr Leu Gln Asp Lys  
100 105 110  
Phe Gly Val Ser Pro Leu Ser Leu Ala Pro Ala Ala Ala Val Ala  
115 120 125  
Ala Pro Ala Asp Gly Gly Ala Ala Ala Val Val Glu Glu Gln Thr Glu  
130 135 140  
Phe Asp Val Val Ile Asn Glu Val Pro Ser Ser Ser Arg Ile Ala Val  
145 150 155 160  
Ile Lys Ala Val Arg Ala Leu Thr Ser Leu Ala Leu Lys Glu Ala Lys  
165 170 175  
Glu Leu Ile Glu Gly Leu Pro Lys Lys Phe Lys Glu Gly Ile Thr Lys  
180 185 190  
Asp Glu Ala Glu Glu Ala Lys Lys Thr Leu Glu Glu Ala Gly Ala Lys  
195 200 205  
Val Ser Ile Ala  
210

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1498104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr Ile Arg Ser Ser Ser  
1 5 10 15  
Tyr Pro Thr Leu Ala Ser Ile Asn His Phe Pro Ser Arg Thr Xaa Thr  
20 25 30  
Ile Glu Phe Pro Ser Arg Phe Gly Gly Gly Ser Ser Ser Thr Leu Thr  
35 40 45  
His Arg Ala Thr His Leu Arg Pro Ile Ala Ala Val Glu Ala Pro Glu  
50 55 60  
Lys Ile Glu Lys Ile Gly Ser Glu Ile Ser Ser Leu Thr Leu Glu Glu  
65 70 75 80  
Ala Arg Ile Leu Val Asp Tyr Leu Gln Asp Lys Phe Gly Val Ser Pro  
85 90 95  
Leu Ser Leu Ala Pro Ala Ala Ala Ala Val Ala Ala Pro Ala Asp Gly  
100 105 110  
Gly Ala Ala Ala Val Val Glu Glu Gln Thr Glu Phe Asp Val Val Ile  
115 120 125  
Asn Glu Val Pro Ser Ser Ser Arg Ile Ala Val Ile Lys Ala Val Arg

130 135 140  
Ala Leu Thr Ser Leu Ala Leu Lys Glu Ala Lys Glu Leu Ile Glu Gly  
145 150 155 160  
Leu Pro Lys Lys Phe Lys Glu Gly Ile Thr Lys Asp Glu Ala Glu Glu  
165 170 175  
Ala Lys Lys Thr Leu Glu Glu Ala Gly Ala Lys Val Ser Ile Ala  
180 185 190

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2443

(D) OTHER INFORMATION: / Ceres Seq. ID 1498109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

|            |            |            |             |             |            |      |
|------------|------------|------------|-------------|-------------|------------|------|
| aattgctctc | tcaattttct | tctcctcccg | cttctgcttc  | tctcccttaa  | caagaaccat | 60   |
| gagctcctcc | gatggcgggt | cctctagggt | ttcgattcct  | taccatctcc  | gcaaaaccct | 120  |
| tcagaaaatc | agagagtata | ccggaagaca | gcactcggat  | gaggatatct  | ttgccgtcta | 180  |
| taaggattcc | ttcaatgata | ctcatgagac | cgctcagaag  | ctcctcttct  | tagatacatt | 240  |
| tcatgaggtg | agaagtaaaa | gggagaaaaa | gaaggagcct  | atagtgccag  | ttacacaacc | 300  |
| aagtggcaga | ggtggtcgga | ggaactttgc | ttcaagtaac  | tcttatcaag  | gtagtggaa  | 360  |
| aaatgcttct | tttaaaagg  | aaaatggagc | taatcatgta  | acaagagggt  | ctagaactgc | 420  |
| tcagcctgcc | actaacaagg | camgcaacat | cacagtacct  | aatgaaacaa  | aggtttctgg | 480  |
| tcctgctagt | attctgagtg | aggctcagca | tcataaagct  | caagatgata  | cttctttgat | 540  |
| ttctgcttca | cggtgcagta | gccagtcaga | tcaagccatt  | gaaattgaga  | ctgcgtccaa | 600  |
| acaaggcaaa | aatcaatcgc | ttcctaagcc | agatgttagc  | gaacagtcac  | acgtaacatt | 660  |
| ccctttccac | cttcagggtg | ccaaaggact | gcaaaatggt  | ctgacgtttg  | gcagttttga | 720  |
| ttccaatttt | gtgaaagagg | tatcttctag | caatgggtgct | agtggcggat  | atgactcaaa | 780  |
| ttttgagctc | tctcacggga | caggggatga | tgagagggaa  | tcttctccca  | ctaccaatgg | 840  |
| tattactggg | gttgcttcgg | ctagagaaga | aacatcaaca  | gtttctgaag  | ataaggatta | 900  |
| tgggatatac | aattctgcaa | ctggagctga | gcctgtgggt  | cactcggatc  | acattgtccc | 960  |
| acctgtatga | gaagtacga  | aggaggaagc | tttatcaaac  | acagaaactc  | atcaaattgc | 1020 |
| ttatggtcaa | gaagctccac | tcagtgtgtt | tggtcttgct  | ccctcggtgt  | cagcaatagg | 1080 |
| ccaacccgtt | aacacagaag | cagcggagac | tcagcccggg  | aattccaact  | ctccagctat | 1140 |
| ttcattagta | tcatatcttc | cagatcagag | ctccatagca  | gcagccactc  | aacagacaaa | 1200 |
| ttttcttagg | cagcaatacc | ctcccaattt | cttcccttac  | ggctatttct  | caccgtatta | 1260 |
| tatgccaccg | ccgtacattc | accagttctt | gagcccaaac  | gggatccctc  | agcagcttta | 1320 |
| ttttccacaa | ggagctgctc | taacagcacc | ttctcatgca  | aaaccagttg  | acaacactga | 1380 |
| aaacctctcc | accacaaacc | cttacctaca | cacttctccc  | atggttgcta  | gcagcatccc | 1440 |
| atctacaacc | accttaaat  | ctatccatag | tgaagaaaag  | gcattctcacc | tgactgaaag | 1500 |
| tgcagctgca | tggattgggc | agggatttgg | caacctgcag  | gtgaatccaa  | tgtataacct | 1560 |
| agcataccac | ggtcagccac | ttggttttcc | agtcgtgcag  | gctgggtcat  | gtggcctcat | 1620 |
| gggaatgcac | caaccaaac  | agcccatggc | agctgcttta  | actacatata  | agaccttacc | 1680 |
| accaccgcca | cacacaacaa | cggctatggt | tccgagcgtg  | gtgggtgata  | cggttctcaa | 1740 |
| cgtagtgggt | gtggttacgg | aggttctcaa | cgttccagtt  | atggttcggg  | gtcagggtcc | 1800 |
| ggttcgggct | caggttcagg | aaaccgtctc | tacgtgggca  | acctttcttg  | gggtgttgat | 1860 |
| gacatggcac | ttgagaactt | gtttaacgag | caaggaaagg  | tagttgragc  | tagggttwgc | 1920 |
| gatctacgac | agggacagcg | gtagatccaa | gggttttgga  | tttgtagacac | ttagctcttc | 1980 |
| ccaagagggt | cagaaggcga | tcaattcctt | gaatggagca  | gatttggtat  | gaagacaaat | 2040 |
| aagagtctca | gaggctgagg | ctaggccacc | aagaggccaa  | ttttgagcgg  | tcacacctct | 2100 |
| ttcatattct | caaaaaatgc | aaattctgga | gggttctttg  | aagcatatag  | ggttagtgga | 2160 |
| aaatggcggt | ttcagacagt | aactaaaact | cactgctggt  | gcacgctagg  | ctttatccgc | 2220 |
| ctttgatgca | tgaaggtcgt | taaggaaagg | tctttttttg  | agaaagataa  | caattagatt | 2280 |
| aaagcagaga | acccatgttt | cttgtctgtt | cgaatcctgc  | gagattgggt  | gtagttgaag | 2340 |
| ttgcattttc | ttcttgtctt | ttttgttggt | attttgacac  | aatttggctt  | tttggcatat | 2400 |
| gagagtgact | gtagcagctc | gttttatttg | atgttcttga  | tcc         |            |      |

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 633 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..633  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498110  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ala | Leu | Ser | Ile | Ser | Leu | Ser | Ser | Arg | Phe | Cys | Phe | Ser | Pro | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Arg | Thr | Met | Ser | Ser | Ser | Asp | Gly | Gly | Ser | Ser | Arg | Val | Ser | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Tyr | His | Leu | Arg | Lys | Thr | Leu | Gln | Lys | Ile | Arg | Glu | Tyr | Thr | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Gln | His | Ser | Asp | Glu | Asp | Ile | Phe | Ala | Val | Tyr | Lys | Asp | Ser | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Asp | Pro | His | Glu | Thr | Ala | Gln | Lys | Leu | Leu | Phe | Leu | Asp | Thr | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Glu | Val | Arg | Ser | Lys | Arg | Glu | Lys | Lys | Lys | Glu | Pro | Ile | Val | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Thr | Gln | Pro | Ser | Gly | Arg | Gly | Gly | Arg | Arg | Asn | Phe | Ala | Ser | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Ser | Tyr | Gln | Gly | Ser | Gly | Arg | Asn | Ala | Ser | Phe | Lys | Arg | Glu | Asn |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ala | Asn | His | Val | Thr | Arg | Gly | Ser | Arg | Thr | Ala | Gln | Pro | Ala | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Lys | Ala | Xaa | Asn | Ile | Thr | Val | Pro | Asn | Glu | Thr | Lys | Val | Ser | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Ala | Ser | Ile | Leu | Ser | Glu | Val | Ser | Asn | His | Lys | Ala | Gln | Asp | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Ser | Leu | Ile | Ser | Ala | Ser | Arg | Cys | Ser | Ser | Gln | Ser | Asp | Gln | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Glu | Ile | Glu | Thr | Ala | Ser | Lys | Gln | Gly | Lys | Asn | Gln | Ser | Leu | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Pro | Asp | Val | Ser | Glu | Gln | Ser | His | Val | Thr | Phe | Pro | Phe | His | Leu |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Val | Ala | Lys | Gly | Leu | Gln | Asn | Gly | Leu | Thr | Phe | Gly | Ser | Phe | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Asn | Phe | Val | Lys | Glu | Val | Ser | Ser | Ser | Asn | Gly | Ala | Ser | Gly | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Tyr | Asp | Ser | Asn | Phe | Glu | Ser | Ser | His | Gly | Thr | Gly | Asp | Asp | Glu | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Ser | Ser | Pro | Thr | Thr | Asn | Gly | Ile | Thr | Gly | Val | Ala | Ser | Ala | Arg |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Glu | Glu | Thr | Ser | Thr | Val | Ser | Glu | Asp | Lys | Asp | Tyr | Gly | Ile | Ser | Asn |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Ala | Thr | Gly | Ala | Glu | Pro | Val | Val | His | Ser | Asp | His | Ile | Val | Pro |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro | Val | Glu | Glu | Val | Pro | Lys | Glu | Glu | Ala | Leu | Ser | Asn | Thr | Glu | Thr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| His | Gln | Ile | Ala | Tyr | Gly | Gln | Glu | Ala | Pro | Leu | Ser | Val | Phe | Gly | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val | Pro | Ser | Leu | Ser | Ala | Ile | Gly | Gln | Pro | Val | Asn | Thr | Glu | Ala | Ala |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Glu | Thr | Gln | Pro | Gly | Asn | Ser | Asn | Ser | Pro | Ala | Ile | Ser | Leu | Val | Ser |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Tyr | Pro | Pro | Asp | Gln | Ser | Ser | Ile | Ala | Ala | Ala | Thr | Gln | Gln | Thr | Asn |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |

Phe Leu Arg Gln Gln Tyr Pro Pro Asn Phe Phe Pro Tyr Gly Tyr Xaa  
405 410 415  
Ser Pro Tyr Tyr Met Pro Pro Pro Tyr Ile His Gln Phe Leu Ser Pro  
420 425 430  
Asn Gly Ile Pro Gln Gln Ser Tyr Phe Pro Gln Gly Ala Ala Leu Thr  
435 440 445  
Ala Pro Ser His Ala Lys Pro Val Asp Asn Thr Glu Asn Pro Pro Thr  
450 455 460  
Thr Asn Pro Tyr Leu His Thr Ser Pro Met Val Ala Ser Ser Ile Pro  
465 470 475 480  
Ser Thr Thr Thr Leu Asn Ser Ile His Ser Glu Glu Lys Ala Ser His  
485 490 495  
Leu Thr Glu Ser Ala Ala Ala Trp Ile Gly Gln Gly Phe Gly Asn Leu  
500 505 510  
Gln Val Asn Pro Met Tyr Asn Leu Ala Tyr Gln Gly Gln Pro Leu Gly  
515 520 525  
Phe Pro Val Val Gln Ala Gly His Gly Gly Leu Met Gly Met His Gln  
530 535 540  
Pro Thr Gln Pro Met Ala Ala Ala Leu Thr Thr Tyr Gln Thr Leu Pro  
545 550 555 560  
Pro Pro Pro His Thr Thr Thr Ala Met Val Pro Ser Val Val Val Asp  
565 570 575  
Thr Val Leu Asn Val Val Val Val Val Thr Glu Gly Leu Asn Val Pro  
580 585 590  
Val Met Val Arg Gly Gln Gly Pro Val Arg Ala Gln Val Gln Glu Thr  
595 600 605  
Val Ser Thr Trp Ala Thr Phe Leu Gly Val Leu Met Thr Trp His Leu  
610 615 620  
Arg Thr Cys Leu Thr Ser Lys Glu Arg  
625 630

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 614 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..614

(D) OTHER INFORMATION: / Ceres Seq. ID 1498111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Met Ser Ser Ser Asp Gly Gly Ser Ser Arg Val Ser Ile Pro Tyr His  
1 5 10 15  
Leu Arg Lys Thr Leu Gln Lys Ile Arg Glu Tyr Thr Gly Lys Gln His  
20 25 30  
Ser Asp Glu Asp Ile Phe Ala Val Tyr Lys Asp Ser Phe Asn Asp Pro  
35 40 45  
His Glu Thr Ala Gln Lys Leu Leu Phe Leu Asp Thr Phe His Glu Val  
50 55 60  
Arg Ser Lys Arg Glu Lys Lys Lys Glu Pro Ile Val Pro Val Thr Gln  
65 70 75 80  
Pro Ser Gly Arg Gly Gly Arg Arg Asn Phe Ala Ser Ser Asn Ser Tyr  
85 90 95  
Gln Gly Ser Gly Arg Asn Ala Ser Phe Lys Arg Glu Asn Gly Ala Asn  
100 105 110  
His Val Thr Arg Gly Ser Arg Thr Ala Gln Pro Ala Thr Asn Lys Ala  
115 120 125  
Xaa Asn Ile Thr Val Pro Asn Glu Thr Lys Val Ser Gly Pro Ala Ser  
130 135 140  
Ile Leu Ser Glu Val Ser Asn His Lys Ala Gln Asp Asp Pro Ser Leu

|                                                                 |  |     |  |     |  |     |
|-----------------------------------------------------------------|--|-----|--|-----|--|-----|
| 145                                                             |  | 150 |  | 155 |  | 160 |
| Ile Ser Ala Ser Arg Cys Ser Ser Gln Ser Asp Gln Ala Ile Glu Ile |  |     |  |     |  |     |
|                                                                 |  | 165 |  | 170 |  | 175 |
| Glu Thr Ala Ser Lys Gln Gly Lys Asn Gln Ser Leu Pro Lys Pro Asp |  |     |  |     |  |     |
|                                                                 |  | 180 |  | 185 |  | 190 |
| Val Ser Glu Gln Ser His Val Thr Phe Pro Phe His Leu Gln Val Ala |  |     |  |     |  |     |
|                                                                 |  | 195 |  | 200 |  | 205 |
| Lys Gly Leu Gln Asn Gly Leu Thr Phe Gly Ser Phe Asp Ser Asn Phe |  |     |  |     |  |     |
|                                                                 |  | 210 |  | 215 |  | 220 |
| Val Lys Glu Val Ser Ser Ser Asn Gly Ala Ser Gly Gly Tyr Asp Ser |  |     |  |     |  |     |
| 225                                                             |  | 230 |  | 235 |  | 240 |
| Asn Phe Glu Ser Ser His Gly Thr Gly Asp Asp Glu Arg Glu Ser Ser |  |     |  |     |  |     |
|                                                                 |  | 245 |  | 250 |  | 255 |
| Pro Thr Thr Asn Gly Ile Thr Gly Val Ala Ser Ala Arg Glu Glu Thr |  |     |  |     |  |     |
|                                                                 |  | 260 |  | 265 |  | 270 |
| Ser Thr Val Ser Glu Asp Lys Asp Tyr Gly Ile Ser Asn Ser Ala Thr |  |     |  |     |  |     |
|                                                                 |  | 275 |  | 280 |  | 285 |
| Gly Ala Glu Pro Val Val His Ser Asp His Ile Val Pro Pro Val Glu |  |     |  |     |  |     |
|                                                                 |  | 290 |  | 295 |  | 300 |
| Glu Val Pro Lys Glu Glu Ala Leu Ser Asn Thr Glu Thr His Gln Ile |  |     |  |     |  |     |
| 305                                                             |  | 310 |  | 315 |  | 320 |
| Ala Tyr Gly Gln Glu Ala Pro Leu Ser Val Phe Gly Leu Val Pro Ser |  |     |  |     |  |     |
|                                                                 |  | 325 |  | 330 |  | 335 |
| Leu Ser Ala Ile Gly Gln Pro Val Asn Thr Glu Ala Ala Glu Thr Gln |  |     |  |     |  |     |
|                                                                 |  | 340 |  | 345 |  | 350 |
| Pro Gly Asn Ser Asn Ser Pro Ala Ile Ser Leu Val Ser Tyr Pro Pro |  |     |  |     |  |     |
|                                                                 |  | 355 |  | 360 |  | 365 |
| Asp Gln Ser Ser Ile Ala Ala Thr Gln Gln Thr Asn Phe Leu Arg     |  |     |  |     |  |     |
|                                                                 |  | 370 |  | 375 |  | 380 |
| Gln Gln Tyr Pro Pro Asn Phe Phe Pro Tyr Gly Tyr Xaa Ser Pro Tyr |  |     |  |     |  |     |
| 385                                                             |  | 390 |  | 395 |  | 400 |
| Tyr Met Pro Pro Pro Tyr Ile His Gln Phe Leu Ser Pro Asn Gly Ile |  |     |  |     |  |     |
|                                                                 |  | 405 |  | 410 |  | 415 |
| Pro Gln Gln Ser Tyr Phe Pro Gln Gly Ala Ala Leu Thr Ala Pro Ser |  |     |  |     |  |     |
|                                                                 |  | 420 |  | 425 |  | 430 |
| His Ala Lys Pro Val Asp Asn Thr Glu Asn Pro Pro Thr Thr Asn Pro |  |     |  |     |  |     |
|                                                                 |  | 435 |  | 440 |  | 445 |
| Tyr Leu His Thr Ser Pro Met Val Ala Ser Ser Ile Pro Ser Thr Thr |  |     |  |     |  |     |
|                                                                 |  | 450 |  | 455 |  | 460 |
| Thr Leu Asn Ser Ile His Ser Glu Glu Lys Ala Ser His Leu Thr Glu |  |     |  |     |  |     |
| 465                                                             |  | 470 |  | 475 |  | 480 |
| Ser Ala Ala Ala Trp Ile Gly Gln Gly Phe Gly Asn Leu Gln Val Asn |  |     |  |     |  |     |
|                                                                 |  | 485 |  | 490 |  | 495 |
| Pro Met Tyr Asn Leu Ala Tyr Gln Gly Gln Pro Leu Gly Phe Pro Val |  |     |  |     |  |     |
|                                                                 |  | 500 |  | 505 |  | 510 |
| Val Gln Ala Gly His Gly Gly Leu Met Gly Met His Gln Pro Thr Gln |  |     |  |     |  |     |
|                                                                 |  | 515 |  | 520 |  | 525 |
| Pro Met Ala Ala Ala Leu Thr Tyr Gln Thr Leu Pro Pro Pro Pro     |  |     |  |     |  |     |
|                                                                 |  | 530 |  | 535 |  | 540 |
| His Thr Thr Thr Ala Met Val Pro Ser Val Val Val Asp Thr Val Leu |  |     |  |     |  |     |
| 545                                                             |  | 550 |  | 555 |  | 560 |
| Asn Val Val Val Val Val Thr Glu Gly Leu Asn Val Pro Val Met Val |  |     |  |     |  |     |
|                                                                 |  | 565 |  | 570 |  | 575 |
| Arg Gly Gln Gly Pro Val Arg Ala Gln Val Gln Glu Thr Val Ser Thr |  |     |  |     |  |     |
|                                                                 |  | 580 |  | 585 |  | 590 |
| Trp Ala Thr Phe Leu Gly Val Leu Met Thr Trp His Leu Arg Thr Cys |  |     |  |     |  |     |
|                                                                 |  | 595 |  | 600 |  | 605 |
| Leu Thr Ser Lys Glu Arg                                         |  |     |  |     |  |     |
| 610                                                             |  |     |  |     |  |     |

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 657 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..657  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498112  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:  
actcaactta aactctttta gtaacaatgg tttcttcttc ttttaaccaag cttgtgttct 60  
ttggttgtct cctcctgctc acattcacgg acaaccttgt ggctggaaaa tctggcaaag 120  
tgaagctcaa tctttactac gaatcacttt gtccccggttg tcaggaattc atcgtcgatg 180  
acctaggtaa aatctttgac tacgatctct acacaatcac tgatctcaag ctgtttccat 240  
ttggtaatgc cgaactctcc gataatctga ctgtcacttg ccagcatggt gaagaggaat 300  
gcaaaactaaa cgcccttgaa gcttgagatc agtgattgtg tagagatcgt agtcaaagat 360  
tttacagaag tcattctcca gtcccaagag gaagaccttg atcaatgcag aaaacagaag 420  
cttcgaagaa tgagtttttc gaaagggtaa atttatctat gttgtgtttt gagttagaag 480  
atgctttttg atgttttgaa atccttgtaa actttgggat cttagacttt tatcttaaaa 540  
tcagtataaa cttcataatg gcgctttgtc acgatctgtt acttggttca tatactcttt 600  
tcattcgtca ttaattattc taartcccat ataaattaac aatgacacaa gtttgcc

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..59  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498113  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:  
Leu Asn Leu Asn Ser Phe Ser Asn Asn Gly Phe Phe Phe Asn Gln  
1 5 10 15  
Ala Cys Val Leu Trp Leu Ser Pro Pro Ala His Ile His Gly Gln Pro  
20 25 30  
Cys Gly Trp Lys Ile Trp Gln Ser Glu Ala Gln Ser Leu Leu Arg Ile  
35 40 45  
Thr Leu Ser Arg Leu Ser Gly Ile His Arg Arg  
50 55

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 99 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..99  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498114  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:  
Met Val Ser Ser Ser Leu Thr Lys Leu Val Phe Phe Gly Cys Leu Leu  
1 5 10 15  
Leu Leu Thr Phe Thr Asp Asn Leu Val Ala Gly Lys Ser Gly Lys Val  
20 25 30  
Lys Leu Asn Leu Tyr Tyr Glu Ser Leu Cys Pro Gly Cys Gln Glu Phe  
35 40 45  
Ile Val Asp Asp Leu Gly Lys Ile Phe Asp Tyr Asp Leu Tyr Thr Ile  
50 55 60



Thr Asp Leu Lys Leu Phe Pro Phe Gly Asn Ala Glu Leu Ser Asp Asn  
65 70 75 80  
Leu Thr Val Thr Cys Gln His Gly Glu Glu Glu Cys Lys Leu Asn Ala  
85 90 95  
Leu Glu Ala

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..772
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| tcctttcttt  | gagtcgcttc  | acttctcttg | catccttcaa | actcatccac | agcaaggaat | 60  |
| ggctacagca  | gcagcaccag  | cagtgtattc | atggacaaga | tcaggcattg | tgtccaaatc | 120 |
| cggacaaacc  | cagaagaaat  | ctgagatgaa | agtttcttac | ataactggac | ttactcata  | 180 |
| tgggtggtctc | aaggcacaga  | acaacaagg  | tgtctcaatg | ggatcaccac | tctgcacaga | 240 |
| acagtgtttt  | gctaacgttg  | tgatgtctct | caaaggaaga | agaggtaatg | gaggagcctt | 300 |
| atccaccacg  | tgtaacgctg  | tcggagagat | tttcaagatt | gcagcaaac  | actgttctgt | 360 |
| gaagagtggg  | ataagtatct  | agcaatgttc | tggcaacttg | tacctccgag | tgaagaagac | 420 |
| acacctgagg  | ctaactcaga  | ccacatcctg | aaaacaacca | caggagatga | agaacagggt | 480 |
| tcaagcacat  | tagcagagaa  | gtaaaacct  | cacatttgat | cgtgggttcc | tctttgtaca | 540 |
| gtcaaagtgc  | tgggtggagga | gataagtaag | tctctcagtt | gctgagaaca | taacaattta | 600 |
| caaattcacc  | acttgatttt  | gatgtggttt | taattcggtc | tggactcgca | tatcttttgg | 660 |
| tttacttcgt  | cccagtcacg  | ttagtaataa | aacgaaatcc | agcatgcttg | tactttgtat | 720 |
| ggaaacatca  | ttagtcttcc  | gattcccgat | tattaagaaa | gggttttcga | tt         |     |

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Phe | Phe | Glu | Ser | Leu | His | Phe | Ser | Cys | Ile | Leu | Gln | Thr | His | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Gln | Gly | Met | Ala | Thr | Ala | Ala | Ala | Pro | Ala | Val | Ile | Ser | Trp | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ser | Gly | Ile | Val | Ser | Lys | Ser | Gly | Gln | Thr | Gln | Lys | Lys | Ser | Glu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Met | Lys | Val | Ser | Tyr | Ile | Thr | Gly | Leu | Asn | Ser | Tyr | Gly | Gly | Leu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Gln | Asn | Asn | Lys | Val | Val | Ser | Met | Gly | Ser | Pro | Leu | Cys | Thr | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Cys | Phe | Ala | Asn | Val | Val | Met | Ser | Leu | Lys | Gly | Arg | Arg | Gly | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Gly | Ala | Leu | Ser | Thr | Thr | Cys | Asn | Ala | Val | Gly | Glu | Ile | Phe | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Ala | Ala | Lys | His | Cys | Ser | Val | Lys | Ser | Gly | Ile | Ser | Ile |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..107  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498121  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:  
Met Ala Thr Ala Ala Pro Ala Val Ile Ser Trp Thr Arg Ser Gly  
1 5 10 15  
Ile Val Ser Lys Ser Gly Gln Thr Gln Lys Lys Ser Glu Met Lys Val  
20 25 30  
Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys Ala Gln Asn  
35 40 45  
Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu Gln Cys Phe  
50 55 60  
Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Gly Asn Gly Gly Ala  
65 70 75 80  
Leu Ser Thr Thr Cys Asn Ala Val Gly Glu Ile Phe Lys Ile Ala Ala  
85 90 95  
Lys His Cys Ser Val Lys Ser Gly Ile Ser Ile  
100 105

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1498122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Met Lys Val Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys  
1 5 10 15  
Ala Gln Asn Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu  
20 25 30  
Gln Cys Phe Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Gly Asn  
35 40 45  
Gly Gly Ala Leu Ser Thr Thr Cys Asn Ala Val Gly Glu Ile Phe Lys  
50 55 60  
Ile Ala Ala Lys His Cys Ser Val Lys Ser Gly Ile Ser Ile  
65 70 75

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 671 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..671

(D) OTHER INFORMATION: / Ceres Seq. ID 1498123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cacctakaac atcctaatacg aaaaccggcg ccaccattaa aatctctcga tctctatctg | 60  |
| cgaaatttca cggtaggtat ttgaaatggc gacagttcca ggacaattga tctgggagat  | 120 |
| cgtgaagaac aacaactggt tcttggtgaa gcagttcggg agaggaaact ctaaggttca  | 180 |

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| attcagcaag | gagactaaca | acctcaccaa | cgttcactct  | tacaagcact | ctggctcttg | 240 |
| aaacaaaaag | actgtgacca | tccaggccgc | tgacaaggac  | caagctgttg | tgctcgccac | 300 |
| caccaagacc | aagaagcaga | acaagcctaa | gctctctgtc  | aacaagtcta | tcctcaagaa | 360 |
| ggaattcccc | aggatgtcaa | aggctgttgc | taaccagggtg | gtggacaact | actacaggcc | 420 |
| ggacttgaag | aaagctgcac | ttgctagact | cagcgccatc  | agcaaaggtc | tcagggttgc | 480 |
| caagtccggt | gccaagcaaa | gaaacagaca | agcttaagct  | tcttctttca | caatctgttt | 540 |
| tttttgaagt | aaaagatttt | gtytgaacag | gttttattta  | agttgttgct | ttgaagtttg | 600 |
| aaccataatg | ctattctcct | ttttcattat | ccttattata  | aaggagttag | aagtttatct | 660 |
| tgttatgctt | g          |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1498124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Thr | Val | Pro | Gly | Gln | Leu | Ile | Trp | Glu | Ile | Val | Lys | Asn | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asn | Cys | Phe | Leu | Val | Lys | Gln | Phe | Gly | Arg | Gly | Asn | Ser | Lys | Val | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Ser | Lys | Glu | Thr | Asn | Asn | Leu | Thr | Asn | Val | His | Ser | Tyr | Lys | His |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Gly | Leu | Ala | Asn | Lys | Lys | Thr | Val | Thr | Ile | Gln | Ala | Ala | Asp | Lys |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp | Gln | Ala | Val | Val | Leu | Ala | Thr | Thr | Lys | Thr | Lys | Lys | Gln | Asn | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Pro | Lys | Leu | Ser | Val | Asn | Lys | Ser | Ile | Leu | Lys | Lys | Glu | Phe | Pro | Arg |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Met | Ser | Lys | Ala | Val | Ala | Asn | Gln | Val | Val | Asp | Asn | Tyr | Tyr | Arg | Pro |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asp | Leu | Lys | Lys | Ala | Ala | Leu | Ala | Arg | Leu | Ser | Ala | Ile | Ser | Lys | Gly |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Leu | Arg | Val | Ala | Lys | Ser | Gly | Ala | Lys | Gln | Arg | Asn | Arg | Gln | Ala |     |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1065 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1065

(D) OTHER INFORMATION: / Ceres Seq. ID 1498129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| taatttcgac | ttttgtagat | ctttttctgc  | tctttctctc | tctctctctc | tctctctctc  | 60  |
| tctctctctc | ttgtattatt | tctatctccc  | ccgccgtcga | aagagaaacg | tcgatcgag   | 120 |
| aacctttgaa | atgtcgactg | gattagatat  | gtctctcgac | gacatgatcg | ccaagaaccg  | 180 |
| taagtctcgt | ggtggagccg | gccccgctcg  | tggaaccgga | tccggatccg | gaccgggtcc  | 240 |
| gactcgccgc | aacaacccta | atcggaatc   | aacccgatct | gctccatacc | aatcagccaa  | 300 |
| ggcgccggag | tccacctggg | gtcacgacat  | gttctccgat | agatctgaag | atcacggatc  | 360 |
| gggacgttcc | tccgccggaa | tcgaaactgg  | aaccaagctc | tacatttcca | atttggatta  | 420 |
| cggtgtcatg | aacgaagaca | tcaaggaaact | gtttggctga | aggttggaga | acttaaaccgc | 480 |
| tacacagttc | attttgatag | aagtgggaaga | tcaaagggaa | ctgctgaagt | agtgatttct  | 540 |
| cggcgtggcg | atgcactcgc | agctgtgaag  | aagtataatg | atgttcasct | ggatggaaaa  | 600 |

```
cccatgaaga tagagattgt gggcactaat cttcaaactg ctgcagcccc gtctggtaga 660
cctgcgaatg gaaactccaa tgggtgctcca tggagaggag gacaagggag aggaggtcaa 720
caacgaggtg gtggacgagg aggcgggtggc cgaggtggtg gtggtcgtgg taggcgtcct 780
ggtaagggcc ctgcagagaa gatttctgcg gaagatcttg atgcggatct tgataagtac 840
cattctggag atatggagac aaactaagga acgtgactga tcttctcaaa ccggtagggg 900
ttttaggagg aagagaatcg agaaaatggt tgccagaggc tttaccactt agcgcctttt 960
tggtctgtgt gttcatttgt ttcattagaa tgactttaca gaattgagaa tatgtgttat 1020
ttaaagttgt tgtctatctt aataccctca agtgaaaggc agagg
```

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```
Asn Phe Asp Phe Cys Arg Ser Phe Ser Ala Leu Ser Leu Ser Leu Ser
1 5 10 15
Leu Ser Leu Ser Leu Ser Leu Leu Tyr Tyr Phe Tyr Leu Pro Arg Arg
20 25 30
Arg Lys Arg Asn Val Asp Arg Arg Thr Phe Glu Met Ser Thr Gly Leu
35 40 45
Asp Met Ser Leu Asp Asp Met Ile Ala Lys Asn Arg Lys Ser Arg Gly
50 55 60
Gly Ala Gly Pro Ala Arg Gly Thr Gly Ser Gly Ser Gly Pro Gly Pro
65 70 75 80
Thr Arg Arg Asn Asn Pro Asn Arg Lys Ser Thr Arg Ser Ala Pro Tyr
85 90 95
Gln Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly His Asp Met Phe Ser
100 105 110
Asp Arg Ser Glu Asp His Arg Ser Gly Arg Ser Ser Ala Gly Ile Glu
115 120 125
Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Tyr Gly Val Met Asn
130 135 140
Glu Asp Ile Lys Glu Leu Phe Gly
145 150
```

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

```
Met Ser Thr Gly Leu Asp Met Ser Leu Asp Asp Met Ile Ala Lys Asn
1 5 10 15
Arg Lys Ser Arg Gly Gly Ala Gly Pro Ala Arg Gly Thr Gly Ser Gly
20 25 30
Ser Gly Pro Gly Pro Thr Arg Arg Asn Asn Pro Asn Arg Lys Ser Thr
35 40 45
Arg Ser Ala Pro Tyr Gln Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly
50 55 60
His Asp Met Phe Ser Asp Arg Ser Glu Asp His Arg Ser Gly Arg Ser
```

(2) INFORMATION FOR SEQ ID NO:206:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1498132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

(2) INFORMATION FOR SEQ ID NO:207:

(A) LENGTH: 1247 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1247

(D) OTHER INFORMATION: / Ceres Seq. ID 1498133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| ctcttgcgttc | tcttcactca  | caatctcaca  | gcaaagcctc  | tcgttgctag  | aggaatcaaa | 60   |
| caatgggtgtt | tgtgaagtcc  | accaagtcga  | atgcttactt  | caagaggtag  | caagtgaagt | 120  |
| tcaggagaag  | aagagatgga  | aagactgact  | acagggcaag  | gatccgtctt  | atcaaccaag | 180  |
| acaagaacaa  | gtacaatata  | cctaagtatc  | gttttggtgt  | ccgggtttacc | aacaaagaca | 240  |
| tagtggcaca  | gattgtatct  | gcaagcattg  | ctggtgacat  | tgttaaagct  | tctgcttacg | 300  |
| cacatgaact  | gcctcagtat  | ggtctcactg  | ttgggtcttac | aaactatgct  | gcagcttact | 360  |
| gtactggcct  | tcttttggtt  | cgccgtgttt  | taaagatggt  | ggaaattggt  | gacgagtagt | 420  |
| agggaaacgt  | tgaggccact  | ggagaggact  | tttccgttga  | gccaactgat  | tcaaggagac | 480  |
| ctttccgtgc  | tcttcttgat  | gttggaacta  | tcaggaccac  | aacaggaaac  | cgtgtgttcg | 540  |
| gtgctcttaa  | gggtgctttg  | gatggtggtc  | ttgatatccc  | tcacagtga   | aagagatttg | 600  |
| ctgggttcca  | caaggagaac  | aagcaacttg  | atgctgaaat  | ccacagggaac | tacatctatg | 660  |
| gtggccatgt  | ctcaaaactac | atgaagctgt  | tgggagaaga  | tgagccagag  | aagttacaaa | 720  |
| ctcacttcag  | tgcttacatc  | aagaaaggag  | ttgaagctga  | gagcattgag  | gagttgtaca | 780  |
| agaaggttca  | cgcagctatt  | cgtgctgrcc  | ccaaccsaag  | gaaaaccgtg  | aaacctgctc | 840  |
| ccaagcaaca  | caagaggtag  | aacttgaaga  | aacttactta  | cgaggagagg  | aagaacaagt | 900  |
| tgatctagag  | agtcaggcat  | tgaattggag  | aggtggtgat  | gatgatgatg  | aggacgatga | 960  |
| asagtaaatac | agtcagaacct | tctttatactc | atgcctcttg  | tgtgttttta  | tcttttgagc | 1020 |
| ttaatgcctc  | aaattttctg  | ttttcagact  | aaaacactca  | gcttttgtgt  | tcacatttta | 1080 |

attgtgttcg aggattttga tattgaggat acattttctt tgaagtatca ttatcttatt 1140  
attacctcca tcataatttt caagaatttg tatgacaata gtttgatgac ttgattttat 1200  
ctgtagtttg ctattgttaa atgtaagaac tgttagactt catctat

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..286
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Phe | Val | Lys | Ser | Thr | Lys | Ser | Asn | Ala | Tyr | Phe | Lys | Arg | Tyr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Val | Lys | Phe | Arg | Arg | Arg | Arg | Asp | Gly | Lys | Thr | Asp | Tyr | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ile | Arg | Leu | Ile | Asn | Gln | Asp | Lys | Asn | Lys | Tyr | Asn | Thr | Pro | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Arg | Phe | Val | Val | Arg | Phe | Thr | Asn | Lys | Asp | Ile | Val | Ala | Gln | Ile |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ser | Ala | Ser | Ile | Ala | Gly | Asp | Ile | Val | Lys | Ala | Ser | Ala | Tyr | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Glu | Leu | Pro | Gln | Tyr | Gly | Leu | Thr | Val | Gly | Leu | Thr | Asn | Tyr | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ala | Tyr | Cys | Thr | Gly | Leu | Leu | Leu | Ala | Arg | Arg | Val | Leu | Lys | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Glu | Met | Asp | Asp | Glu | Tyr | Glu | Gly | Asn | Val | Glu | Ala | Thr | Gly | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Phe | Ser | Val | Glu | Pro | Thr | Asp | Ser | Arg | Arg | Pro | Phe | Arg | Ala | Leu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Leu | Asp | Val | Gly | Leu | Ile | Arg | Thr | Thr | Thr | Gly | Asn | Arg | Val | Phe | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Leu | Lys | Gly | Ala | Leu | Asp | Gly | Gly | Leu | Asp | Ile | Pro | His | Ser | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Arg | Phe | Ala | Gly | Phe | His | Lys | Glu | Asn | Lys | Gln | Leu | Asp | Ala | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | His | Arg | Asn | Tyr | Ile | Tyr | Gly | His | Val | Ser | Asn | Tyr | Met | Lys |     |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Leu | Gly | Glu | Asp | Glu | Pro | Glu | Lys | Leu | Gln | Thr | His | Phe | Ser | Ala |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Tyr | Ile | Lys | Lys | Gly | Val | Glu | Ala | Glu | Ser | Ile | Glu | Glu | Leu | Tyr | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Lys | Val | His | Ala | Ala | Ile | Arg | Ala | Xaa | Pro | Asn | Xaa | Arg | Lys | Thr | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Pro | Ala | Pro | Lys | Gln | His | Lys | Arg | Tyr | Asn | Leu | Lys | Lys | Leu | Thr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Tyr | Glu | Glu | Arg | Lys | Asn | Lys | Leu | Ile | Glu | Arg | Val | Arg | His |     |     |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Met Leu Glu Met Asp Asp Glu Tyr Glu Gly Asn Val Glu Ala Thr Gly  
1 5 10 15  
Glu Asp Phe Ser Val Glu Pro Thr Asp Ser Arg Arg Pro Phe Arg Ala  
20 25 30  
Leu Leu Asp Val Gly Leu Ile Arg Thr Thr Thr Gly Asn Arg Val Phe  
35 40 45  
Gly Ala Leu Lys Gly Ala Leu Asp Gly Gly Leu Asp Ile Pro His Ser  
50 55 60  
Asp Lys Arg Phe Ala Gly Phe His Lys Glu Asn Lys Gln Leu Asp Ala  
65 70 75 80  
Glu Ile His Arg Asn Tyr Ile Tyr Gly Gly His Val Ser Asn Tyr Met  
85 90 95  
Lys Leu Leu Gly Glu Asp Glu Pro Glu Lys Leu Gln Thr His Phe Ser  
100 105 110  
Ala Tyr Ile Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Leu Tyr  
115 120 125  
Lys Lys Val His Ala Ala Ile Arg Ala Xaa Pro Asn Xaa Arg Lys Thr  
130 135 140  
Val Lys Pro Ala Pro Lys Gln His Lys Arg Tyr Asn Leu Lys Lys Leu  
145 150 155 160  
Thr Tyr Glu Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Arg His  
165 170 175

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1498136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Met Asp Asp Glu Tyr Glu Gly Asn Val Glu Ala Thr Gly Glu Asp Phe  
1 5 10 15  
Ser Val Glu Pro Thr Asp Ser Arg Arg Pro Phe Arg Ala Leu Leu Asp  
20 25 30  
Val Gly Leu Ile Arg Thr Thr Thr Thr Gly Asn Arg Val Phe Gly Ala Leu  
35 40 45  
Lys Gly Ala Leu Asp Gly Gly Leu Asp Ile Pro His Ser Asp Lys Arg  
50 55 60  
Phe Ala Gly Phe His Lys Glu Asn Lys Gln Leu Asp Ala Glu Ile His  
65 70 75 80  
Arg Asn Tyr Ile Tyr Gly Gly His Val Ser Asn Tyr Met Lys Leu Leu  
85 90 95  
Gly Glu Asp Glu Pro Glu Lys Leu Gln Thr His Phe Ser Ala Tyr Ile  
100 105 110  
Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Leu Tyr Lys Lys Val  
115 120 125  
His Ala Ala Ile Arg Ala Xaa Pro Asn Xaa Arg Lys Thr Val Lys Pro  
130 135 140  
Ala Pro Lys Gln His Lys Arg Tyr Asn Leu Lys Lys Leu Thr Tyr Glu  
145 150 155 160  
Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Arg His  
165 170

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1186 base pairs

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- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1186  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498137  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```
aaaaaattcg ctattcaatt ccttttagtaa gcttcacttt tcacacttct ctcactttct 60
ggtcagaaac tttgtggatc tagaagaaca cacaaatcac aagagtgaac aaagatgaac 120
gacttgatga cgaaatcggt tatgagttac gttgacttga aaaaagcagc gatgaaggat 180
atggaagcag gacctgactt tgatcttgag atggcttcga cgaaagcaga caagatggat 240
gagaatctgt catctttctt acaagaagca gagtatgtga aagcagagat gggttttatt 300
agtagacact ggctcggatt gaavcragta ccatgaagag agtaaagggtg ttcacaaggc 360
agagtctgtg aagtctcttc gtaacaagat ctctaakgag attgtgtctg gtttgaggaa 420
ggcgaaatcg attaagtcga agctggaaga gatggataaa gcaaacaagg agattaaaag 480
gctctctggg actccgggtt acaggagcag aaccgctgtg actaacgggc tgaggaagaa 540
acttaaggra gtgmtgatgg agtttcaggg gctgaggcaa aagatgatga gtgagtacaa 600
ggagactggt gagagaaggt acttcactgt cactggagaa catgctaata atgagatgat 660
tgagaagatc attacttgata acgctggaga tgaagagtgt ctcacgcgag caattcagga 720
acatggtaaa ggaaagggtc tggaaactgt ggttgagatt caagataggt acgatgcagc 780
aaaggagatt gagaagagtc tgttgagagc tcaccaagtg tttcttgata tggctgtgat 840
ggttgaatcg caaggtgaac agatggacga gatcgagcat catgtgatta atgcgagcca 900
ttacgtggct gatggagcta atgagctgaa gactgcaaag agtcatcaga gaaacagcag 960
aaaatggatg tgcattggta tcattgtgct gcttttgatc attctcattg ttgttatccc 1020
catcattacc agtttcagct cttcttgaga tactggctat gttcactcct tttgttttgt 1080
ttcgctcttc tttgtaccaa tggatgtctt aatccttttg tgttcttaaa ggatgtctta 1140
atcctttcgt gtcttgatc caatttcaat gaaatgggtg atgttt
```

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..198  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```
Met Asp Lys Ala Asn Lys Glu Ile Lys Arg Leu Ser Gly Thr Pro Val
1 5 10 15
Tyr Arg Ser Arg Thr Ala Val Thr Asn Gly Leu Arg Lys Lys Leu Lys
20 25 30
Xaa Val Xaa Met Glu Phe Gln Gly Leu Arg Gln Lys Met Met Ser Glu
35 40 45
Tyr Lys Glu Thr Val Glu Arg Tyr Phe Thr Val Thr Gly Glu His
50 55 60
Ala Asn Asp Glu Met Ile Glu Lys Ile Ile Thr Asp Asn Ala Gly Gly
65 70 75 80
Glu Glu Phe Leu Thr Arg Ala Ile Gln Glu His Gly Lys Gly Lys Val
85 90 95
Leu Glu Thr Val Val Glu Ile Gln Asp Arg Tyr Asp Ala Ala Lys Glu
100 105 110
Ile Glu Lys Ser Leu Leu Glu Leu His Gln Val Phe Leu Asp Met Ala
115 120 125
Val Met Val Glu Ser Gln Gly Glu Gln Met Asp Glu Ile Glu His His
130 135 140
Val Ile Asn Ala Ser His Tyr Val Ala Asp Gly Ala Asn Glu Leu Lys
145 150 155 160
```



Thr Ala Lys Ser His Gln Arg Asn Ser Arg Lys Trp Met Cys Ile Gly  
165 170 175  
Ile Ile Val Leu Leu Leu Ile Ile Leu Ile Val Val Ile Pro Ile Ile  
180 185 190  
Thr Ser Phe Ser Ser Ser  
195

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Met Glu Phe Gln Gly Leu Arg Gln Lys Met Met Ser Glu Tyr Lys Glu  
1 5 10 15  
Thr Val Glu Arg Arg Tyr Phe Thr Val Thr Gly Glu His Ala Asn Asp  
20 25 30  
Glu Met Ile Glu Lys Ile Ile Thr Asp Asn Ala Gly Gly Glu Glu Phe  
35 40 45  
Leu Thr Arg Ala Ile Gln Glu His Gly Lys Gly Lys Val Leu Glu Thr  
50 55 60  
Val Val Glu Ile Gln Asp Arg Tyr Asp Ala Ala Lys Glu Ile Glu Lys  
65 70 75 80  
Ser Leu Leu Glu Leu His Gln Val Phe Leu Asp Met Ala Val Met Val  
85 90 95  
Glu Ser Gln Gly Glu Gln Met Asp Glu Ile Glu His His Val Ile Asn  
100 105 110  
Ala Ser His Tyr Val Ala Asp Gly Ala Asn Glu Leu Lys Thr Ala Lys  
115 120 125  
Ser His Gln Arg Asn Ser Arg Lys Trp Met Cys Ile Gly Ile Ile Val  
130 135 140  
Leu Leu Leu Ile Ile Leu Ile Val Val Ile Pro Ile Ile Thr Ser Phe  
145 150 155 160  
Ser Ser Ser

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Met Ser Glu Tyr Lys Glu Thr Val Glu Arg Arg Tyr Phe Thr Val  
1 5 10 15  
Thr Gly Glu His Ala Asn Asp Glu Met Ile Glu Lys Ile Ile Thr Asp  
20 25 30  
Asn Ala Gly Gly Glu Glu Phe Leu Thr Arg Ala Ile Gln Glu His Gly  
35 40 45  
Lys Gly Lys Val Leu Glu Thr Val Val Glu Ile Gln Asp Arg Tyr Asp  
50 55 60  
Ala Ala Lys Glu Ile Glu Lys Ser Leu Leu Glu Leu His Gln Val Phe

[illegible]

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..768  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

|             |             |            |            |    |            |            |     |
|-------------|-------------|------------|------------|----|------------|------------|-----|
| accaaaatct  | cttctctctc  | ttccattgtc | ttcctcta   | at | ggaaccaacc | gagaaatcta | 60  |
| tgttactaga  | aactactagt  | accacgaaga | tggagaccaa | at | atacgaagat | atgttaccag | 120 |
| ttatggcgga  | gaagatggat  | gttgaagagt | ttgtatcaga | gt | ttatgcaa   | ggtttcagtt | 180 |
| tgcttgcgga  | tccagagaga  | catctcatca | cagctgagtc | t  | ctaagacga  | aactcagggg | 240 |
| tacttggaat  | tgaaggtat   | agcaaggaag | atgctcaagg | a  | aatggttaga | gaaggagacs | 300 |
| tcgatggaga  | tgkgctctt   | aaccaaaccg | aattctgcgt | t  | ctctatgggt | cggttaagcc | 360 |
| ctgagatgat  | ggaagacgcc  | graacctggk | tggaatgggg | t  | tgggctatg  | ggatcctttc | 420 |
| aagaaaacct  | atattcatca  | gagatcttga | gcttaacaaa | g  | gacgaagct  | aaatcgattg | 480 |
| gttcacaaaa  | cagaggaagt  | ataatgcacg | ttttcttcaa | a  | ctccgatct  | cagatccgta | 540 |
| atttcatggg  | accttcttca  | gaagattctc | ttcctctttc | t  | tgcaaatac  | aagcgtcaac | 600 |
| gataaaatga  | ttcatataag  | gttgagattt | tgtgattttg | c  | tgttctttt  | tttacttttg | 660 |
| tgcaatggag  | tataattgaat | gtataattcg | tctttttttt | t  | taaacttga  | tgttgatatt | 720 |
| tgctataaatt | aaatttgccta | gattattatt | aatcaattta | t  | tttatttt   |            |     |

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..200  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Asn | Leu | Phe | Ser | Leu | Phe | His | Cys | Leu | Pro | Leu | Met | Glu | Pro | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Lys | Ser | Met | Leu | Leu | Glu | Thr | Thr | Ser | Thr | Thr | Lys | Met | Glu | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Tyr | Glu | Asp | Met | Leu | Pro | Val | Met | Ala | Glu | Lys | Met | Asp | Val | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Phe | Val | Ser | Glu | Leu | Cys | Lys | Gly | Phe | Ser | Leu | Leu | Ala | Asp | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Arg | His | Leu | Ile | Thr | Ala | Glu | Ser | Leu | Arg | Arg | Asn | Ser | Gly | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Gly | Ile | Glu | Gly | Met | Ser | Lys | Glu | Asp | Ala | Gln | Gly | Met | Val | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Glu | Gly | Asp | Xaa | Asp | Gly | Asp | Xaa | Ala | Leu | Asn | Gln | Thr | Glu | Phe | Cys |

(2) INFORMATION FOR SEQ ID NO:217:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1498143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1498144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Leu Leu Glu Thr Thr Ser Thr Thr Lys Met Glu Thr Lys Tyr Glu  
1 5 10 15  
Asp Met Leu Pro Val Met Ala Glu Lys Met Asp Val Glu Glu Phe Val  
20 25 30  
Ser Glu Leu Cys Lys Gly Phe Ser Leu Leu Ala Asp Pro Glu Arg His  
35 40 45  
Leu Ile Thr Ala Glu Ser Leu Arg Arg Asn Ser Gly Ile Leu Gly Ile  
50 55 60  
Glu Gly Met Ser Lys Glu Asp Ala Gln Gly Met Val Arg Glu Gly Asp  
65 70 75 80  
Xaa Asp Gly Asp Xaa Ala Leu Asn Gln Thr Glu Phe Cys Val Leu Met  
85 90 95  
Val Arg Leu Ser Pro Glu Met Met Glu Asp Ala Xaa Thr Trp Xaa Glu  
100 105 110  
Trp Gly Trp Val Met Gly Ser Phe Gln Glu Asn Leu Tyr Ser Ser Glu  
115 120 125  
Ile Leu Ser Leu Thr Lys Asp Glu Ala Lys Ser Ile Gly Ser Gln Asn  
130 135 140  
Arg Gly Ser Ile Met His Val Phe Phe Lys Leu Arg Ser Gln Ile Arg  
145 150 155 160  
Asn Phe Met Gly Pro Ser Ser Glu Asp Ser Leu Pro Leu Ser Cys Lys  
165 170 175  
Tyr Lys Arg Gln Arg  
180

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

|             |             |            |             |             |            |      |
|-------------|-------------|------------|-------------|-------------|------------|------|
| atttcgagat  | cctctcggct  | tggtcgttct | tcgtgaacga  | tcccatctat  | tgtttctcgc | 60   |
| tggtctcaga  | ttcgactaac  | ttggatatct | ccgatactga  | agaagcctcc  | ttcttctttt | 120  |
| tccgctcttc  | ccgatgccga  | tcgataagat | cttcaaagat  | gatgctagt   | aagagaaggg | 180  |
| agaacgtg    | aggaatggcat | catttggttg | tgcaatggct  | atcagtgatc  | tggttaagtc | 240  |
| tactttagg   | ccaaagggca  | tggataaaat | cttacaatct  | actggtagag  | gtcatgcggt | 300  |
| cactgttact  | aacgatgggt  | ctactattct | caagtcactt  | cacatagaca  | accctgcagc | 360  |
| taaagttctt  | gttgacatct  | cgaaagttca | agatgatgag  | gttggtgatg  | gaactacctc | 420  |
| tggtgtgtgc  | ttggccggcg  | agcttctgag | ggaagcagaa  | aagcttgtgg  | cttctaagat | 480  |
| tcaccctatg  | accatcatag  | caggttacag | aatggcttcg  | gaatgtgctc  | gtaatgcctt | 540  |
| actgaaaaga  | gtcattgata  | acaaggacaa | tcagagagaag | tttaggtcag  | acttggtgaa | 600  |
| gattgcgatg  | actactttat  | gttccaaaat | tctctcacag  | gacaaggaac  | attttgcaga | 660  |
| aatggccgtg  | gatgctgttt  | tcaggctaaa | gggaagcaca  | aacttggaag  | ctattcagat | 720  |
| catcaaaaaa  | cctggagggt  | ctctgaagga | ttcgtttttg  | gatgaagggt  | ttattcttga | 780  |
| caagaaaata  | ggaattgggc  | agcctaagcg | catagagaat  | gcaaatactt  | tagtagctaa | 840  |
| tactgctatg  | gataccgata  | aagtgaagat | ttacggtgca  | cgtgtccgtg  | tggattccat | 900  |
| gaccaagggt  | gctgagattg  | aaggtcaaca | gtttgacctt  | aacgcctcta  | agcttgctt  | 960  |
| cgagcgtg    | tttaaaggca  | tggtcggcat | gaccactgac  | cctgccgctg  | tccaagagct | 1020 |
| cgaaggttaag | ctccagaaag  | tcttggaatg | ctacgaggct  | aggctcgcca  | aatctgagtt | 1080 |
| cttggctggt  | gattccttca  | ctcttgctga | tcttcaccac  | ctcccagcca  | tccattactt | 1140 |
| gttgggtact  | gactccaagg  | tgctctttga | ctctcgccct  | aagggttagcg | agtgaattaa | 1200 |
| gaagatctct  | gccaggcctg  | cttgggctaa | ggttattgac  | ctccagaagc  | agtagtgacc | 1260 |
| ctctctcttt  | cttcacttct  | tttcttttcc | ttttgcccaa  | ataaacgagt  | ccagtgattt | 1320 |
| tcttttcttg  | gcttatgtac  | ttgtgttttc | agtattattt  | atgtcatcat  | catcctcttc | 1380 |
| ttttgtgtta  | ttgttggtt   | cattcacatt | tgtgcaatta  | aaaaccagag  | tttaaaccgc | 1440 |

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..353

(D) OTHER INFORMATION: / Ceres Seq. ID 1498146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ile | Asp | Lys | Ile | Phe | Lys | Asp | Asp | Ala | Ser | Glu | Glu | Lys | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Arg | Ala | Arg | Met | Ala | Ser | Phe | Val | Gly | Ala | Met | Ala | Ile | Ser | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Leu | Val | Lys | Ser | Thr | Leu | Gly | Pro | Lys | Gly | Met | Asp | Lys | Ile | Leu | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Thr | Gly | Arg | Gly | His | Ala | Val | Thr | Val | Thr | Asn | Asp | Gly | Ala | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Lys | Ser | Leu | His | Ile | Asp | Asn | Pro | Ala | Ala | Lys | Val | Leu | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Ile | Ser | Lys | Val | Gln | Asp | Asp | Glu | Val | Gly | Asp | Gly | Thr | Thr | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Val | Val | Leu | Ala | Gly | Glu | Leu | Leu | Arg | Glu | Ala | Glu | Lys | Leu | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ser | Lys | Ile | His | Pro | Met | Thr | Ile | Ile | Ala | Gly | Tyr | Arg | Met | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Glu | Cys | Ala | Arg | Asn | Ala | Leu | Leu | Lys | Arg | Val | Ile | Asp | Asn | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Asn | Ala | Glu | Lys | Phe | Arg | Ser | Asp | Leu | Leu | Lys | Ile | Ala | Met | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Leu | Cys | Ser | Lys | Ile | Leu | Ser | Gln | Asp | Lys | Glu | His | Phe | Ala | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Ala | Val | Asp | Ala | Val | Phe | Arg | Leu | Lys | Gly | Ser | Thr | Asn | Leu | Glu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ile | Gln | Ile | Ile | Lys | Lys | Pro | Gly | Gly | Ser | Leu | Lys | Asp | Ser | Phe |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Asp | Glu | Gly | Phe | Ile | Leu | Asp | Lys | Lys | Ile | Gly | Ile | Gly | Gln | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Arg | Ile | Glu | Asn | Ala | Asn | Ile | Leu | Val | Ala | Asn | Thr | Ala | Met | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Thr | Asp | Lys | Val | Lys | Ile | Tyr | Gly | Ala | Arg | Val | Arg | Val | Asp | Ser | Met |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Thr | Lys | Val | Ala | Glu | Ile | Glu | Gly | Gln | Gln | Phe | Asp | Pro | Asn | Ala | Ser |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Lys | Leu | Ala | Phe | Glu | Arg | Val | Phe | Lys | Gly | Met | Phe | Gly | Met | Thr | Thr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Pro | Ala | Ala | Val | Gln | Glu | Leu | Glu | Gly | Lys | Leu | Gln | Lys | Val | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Val | Tyr | Glu | Ala | Arg | Leu | Ala | Lys | Ser | Glu | Phe | Leu | Ala | Gly | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Ser | Phe | Thr | Leu | Ala | Asp | Leu | His | His | Leu | Pro | Ala | Ile | His | Tyr | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Gly | Thr | Asp | Ser | Lys | Val | Leu | Phe | Asp | Ser | Arg | Pro | Lys | Val | Ser |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |

Glu

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..333
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498147
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Phe | Val | Gly | Ala | Met | Ala | Ile | Ser | Asp | Leu | Val | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Leu | Gly | Pro | Lys | Gly | Met | Asp | Lys | Ile | Leu | Gln | Ser | Thr | Gly | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | His | Ala | Val | Thr | Val | Thr | Asn | Asp | Gly | Ala | Thr | Ile | Leu | Lys | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | His | Ile | Asp | Asn | Pro | Ala | Ala | Lys | Val | Leu | Val | Asp | Ile | Ser | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Gln | Asp | Asp | Glu | Val | Gly | Asp | Gly | Thr | Thr | Ser | Val | Val | Val | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Gly | Glu | Leu | Leu | Arg | Glu | Ala | Glu | Lys | Leu | Val | Ala | Ser | Lys | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| His | Pro | Met | Thr | Ile | Ile | Ala | Gly | Tyr | Arg | Met | Ala | Ser | Glu | Cys | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Asn | Ala | Leu | Leu | Lys | Arg | Val | Ile | Asp | Asn | Lys | Asp | Asn | Ala | Glu |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Phe | Arg | Ser | Asp | Leu | Leu | Lys | Ile | Ala | Met | Thr | Thr | Leu | Cys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ile | Leu | Ser | Gln | Asp | Lys | Glu | His | Phe | Ala | Glu | Met | Ala | Val | Asp |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Val | Phe | Arg | Leu | Lys | Gly | Ser | Thr | Asn | Leu | Glu | Ala | Ile | Gln | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Lys | Lys | Pro | Gly | Gly | Ser | Leu | Lys | Asp | Ser | Phe | Leu | Asp | Glu | Gly |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Ile | Leu | Asp | Lys | Lys | Ile | Gly | Ile | Gly | Gln | Pro | Lys | Arg | Ile | Glu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Ala | Asn | Ile | Leu | Val | Ala | Asn | Thr | Ala | Met | Asp | Thr | Asp | Lys | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Ile | Tyr | Gly | Ala | Arg | Val | Arg | Val | Asp | Ser | Met | Thr | Lys | Val | Ala |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Glu | Ile | Glu | Gly | Gln | Phe | Asp | Pro | Asn | Ala | Ser | Lys | Leu | Ala | Phe |     |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Arg | Val | Phe | Lys | Gly | Met | Phe | Gly | Met | Thr | Thr | Asp | Pro | Ala | Ala |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Gln | Glu | Leu | Glu | Gly | Lys | Leu | Gln | Lys | Val | Leu | Asp | Val | Tyr | Glu |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Arg | Leu | Ala | Lys | Ser | Glu | Phe | Leu | Ala | Gly | Asp | Ser | Phe | Thr | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Asp | Leu | His | His | Leu | Pro | Ala | Ile | His | Tyr | Leu | Leu | Gly | Thr | Asp |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Lys | Val | Leu | Phe | Asp | Ser | Arg | Pro | Lys | Val | Ser | Glu |     |     |     |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:222:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 326 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1498148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Met Ala Ile Ser Asp Leu Val Lys Ser Thr Leu Gly Pro Lys Gly Met  
1 5 10 15  
Asp Lys Ile Leu Gln Ser Thr Gly Arg Gly His Ala Val Thr Val Thr  
20 25 30  
Asn Asp Gly Ala Thr Ile Leu Lys Ser Leu His Ile Asp Asn Pro Ala  
35 40 45  
Ala Lys Val Leu Val Asp Ile Ser Lys Val Gln Asp Asp Glu Val Gly  
50 55 60  
Asp Gly Thr Thr Ser Val Val Val Leu Ala Gly Glu Leu Leu Arg Glu  
65 70 75 80  
Ala Glu Lys Leu Val Ala Ser Lys Ile His Pro Met Thr Ile Ile Ala  
85 90 95  
Gly Tyr Arg Met Ala Ser Glu Cys Ala Arg Asn Ala Leu Leu Lys Arg  
100 105 110  
Val Ile Asp Asn Lys Asp Asn Ala Glu Lys Phe Arg Ser Asp Leu Leu  
115 120 125  
Lys Ile Ala Met Thr Thr Leu Cys Ser Lys Ile Leu Ser Gln Asp Lys  
130 135 140  
Glu His Phe Ala Glu Met Ala Val Asp Ala Val Phe Arg Leu Lys Gly  
145 150 155 160  
Ser Thr Asn Leu Glu Ala Ile Gln Ile Ile Lys Lys Pro Gly Gly Ser  
165 170 175  
Leu Lys Asp Ser Phe Leu Asp Glu Gly Phe Ile Leu Asp Lys Lys Ile  
180 185 190  
Gly Ile Gly Gln Pro Lys Arg Ile Glu Asn Ala Asn Ile Leu Val Ala  
195 200 205  
Asn Thr Ala Met Asp Thr Asp Lys Val Lys Ile Tyr Gly Ala Arg Val  
210 215 220  
Arg Val Asp Ser Met Thr Lys Val Ala Glu Ile Glu Gly Gln Gln Phe  
225 230 235 240  
Asp Pro Asn Ala Ser Lys Leu Ala Phe Glu Arg Val Phe Lys Gly Met  
245 250 255  
Phe Gly Met Thr Thr Asp Pro Ala Ala Val Gln Glu Leu Glu Gly Lys  
260 265 270  
Leu Gln Lys Val Leu Asp Val Tyr Glu Ala Arg Leu Ala Lys Ser Glu  
275 280 285  
Phe Leu Ala Gly Asp Ser Phe Thr Leu Ala Asp Leu His His Leu Pro  
290 295 300  
Ala Ile His Tyr Leu Leu Gly Thr Asp Ser Lys Val Leu Phe Asp Ser  
305 310 315 320  
Arg Pro Lys Val Ser Glu  
325

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 964 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..964

(D) OTHER INFORMATION: / Ceres Seq. ID 1498149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aatccattcc tttccaatcc acgtccaaaa aacaaaacca aaaaaaaaaa aaaaaaaaaaag | 60  |
| acaaaaaaaa atgaacactc caataaaact cgcctttctc attctctgca ttgccctaac   | 120 |
| cgcaaccgca tttatagtc cagcaaaacg tgacgccgtt tcaccacacc accaaaaagc    | 180 |
| cgtcgatgga atctgcagcg ttgtgcaaga caaacgtcta tgcagcatta ccttaagaaa   | 240 |
| cgtcccaagc gatgatccc cgttttgggt tcgttactta gccacggcag cagaagcgtc    | 300 |

|             |            |            |             |             |             |     |
|-------------|------------|------------|-------------|-------------|-------------|-----|
| cgttaaaaag  | ggtttgaagt | tcctctccgg | aatcaaacca  | aaatacaaag  | gaaacgcctt  | 360 |
| cgccacaaca  | tgcataccg  | gctgckwgaa | acagctacac  | aacgccttgg  | acgactttgc  | 420 |
| agattttctgg | aaagccgcag | gaaaaaatct | aacgagcatg  | gctgagaatt  | mcttcacatg  | 480 |
| taagaagaag  | atgacttcca | tcttcactta | ccattccact  | tgtctcgatg  | acattttacga | 540 |
| caagacgttg  | cacaaagtgg | tcgaaggagg | gattggcctt  | gggaaaagaa  | tgagtgggtga | 600 |
| gtctgtggat  | gtgttcgctg | gaatgggcaa | agtcctttaac | actttcaaca  | ttaagaccaa  | 660 |
| acttaaccag  | aaagataccg | acacgttgct | cccaccacct  | ttgtcctttt  | actactattg  | 720 |
| attttatttta | tcaatatata | ttatatatca | taaaacacaa  | caaaatgtac  | tgcttcggtc  | 780 |
| gatggtgatg  | aataattttc | atcgattggg | ttttcagata  | ttttgggggat | cttgtaacca  | 840 |
| aaggttcctt  | ttgatgtatg | tttgatttta | atatgttatg  | gattataatc  | atgtatggac  | 900 |
| ctcgtgattg  | gaaaggatat | ggaataatgt | gattatctaa  | taataaaaaac | gtaattaata  | 960 |
| tcgc        |            |            |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | His | Ser | Phe | Pro | Ile | His | Val | Gln | Lys | Thr | Lys | Pro | Lys | Lys | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Lys | Lys | Arg | Gln | Lys | Lys | Met | Asn | Thr | Pro | Ile | Lys | Leu | Ala | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ile | Leu | Cys | Ile | Ala | Leu | Thr | Ala | Thr | Ala | Phe | Ile | Val | Pro | Ala |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Lys | Arg | Asp | Ala | Val | Ser | Pro | His | His | Gln | Lys | Ala | Val | Asp | Gly | Ile |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Cys | Ser | Val | Val | Gln | Asp | Lys | Arg | Leu | Cys | Ser | Ile | Thr | Leu | Arg | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Pro | Ser | Asp | Asp | Pro | Ala | Val | Leu | Val | Arg | Tyr | Leu | Ala | Thr | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Glu | Ala | Ser | Val | Lys | Lys | Gly | Leu | Lys | Phe | Leu | Ser | Gly | Ile | Lys |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Lys | Tyr | Lys | Gly | Asn | Ala | Phe | Ala | Thr | Thr | Cys | Ile | Thr | Gly | Cys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Xaa | Lys | Gln | Leu | His | Asn | Ala | Leu | Asp | Asp | Phe | Ala | Asp | Phe | Trp | Lys |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ala | Ala | Gly | Lys | Asn | Leu | Thr | Ser | Met | Ala | Glu | Asn | Xaa | Phe | Thr | Cys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Lys | Lys | Met | Thr | Ser | Ile | Phe | Thr | Tyr | His | Ser | Thr | Cys | Leu | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Ile | Tyr | Asp | Lys | Thr | Leu | His | Lys | Val | Val | Glu | Gly | Gly | Ile | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Gly | Lys | Arg | Met | Ser | Gly | Glu | Ser | Val | Asp | Val | Phe | Ala | Gly | Met |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Lys | Val | Phe | Asn | Thr | Phe | Asn | Ile | Lys | Thr | Lys | Leu | Asn | Gln | Lys |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Asp | Thr | Asp | Thr | Leu | Leu | Pro | Pro | Pro | Leu | Ser | Phe | Tyr | Tyr | Tyr |     |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1498151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asn | Thr | Pro | Ile | Lys | Leu | Ala | Phe | Leu | Ile | Leu | Cys | Ile | Ala | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Ala | Thr | Ala | Phe | Ile | Val | Pro | Ala | Lys | Arg | Asp | Ala | Val | Ser | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| His | His | Gln | Lys | Ala | Val | Asp | Gly | Ile | Cys | Ser | Val | Val | Gln | Asp | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Leu | Cys | Ser | Ile | Thr | Leu | Arg | Asn | Val | Pro | Ser | Asp | Asp | Pro | Ala |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Val | Leu | Val | Arg | Tyr | Leu | Ala | Thr | Ala | Ala | Glu | Ala | Ser | Val | Lys | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Gly | Leu | Lys | Phe | Leu | Ser | Gly | Ile | Lys | Pro | Lys | Tyr | Lys | Gly | Asn | Ala |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Phe | Ala | Thr | Thr | Cys | Ile | Thr | Gly | Cys | Xaa | Lys | Gln | Leu | His | Asn | Ala |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Asp | Asp | Phe | Ala | Asp | Phe | Trp | Lys | Ala | Ala | Gly | Lys | Asn | Leu | Thr |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Met | Ala | Glu | Asn | Xaa | Phe | Thr | Cys | Lys | Lys | Lys | Met | Thr | Ser | Ile |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Phe | Thr | Tyr | His | Ser | Thr | Cys | Leu | Asp | Asp | Ile | Tyr | Asp | Lys | Thr | Leu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| His | Lys | Val | Val | Glu | Gly | Gly | Ile | Gly | Leu | Gly | Lys | Arg | Met | Ser | Gly |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Glu | Ser | Val | Asp | Val | Phe | Ala | Gly | Met | Gly | Lys | Val | Phe | Asn | Thr | Phe |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Asn | Ile | Lys | Thr | Lys | Leu | Asn | Gln | Lys | Asp | Thr | Asp | Thr | Leu | Leu | Pro |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Pro | Pro | Leu | Ser | Phe | Tyr | Tyr | Tyr |     |     |     |     |     |     |     |     |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1498152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaaaacatta | ctcattcaca | aaaccatctt | aaagcaacta | cacaaatctt | gaaattttct | 60  |
| catattttct | atttactata | taaactttta | atcaaataca | gattaactat | ggctgaggag | 120 |
| tacaagaaca | acgttcccga | gcacgagaca | ccaacggtcg | caacagagga | atcaccagcg | 180 |
| acgacaacag | aggttacgga | tcgtggattg | tttgatttct | tggggaagaa | ggaagaggaa | 240 |
| gtgaaacctc | aagagacaac | gacgctcgag | tctgagttcg | atcataaggc | tcagatctct | 300 |
| gaaccggagt | tagctgcgga | sacgaggaag | tgaaggagaa | caagattact | ctgctcaacr | 360 |
| agtcctcagt | ggctctcctg | aatacwtgca | tcccatgaat | cttagcacca | tcctcaccgt | 420 |
| tgrttc     |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1498153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```
Lys Asn Ile Thr His Ser Gln Asn His Leu Lys Ala Thr Thr Gln Ile
1 5 10 15
Leu Lys Phe Ser His Ile Phe Tyr Leu Leu Tyr Lys Leu Leu Ile Lys
20 25 30
Ser Arg Leu Thr Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His
35 40 45
Glu Thr Pro Thr Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu
50 55 60
Val Thr Asp Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu
65 70 75 80
Val Lys Pro Gln Glu Thr Thr Thr Leu Glu Ser Glu Phe Asp His Lys
85 90 95
Ala Gln Ile Ser Glu Pro Glu Leu Ala Ala Xaa Thr Arg Lys
100 105 110
```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1498154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```
Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His Glu Thr Pro Thr
1 5 10 15
Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu Val Thr Asp Arg
20 25 30
Gly Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu Val Lys Pro Gln
35 40 45
Glu Thr Thr Thr Leu Glu Ser Glu Phe Asp His Lys Ala Gln Ile Ser
50 55 60
Glu Pro Glu Leu Ala Ala Xaa Thr Arg Lys
65 70
```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1011 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1011

(D) OTHER INFORMATION: / Ceres Seq. ID 1498155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```
tcttcatata ttattatatt cgatttttgca tcctgctctg aagacgatat tagcaatcat 60
ggagcgtcta acatctcctc ctcgtttgat gattgtctct gatcttgatc atactatggt 120
tgatcatcat gactcctgaga atctatctct gctgagattc aattcgttgt gggaacacgc 180
ttatcgccat gactctcttc ttgtgttttc tacgggaaga tcaccgacat tgtataaaga 240
actgagaaaag gagaaacctt tggtgacccc tgatattacc attatgtctg taggaactga 300
gattacttat ggtaactcta tggttcctga tcatggttgg gttgaggctc tgaacaataa 360
atgggatttg ggtattgtca aacaagaagc tagcaacttc cctgagttaa agcttcaggc 420
agaaactgag cagaggccac acaagggttag cttttatggt gaaaagagta aggctcagga 480
agttactaag gagctatcac agagggttct gaaacgtggg ctggatgtca aaataattta 540
```

```
cagtggaggt atggatttgg atatttttacc acaaggtgcc ggaaagggac aagcgcttgc 600
atatctgctg aagaaactga agactgaggg gaaactccct gtcaatactc ttgcttgtgg 660
cgactctggg aatgatgctg agctgttttag tattcccgat gtttatgggtg ttatggtaag 720
caatgctcaa gaagagctgt tgaagtggca tgctgaaaat gcaaaagaca accctaaggt 780
aatccatgca aaggagaggt gtgcaggtgg gattatacaa gccattgggtc acttcaagct 840
tggtccaaac ctttctccaa gagatgtctc tgacttctta gagatcaagg cagagaatgt 900
gaaccctggg cacgaggttg tgaagttttt tttgttctac gagaaatgga gacggggcga 960
ggttgagaac tctgaggcat acacagcaag ccccgctctc atttctcgta g
```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..336

(D) OTHER INFORMATION: / Ceres Seq. ID 1498156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```
Leu His Ile Leu Leu Tyr Ser Ile Leu His Pro Ala Leu Lys Thr Ile
1 5 10 15
Leu Ala Ile Met Glu Arg Leu Thr Ser Pro Pro Arg Leu Met Ile Val
20 25 30
Ser Asp Leu Asp His Thr Met Val Asp His His Asp Pro Glu Asn Leu
35 40 45
Ser Leu Leu Arg Phe Asn Ser Leu Trp Glu His Ala Tyr Arg His Asp
50 55 60
Ser Leu Leu Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu
65 70 75 80
Leu Arg Lys Glu Lys Pro Leu Leu Thr Pro Asp Ile Thr Ile Met Ser
85 90 95
Val Gly Thr Glu Ile Thr Tyr Gly Asn Ser Met Val Pro Asp His Gly
100 105 110
Trp Val Glu Ala Leu Asn Asn Lys Trp Asp Leu Gly Ile Val Lys Gln
115 120 125
Glu Ala Ser Asn Phe Pro Glu Leu Lys Leu Gln Ala Glu Thr Glu Gln
130 135 140
Arg Pro His Lys Val Ser Phe Tyr Val Glu Lys Ser Lys Ala Gln Glu
145 150 155 160
Val Thr Lys Glu Leu Ser Gln Arg Phe Leu Lys Arg Gly Leu Asp Val
165 170 175
Lys Ile Ile Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly
180 185 190
Ala Gly Lys Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Thr
195 200 205
Glu Gly Lys Leu Pro Val Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn
210 215 220
Asp Ala Glu Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ser
225 230 235 240
Asn Ala Gln Glu Glu Leu Leu Lys Trp His Ala Glu Asn Ala Lys Asp
245 250 255
Asn Pro Lys Val Ile His Ala Lys Glu Arg Cys Ala Gly Gly Ile Ile
260 265 270
Gln Ala Ile Gly His Phe Lys Leu Gly Pro Asn Leu Ser Pro Arg Asp
275 280 285
Val Ser Asp Phe Leu Glu Ile Lys Ala Glu Asn Val Asn Pro Gly His
290 295 300
Glu Val Val Lys Phe Phe Leu Phe Tyr Glu Lys Trp Arg Arg Gly Glu
305 310 315 320
Val Glu Asn Ser Glu Ala Tyr Thr Ala Ser Pro Val Ser Ile Ser Arg
```

325

330

335

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..317

(D) OTHER INFORMATION: / Ceres Seq. ID 1498157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Arg | Leu | Thr | Ser | Pro | Pro | Arg | Leu | Met | Ile | Val | Ser | Asp | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | His | Thr | Met | Val | Asp | His | His | Asp | Pro | Glu | Asn | Leu | Ser | Leu | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Phe | Asn | Ser | Leu | Trp | Glu | His | Ala | Tyr | Arg | His | Asp | Ser | Leu | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Phe | Ser | Thr | Gly | Arg | Ser | Pro | Thr | Leu | Tyr | Lys | Glu | Leu | Arg | Lys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu | Lys | Pro | Leu | Leu | Thr | Pro | Asp | Ile | Thr | Ile | Met | Ser | Val | Gly | Thr |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Glu | Ile | Thr | Tyr | Gly | Asn | Ser | Met | Val | Pro | Asp | His | Gly | Trp | Val | Glu |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ala | Leu | Asn | Asn | Lys | Trp | Asp | Leu | Gly | Ile | Val | Lys | Gln | Glu | Ala | Ser |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asn | Phe | Pro | Glu | Leu | Lys | Leu | Gln | Ala | Glu | Thr | Glu | Gln | Arg | Pro | His |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Lys | Val | Ser | Phe | Tyr | Val | Glu | Lys | Ser | Lys | Ala | Gln | Glu | Val | Thr | Lys |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Leu | Ser | Gln | Arg | Phe | Leu | Lys | Arg | Gly | Leu | Asp | Val | Lys | Ile | Ile |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Tyr | Ser | Gly | Gly | Met | Asp | Leu | Asp | Ile | Leu | Pro | Gln | Gly | Ala | Gly | Lys |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Gly | Gln | Ala | Leu | Ala | Tyr | Leu | Leu | Lys | Lys | Leu | Lys | Thr | Glu | Gly | Lys |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Leu | Pro | Val | Asn | Thr | Leu | Ala | Cys | Gly | Asp | Ser | Gly | Asn | Asp | Ala | Glu |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Leu | Phe | Ser | Ile | Pro | Asp | Val | Tyr | Gly | Val | Met | Val | Ser | Asn | Ala | Gln |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Glu | Glu | Leu | Leu | Lys | Trp | His | Ala | Glu | Asn | Ala | Lys | Asp | Asn | Pro | Lys |  |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |  |
| Val | Ile | His | Ala | Lys | Glu | Arg | Cys | Ala | Gly | Gly | Ile | Ile | Gln | Ala | Ile |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Gly | His | Phe | Lys | Leu | Gly | Pro | Asn | Leu | Ser | Pro | Arg | Asp | Val | Ser | Asp |  |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |  |
| Phe | Leu | Glu | Ile | Lys | Ala | Glu | Asn | Val | Asn | Pro | Gly | His | Glu | Val | Val |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Lys | Phe | Phe | Leu | Phe | Tyr | Glu | Lys | Trp | Arg | Arg | Gly | Glu | Val | Glu | Asn |  |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |  |
| Ser | Glu | Ala | Tyr | Thr | Ala | Ser | Pro | Val | Ser | Ile | Ser | Arg |     |     |     |  |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..307

(D) OTHER INFORMATION: / Ceres Seq. ID 1498158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```
Met Ile Val Ser Asp Leu Asp His Thr Met Val Asp His His Asp Pro
1 5 10 15
Glu Asn Leu Ser Leu Leu Arg Phe Asn Ser Leu Trp Glu His Ala Tyr
 20 25 30
Arg His Asp Ser Leu Leu Val Phe Ser Thr Gly Arg Ser Pro Thr Leu
 35 40 45
Tyr Lys Glu Leu Arg Lys Glu Lys Pro Leu Leu Thr Pro Asp Ile Thr
 50 55 60
Ile Met Ser Val Gly Thr Glu Ile Thr Tyr Gly Asn Ser Met Val Pro
65 70 75 80
Asp His Gly Trp Val Glu Ala Leu Asn Asn Lys Trp Asp Leu Gly Ile
 85 90 95
Val Lys Gln Glu Ala Ser Asn Phe Pro Glu Leu Lys Leu Gln Ala Glu
 100 105 110
Thr Glu Gln Arg Pro His Lys Val Ser Phe Tyr Val Glu Lys Ser Lys
 115 120 125
Ala Gln Glu Val Thr Lys Glu Leu Ser Gln Arg Phe Leu Lys Arg Gly
 130 135 140
Leu Asp Val Lys Ile Ile Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu
145 150 155 160
Pro Gln Gly Ala Gly Lys Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys
 165 170 175
Leu Lys Thr Glu Gly Lys Leu Pro Val Asn Thr Leu Ala Cys Gly Asp
 180 185 190
Ser Gly Asn Asp Ala Glu Leu Phe Ser Ile Pro Asp Val Tyr Gly Val
 195 200 205
Met Val Ser Asn Ala Gln Glu Leu Leu Lys Trp His Ala Glu Asn
 210 215 220
Ala Lys Asp Asn Pro Lys Val Ile His Ala Lys Glu Arg Cys Ala Gly
225 230 235 240
Gly Ile Ile Gln Ala Ile Gly His Phe Lys Leu Gly Pro Asn Leu Ser
 245 250 255
Pro Arg Asp Val Ser Asp Phe Leu Glu Ile Lys Ala Glu Asn Val Asn
 260 265 270
Pro Gly His Glu Val Val Lys Phe Leu Phe Tyr Glu Lys Trp Arg
 275 280 285
Arg Gly Glu Val Glu Asn Ser Glu Ala Tyr Thr Ala Ser Pro Val Ser
290 295 300
Ile Ser Arg
305
```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1220 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1220

(D) OTHER INFORMATION: / Ceres Seq. ID 1498159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```
gtaatttctc ttctgttcaa tgttattctt ttagatctcg aacaaaacaa aatctccaga 60
agaaaaaaccc aaattccatg gcgtctaaat cgaagcagca tcttcgttat cagccgcgaa 120
aatctgtgtc acgatcaaca caagctttca cggtgcttat acttcttctc gtagtgattc 180
```

|            |             |            |             |            |            |      |
|------------|-------------|------------|-------------|------------|------------|------|
| tgattcttct | gggtctcggg  | attttgtcac | tacctaattgc | taatagaaac | tcttccaaga | 240  |
| cgaatgattt | gaccaacatt  | gtacgaaaga | gtgagacgag  | ttctggagat | gaagaagggg | 300  |
| atggtgaacg | ttgggttgaa  | gttatttctt | gggagcctcg  | tgctgttggt | tatcacaatt | 360  |
| tcttgactaa | tgaagaatgt  | gagcacttga | tcagccttgc  | taaaccgagt | atggttaagt | 420  |
| caaccgtggt | agatgagaaa  | accggtggga | gcaaagatag  | cagagtgaga | actagctcag | 480  |
| gaacttttct | tagaagagga  | catgacgaag | ttgtcgaggt  | gattgagaaa | aggatttcag | 540  |
| atttcacctt | cattcctggt  | gaaaatgggt | aaggtcttca  | agttcttcac | taccaagttg | 600  |
| ggcagaagta | tgagcctcac  | tatgactatt | tcttagatga  | gttcaacacc | aagaatggag | 660  |
| gacaacgaat | agctactgtg  | cttatgtacc | tctctgatgt  | cgatgatggt | ggcgagactg | 720  |
| tgttccctgc | agcaagagga  | aacattagtg | ctgtcccatg  | gtggaacgag | ctctcaaaat | 780  |
| gtggtaaaga | aggactatct  | gttctaccaa | agragcgaga  | tgctttactt | ttctggaaca | 840  |
| tgaggcctga | tgcattctcta | gaccttcga  | gcttgacagg  | tggatgtcca | gtggtgaaag | 900  |
| gaaacaaatg | gtcatccacg  | aaatggttcc | atgtccacga  | gttcaaggtt | taagagmaac | 960  |
| caaacaaasa | aagctaaaat  | atgaggaggt | atgtccacga  | gttcaaggtt | taagagmaac | 1020 |
| acagttaaac | aggtataatg  | tgtatttccc | ttttcatgga  | agcttcgaat | gtgtgtggat | 1080 |
| aggctgttct | ttcatggggg  | atatttgaac | ttttgtact   | ttttcttcta | aattattttg | 1140 |
| aatgatttgt | actttacgac  | atattcgaat | ctgagtcttg  | taacttttaa | caactcaata | 1200 |
| cgaaccatga | attttccgtt  |            |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Phe | Ser | Phe | Val | Gln | Cys | Tyr | Ser | Phe | Arg | Ser | Arg | Thr | Lys | Gln |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asn | Leu | Gln | Lys | Lys | Lys | Pro | Asn | Ser | Met | Ala | Ser | Lys | Ser | Lys | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| His | Leu | Arg | Tyr | Gln | Pro | Arg | Lys | Ser | Val | Ser | Arg | Ser | Thr | Gln | Ala |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Phe | Thr | Val | Leu | Ile | Leu | Leu | Leu | Val | Val | Ile | Leu | Ile | Leu | Leu | Gly |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Leu | Gly | Ile | Leu | Ser | Leu | Pro | Asn | Ala | Asn | Arg | Asn | Ser | Ser | Lys | Thr |  |
| 65  |     |     |     |     | 70  |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Asn | Asp | Leu | Thr | Asn | Ile | Val | Arg | Lys | Ser | Glu | Thr | Ser | Ser | Gly | Asp |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Glu | Glu | Gly | Asn | Gly | Glu | Arg | Trp | Val | Glu | Val | Ile | Ser | Trp | Glu | Pro |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Arg | Ala | Val | Val | Tyr | His | Asn | Phe | Leu | Thr | Asn | Glu | Glu | Cys | Glu | His |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Ile | Ser | Leu | Ala | Lys | Pro | Ser | Met | Val | Lys | Ser | Thr | Val | Val | Asp |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Lys | Thr | Gly | Gly | Ser | Lys | Asp | Ser | Arg | Val | Arg | Thr | Ser | Ser | Gly |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Thr | Phe | Leu | Arg | Arg | Gly | His | Asp | Glu | Val | Val | Glu | Val | Ile | Glu | Lys |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Arg | Ile | Ser | Asp | Phe | Thr | Phe | Ile | Pro | Val | Glu | Asn | Gly | Glu | Gly | Leu |  |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Gln | Val | Leu | His | Tyr | Gln | Val | Gly | Gln | Lys | Tyr | Glu | Pro | His | Tyr | Asp |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Tyr | Phe | Leu | Asp | Glu | Phe | Asn | Thr | Lys | Asn | Gly | Gly | Gln | Arg | Ile | Ala |  |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Thr | Val | Leu | Met | Tyr | Leu | Ser | Asp | Val | Asp | Asp | Gly | Gly | Glu | Thr | Val |  |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |  |
| Phe | Pro | Ala | Ala | Arg | Gly | Asn | Ile | Ser | Ala | Val | Pro | Trp | Trp | Asn | Glu |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |
| Leu | Ser | Lys | Cys | Gly | Lys | Glu | Gly | Leu | Ser | Val | Leu | Pro | Lys | Xaa | Arg |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Asp | Ala | Leu | Leu | Phe | Trp | Asn | Met | Arg | Pro | Asp | Ala | Ser | Leu | Asp | Pro |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Ser | Ser | Leu | His | Gly | Gly | Cys | Pro | Val | Val | Lys | Gly | Asn | Lys | Trp | Ser |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Ser | Thr | Lys | Trp | Phe | His | Val | His | Glu | Phe | Lys | Val |     |     |     |     |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..291

(D) OTHER INFORMATION: / Ceres Seq. ID 1498161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ser | Lys | Ser | Lys | Gln | His | Leu | Arg | Tyr | Gln | Pro | Arg | Lys | Ser |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Val | Ser | Arg | Ser | Thr | Gln | Ala | Phe | Thr | Val | Leu | Ile | Leu | Leu | Leu | Val |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Val | Ile | Leu | Ile | Leu | Leu | Gly | Leu | Gly | Ile | Leu | Ser | Leu | Pro | Asn | Ala |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Asn | Arg | Asn | Ser | Ser | Lys | Thr | Asn | Asp | Leu | Thr | Asn | Ile | Val | Arg | Lys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Glu | Thr | Ser | Ser | Gly | Asp | Glu | Glu | Gly | Asn | Gly | Glu | Arg | Trp | Val |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Glu | Val | Ile | Ser | Trp | Glu | Pro | Arg | Ala | Val | Val | Tyr | His | Asn | Phe | Leu |  |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Thr | Asn | Glu | Glu | Cys | Glu | His | Leu | Ile | Ser | Leu | Ala | Lys | Pro | Ser | Met |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Lys | Ser | Thr | Val | Val | Asp | Glu | Lys | Thr | Gly | Gly | Ser | Lys | Asp | Ser |  |
|     | 115 |     |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |  |
| Arg | Val | Arg | Thr | Ser | Ser | Gly | Thr | Phe | Leu | Arg | Arg | Gly | His | Asp | Glu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | Val | Glu | Val | Ile | Glu | Lys | Arg | Ile | Ser | Asp | Phe | Thr | Phe | Ile | Pro |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Val | Glu | Asn | Gly | Glu | Gly | Leu | Gln | Val | Leu | His | Tyr | Gln | Val | Gly | Gln |  |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Lys | Tyr | Glu | Pro | His | Tyr | Asp | Tyr | Phe | Leu | Asp | Glu | Phe | Asn | Thr | Lys |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Asn | Gly | Gly | Gln | Arg | Ile | Ala | Thr | Val | Leu | Met | Tyr | Leu | Ser | Asp | Val |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Asp | Asp | Gly | Gly | Glu | Thr | Val | Phe | Pro | Ala | Ala | Arg | Gly | Asn | Ile | Ser |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |  |
| Ala | Val | Pro | Trp | Trp | Asn | Glu | Leu | Ser | Lys | Cys | Gly | Lys | Glu | Gly | Leu |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Ser | Val | Leu | Pro | Lys | Xaa | Arg | Asp | Ala | Leu | Leu | Phe | Trp | Asn | Met | Arg |  |
|     |     | 245 |     |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Pro | Asp | Ala | Ser | Leu | Asp | Pro | Ser | Ser | Leu | His | Gly | Gly | Cys | Pro | Val |  |
|     | 260 |     |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Val | Lys | Gly | Asn | Lys | Trp | Ser | Ser | Thr | Lys | Trp | Phe | His | Val | His | Glu |  |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |  |
| Phe | Lys | Val |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     | 290 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..180
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498162
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Met Val Lys Ser Thr Val Val Asp Glu Lys Thr Gly Gly Ser Lys Asp  
1 5 10 15  
Ser Arg Val Arg Thr Ser Ser Gly Thr Phe Leu Arg Arg Gly His Asp  
20 25 30  
Glu Val Val Glu Val Ile Glu Lys Arg Ile Ser Asp Phe Thr Phe Ile  
35 40 45  
Pro Val Glu Asn Gly Glu Gly Leu Gln Val Leu His Tyr Gln Val Gly  
50 55 60  
Gln Lys Tyr Glu Pro His Tyr Asp Tyr Phe Leu Asp Glu Phe Asn Thr  
65 70 75 80  
Lys Asn Gly Gly Gln Arg Ile Ala Thr Val Leu Met Tyr Leu Ser Asp  
85 90 95  
Val Asp Asp Gly Gly Glu Thr Val Phe Pro Ala Ala Arg Gly Asn Ile  
100 105 110  
Ser Ala Val Pro Trp Trp Asn Glu Leu Ser Lys Cys Gly Lys Glu Gly  
115 120 125  
Leu Ser Val Leu Pro Lys Xaa Arg Asp Ala Leu Leu Phe Trp Asn Met  
130 135 140  
Arg Pro Asp Ala Ser Leu Asp Pro Ser Ser Leu His Gly Gly Cys Pro  
145 150 155 160  
Val Val Lys Gly Asn Lys Trp Ser Ser Thr Lys Trp Phe His Val His  
165 170 175  
Glu Phe Lys Val  
180

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 496 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..496
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498163
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aagagagaaa aaaggttgaa tcgaaacaga tcggaaaatc gtcgagagag agagagagag | 60  |
| aagtcgaacg acaggcagct aatgctaagg agtttgctga ggaaatgggt cttgaagaca | 120 |
| tctctatgca gagagggtt tcgataaacg ctgctcgtaa cttccttggt ggtgggtgctg | 180 |
| agaaggattc agacattatt ttctgaggtg tgggctctct ctctctctct ctctctctct | 240 |
| ctctctctct ctctctctct ctctctctct ctctctctct ctctctctct ctttgtgcct | 300 |
| tctgtgtttg ctcggtttct attttcgcct tcgcgctggt attactctct tcatcagact | 360 |
| tatgtttctt caaataaaat ggatttgatg tagatgaaat actgtatcat cttggattgt | 420 |
| gctttgatat aaatttttgc gagagatttg tgattattac tgttttgagt aattataatt | 480 |
| cccctgtttc aagact                                                 |     |

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..48

(D) OTHER INFORMATION: / Ceres Seq. ID 1498164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Arg | Glu | Lys | Arg | Leu | Asn | Arg | Asn | Arg | Ser | Glu | Asn | Arg | Arg | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Glu | Arg | Glu | Lys | Ser | Asn | Asp | Arg | Gln | Leu | Met | Leu | Arg | Ser | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Arg | Lys | Trp | Phe | Leu | Lys | Thr | Ser | Leu | Cys | Arg | Glu | Gly | Phe | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1498165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Arg | Lys | Lys | Val | Glu | Ser | Lys | Gln | Ile | Gly | Lys | Ser | Ser | Arg | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Glu | Arg | Glu | Val | Glu | Arg | Gln | Ala | Asn | Ala | Lys | Glu | Phe | Ala |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Glu | Glu | Met | Val | Leu | Glu | Asp | Ile | Ser | Met | Gln | Arg | Gly | Ile | Ser | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asn | Ala | Ala | Arg | Asn | Phe | Leu | Val | Gly | Gly | Ala | Glu | Lys | Asp | Ser | Asp |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Ile | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..33

(D) OTHER INFORMATION: / Ceres Seq. ID 1498166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Glu | Asp | Ile | Ser | Met | Gln | Arg | Gly | Ile | Ser | Ile | Asn | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Arg | Asn | Phe | Leu | Val | Gly | Gly | Ala | Glu | Lys | Asp | Ser | Asp | Ile | Ile |
|     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1121 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1121

(D) OTHER INFORMATION: / Ceres Seq. ID 1498167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

|             |            |             |            |             |            |      |
|-------------|------------|-------------|------------|-------------|------------|------|
| aaacccaac   | tttcgagttt | rccgatgagt  | ctagcctcca | tgatctccgg  | ctaaagatca | 60   |
| atgaatcgac  | gccttcctct | gttcgtttgt  | cgattgatta | caacgacggt  | gatatcctcg | 120  |
| cggtctgtac  | tctctcgatt | cgtctgattt  | tagtgcgttt | gatacagaaat | cggaaasgaa | 180  |
| tcatacaggag | attgttcgta | gattccggtg  | gcagcatgaa | tctctccngg  | tgtaaaaagg | 240  |
| ttaagcgagc  | ctctcttgtt | gaaaaatata  | ttgatggagg | aatctggtga  | cacttgtgaa | 300  |
| ttgacgattg  | tgatcatgac | tgttcatgct  | gttatgttag | aatctggatt  | tttgtgttgt | 360  |
| ttgatcctga  | ttcatctatg | cgtttttagct | tctcgaagaa | gaatttggtg  | tcgcttaact | 420  |
| atactctacc  | ttctgtgaaa | ggaatagtcg  | gtttgaattt | tgagaaggag  | gcgatgttgt | 480  |
| agtttatgga  | tctcttagtg | ttggtagttt  | tgttcgtgtg | gtgtctattg  | ataaacgtag | 540  |
| ctatgtgcac  | attgttgatt | tacttatgga  | aactttgaaa | tctgatgaag  | aagaagatac | 600  |
| tttgagcatt  | gactgtaagg | tactcgtgtg  | gtggagaatg | ataaaagatg  | gtattgttac | 660  |
| gcctctgttg  | gttgatcttt | gctacaaaac  | tgggtagaaa | cttccacctt  | gctttatcag | 720  |
| tctacctcga  | gagctaaaac | acaagatact  | agagtcgctt | cccgggtgtg  | atattgggac | 780  |
| attggcttgt  | gtttcttctg | aactgcgaga  | catggcttcg | tagaatgacc  | tgtggaagca | 840  |
| gaagtgcctg  | gaagagtgcc | aagatcttgt  | gacagaaggc | aatcatgatg  | tggttaactg | 900  |
| gaaggagagg  | tttgctactt | attggaggca  | aaagggaaa  | ttctccttca  | taagcagggc | 960  |
| atttcaaggt  | ttttcaggga | gcattggttc  | gtcataaatc | ctggaagaag  | actaaaaga  | 1020 |
| gaccatattg  | aatccggtgg | agtgaatggt  | tgtttgtatt | caaactcttg  | aaataggcaa | 1080 |
| ttatagggtt  | aagatgggtg | aaagagcatt  | ggaaacttag | t           |            |      |

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1498168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Pro | Thr | Phe | Glu | Phe | Xaa | Asp | Glu | Ser | Ser | Leu | His | Asp | Leu | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Lys | Ile | Asn | Glu | Ser | Thr | Pro | Ser | Ser | Val | Arg | Leu | Ser | Ile | Asp |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Tyr | Asn | Asp | Gly | Asp | Ile | Leu | Ala | Ala | Val | Thr | Leu | Ser | Ile | Arg | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ile | Leu | Val | Arg | Leu | Ile | Arg | Asn | Arg | Lys | Xaa | Ile | Ile | Arg | Arg | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Val | Asp | Ser | Gly | Gly | Ser | Met | Asn | Leu | Ser | Xaa | Cys | Lys | Lys | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Arg | Ala | Ser | Leu | Val | Glu | Lys | Tyr | Ile | Asp | Gly | Gly | Ile | Trp |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1498169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Met Glu Thr Leu Lys Ser Asp Glu Glu Glu Asp Thr Leu Ser Ile Asp

1 5 10 15  
Cys Lys Val Leu Val Trp Trp Arg Met Ile Lys Asp Gly Ile Val Thr  
20 25 30  
Pro Leu Leu Val Asp Leu Cys Tyr Lys Thr Gly Leu Glu Leu Pro Pro  
35 40 45  
Cys Phe Ile Ser Leu Pro Arg Glu Leu Lys His Lys Ile Leu Glu Ser  
50 55 60  
Leu Pro Gly Val Asp Ile Gly Thr Leu Ala Cys Val Ser Ser Glu Leu  
65 70 75 80  
Arg Asp Met Ala Ser  
85

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1498170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Ile Lys Asp Gly Ile Val Thr Pro Leu Leu Val Asp Leu Cys Tyr  
1 5 10 15  
Lys Thr Gly Leu Glu Leu Pro Pro Cys Phe Ile Ser Leu Pro Arg Glu  
20 25 30  
Leu Lys His Lys Ile Leu Glu Ser Leu Pro Gly Val Asp Ile Gly Thr  
35 40 45  
Leu Ala Cys Val Ser Ser Glu Leu Arg Asp Met Ala Ser  
50 55 60

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..775

(D) OTHER INFORMATION: / Ceres Seq. ID 1498173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

actctctata cctcctcaag aaaatcaaag cagcagttat ggccgacgta gcaacaaagc 60  
accccatgga agatgagggtg aagaagacgg aggcgtctag tttggtgggg aagctagaga 120  
cagacgtgga gatcaaggct tcggctgata agtttcacca catgttcgct gggaaaccac 180  
accatgtctc caaagcaagt ccaggcaaca ttcagggatg tgatctgcac gaaggcgact 240  
ggggcacagt cggctctatc gtcttcttga attacgtwca tgatrgggag gcaaagggtg 300  
ctaaggagag gattgaggcr gtggagccrg ataagaactt gatcacgttt agggttatag 360  
acggtgatct gatgaaagag tacaagagct tcttgctcac catccagggtg accccaagc 420  
ytggaggccc tggaagtatt gtgcactggc accttgagta tgagaaaatw agcgaggagg 480  
tagctcatcc ggaaactctc ctccavttct gtgtcgaggt ctccaaagag atcgacgaac 540  
atcttttggc cgaggaatag aggagtacta ctactcttcg tgtttgaatt taaatgcaat 600  
aaataaggac taagagccat gtctttgtga gatatatgaa tgtgagtgtg catcatgaat 660  
gtatgtatac taagatcggt ttacgttggc tactgttaact ttgagaagca atgtgtagta 720  
gctgtgatga agctagtata aatatataat aagtatgtta tatatgtttg ctaat

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..185  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498174  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```
Ser Leu Tyr Leu Leu Lys Lys Ile Lys Ala Ala Val Met Ala Asp Val
1 5 10 15
Ala Thr Lys His Pro Met Glu Asp Glu Val Lys Lys Thr Glu Ala Ser
20 25 30
Ser Leu Val Gly Lys Leu Glu Thr Asp Val Glu Ile Lys Ala Ser Ala
35 40 45
Asp Lys Phe His His Met Phe Ala Gly Lys Pro His His Val Ser Lys
50 55 60
Ala Ser Pro Gly Asn Ile Gln Gly Cys Asp Leu His Glu Gly Asp Trp
65 70 75 80
Gly Thr Val Gly Ser Ile Val Phe Trp Asn Tyr Xaa His Asp Xaa Glu
85 90 95
Ala Lys Val Ala Lys Glu Arg Ile Glu Xaa Val Glu Xaa Asp Lys Asn
100 105 110
Leu Ile Thr Phe Arg Val Ile Asp Gly Asp Leu Met Lys Glu Tyr Lys
115 120 125
Ser Phe Leu Leu Thr Ile Gln Val Thr Xaa Lys Xaa Gly Gly Pro Gly
130 135 140
Ser Ile Val His Trp His Leu Glu Tyr Glu Lys Xaa Ser Glu Glu Val
145 150 155 160
Ala His Pro Glu Thr Leu Leu Xaa Phe Cys Val Glu Val Ser Lys Glu
165 170 175
Ile Asp Glu His Leu Leu Ala Glu Glu
180 185
```

(2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 173 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..173  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```
Met Ala Asp Val Ala Thr Lys His Pro Met Glu Asp Glu Val Lys Lys
1 5 10 15
Thr Glu Ala Ser Ser Leu Val Gly Lys Leu Glu Thr Asp Val Glu Ile
20 25 30
Lys Ala Ser Ala Asp Lys Phe His His Met Phe Ala Gly Lys Pro His
35 40 45
His Val Ser Lys Ala Ser Pro Gly Asn Ile Gln Gly Cys Asp Leu His
50 55 60
Glu Gly Asp Trp Gly Thr Val Gly Ser Ile Val Phe Trp Asn Tyr Xaa
65 70 75 80
His Asp Xaa Glu Ala Lys Val Ala Lys Glu Arg Ile Glu Xaa Val Glu
85 90 95
Xaa Asp Lys Asn Leu Ile Thr Phe Arg Val Ile Asp Gly Asp Leu Met
100 105 110
Lys Glu Tyr Lys Ser Phe Leu Leu Thr Ile Gln Val Thr Xaa Lys Xaa
115 120 125
Gly Gly Pro Gly Ser Ile Val His Trp His Leu Glu Tyr Glu Lys Xaa
130 135 140
```

Ser Glu Glu Val Ala His Pro Glu Thr Leu Leu Xaa Phe Cys Val Glu  
145 150 155 160  
Val Ser Lys Glu Ile Asp Glu His Leu Leu Ala Glu Glu  
165 170

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met Glu Asp Glu Val Lys Lys Thr Glu Ala Ser Ser Leu Val Gly Lys  
1 5 10 15  
Leu Glu Thr Asp Val Glu Ile Lys Ala Ser Ala Asp Lys Phe His His  
20 25 30  
Met Phe Ala Gly Lys Pro His His Val Ser Lys Ala Ser Pro Gly Asn  
35 40 45  
Ile Gln Gly Cys Asp Leu His Glu Gly Asp Trp Gly Thr Val Gly Ser  
50 55 60  
Ile Val Phe Trp Asn Tyr Xaa His Asp Xaa Glu Ala Lys Val Ala Lys  
65 70 75 80  
Glu Arg Ile Glu Xaa Val Glu Xaa Asp Lys Asn Leu Ile Thr Phe Arg  
85 90 95  
Val Ile Asp Gly Asp Leu Met Lys Glu Tyr Lys Ser Phe Leu Leu Thr  
100 105 110  
Ile Gln Val Thr Xaa Lys Xaa Gly Pro Gly Ser Ile Val His Trp  
115 120 125  
His Leu Glu Tyr Glu Lys Xaa Ser Glu Glu Val Ala His Pro Glu Thr  
130 135 140  
Leu Leu Xaa Phe Cys Val Glu Val Ser Lys Glu Ile Asp Glu His Leu  
145 150 155 160  
Leu Ala Glu Glu

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..894
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

attttgaaaa gtttctaacc tctaggccac ccactcatgg ctactctggt catgaagctg 60  
gtgagcttct ttctaattct atctactttt tgtctcacta ctgtgaactc ggagccacag 120  
tgccataatt tcaaatcgat cattagtttc ggtgattcta ttgccgacac tggaaaacttg 180  
ctcgccctct ccgatcctac caatctccct aaggctcgct ttctaccgta cggagaaaacc 240  
ttcttccacc atccgaccgg ccgtttctca aacggccgcc tcatcatcga tttcattgct 300  
gaatTTTTTg gttttccgct tgtgcctcct ttttatggat ctcaaaatgc aaatTTTgag 360  
aaaggagtta atTTTgCGgt tggaggagca acggcactgg aacgttcctt tcttgaagag 420  
agaggcattc attttcctta caccaacgtt agtttagccg tacagcttag tagcttcaag 480  
gagagtttgc ctaacttatg tgtctctcct tcagactgca gagatatgat agaaaattct 540  
ttgattctca tgggagaaat tggagggaat gactataact acgcattctg aaggagagac 600  
acataagtta ggcaaaactct ccttgaagct acggtggtgg aagacgtgag ggaggaggag 660

gatacgggtgg tgggtgaagga ggaggttacg gaggaagcgg tgggtggtgga ggatggtaat 720  
tcctttaatt aggtttggga ttaccaatga atgttctctc tctcgcttgt tatgcttcta 780  
cttggttttg ygtgttctct attttgttct ggttctgctt tagatttgat gtaacagttc 840  
gtgattaggt attttggat ctggaaacgt aatgttaagt cacttgatcat tctc

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1498178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Met Ala Thr Leu Phe Met Lys Leu Val Ser Phe Phe Leu Ile Leu Ser  
1 5 10 15  
Thr Phe Cys Leu Thr Thr Val Asn Ser Glu Pro Gln Cys His Asn Phe  
20 25 30  
Lys Ser Ile Ile Ser Phe Gly Asp Ser Ile Ala Asp Thr Gly Asn Leu  
35 40 45  
Leu Ala Leu Ser Asp Pro Thr Asn Leu Pro Lys Val Ala Phe Leu Pro  
50 55 60  
Tyr Gly Glu Thr Phe Phe His His Pro Thr Gly Arg Phe Ser Asn Gly  
65 70 75 80  
Arg Leu Ile Ile Asp Phe Ile Ala Glu Phe Leu Gly Phe Pro Leu Val  
85 90 95  
Pro Pro Phe Tyr Gly Ser Gln Asn Ala Asn Phe Glu Lys Gly Val Asn  
100 105 110  
Phe Ala Val Gly Gly Ala Thr Ala Leu Glu Arg Ser Phe Leu Glu Glu  
115 120 125  
Arg Gly Ile His Phe Pro Tyr Thr Asn Val Ser Leu Ala Val Gln Leu  
130 135 140  
Ser Ser Phe Lys Glu Ser Leu Pro Asn Leu Cys Val Ser Pro Ser Asp  
145 150 155 160  
Cys Arg Asp Met Ile Glu Asn Ser Leu Ile Leu Met Gly Glu Ile Gly  
165 170 175  
Gly Asn Asp Tyr Asn Tyr Ala Phe  
180

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1498179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Met Lys Leu Val Ser Phe Phe Leu Ile Leu Ser Thr Phe Cys Leu Thr  
1 5 10 15  
Thr Val Asn Ser Glu Pro Gln Cys His Asn Phe Lys Ser Ile Ile Ser  
20 25 30  
Phe Gly Asp Ser Ile Ala Asp Thr Gly Asn Leu Leu Ala Leu Ser Asp  
35 40 45  
Pro Thr Asn Leu Pro Lys Val Ala Phe Leu Pro Tyr Gly Glu Thr Phe  
50 55 60  
Phe His His Pro Thr Gly Arg Phe Ser Asn Gly Arg Leu Ile Ile Asp

[illegible]

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..723  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| agtcgtctag  | ggtttgtttt | tcgtttcttc | tccgattggt | cagaggaatt | gcgaattaag | 60  |
| ataaagatga  | ggccagtggt | cgtcggcaat | ttcgagtatg | aaactcgcca | gtcggatctg | 120 |
| gaacggttgt  | tgcacaagta | tgggagagtc | gaccgagtg  | acatgaaatc | tggatatgct | 180 |
| tttgtgtact  | ttgaggatga | acgtgatgct | gaagacgcta | ttcgcaaact | cgacaatttt | 240 |
| ccttttggat  | atgagaaaac | caggttatca | gttgaatggg | caaagggtga | acgtggcagg | 300 |
| cctcgtggtg  | acgcgaaagc | cccttcaaat | ctgaagccta | caaaagactg | gtttgtcatt | 360 |
| aacttttgacc | ccattagaac | aaaagagcac | gacattgaaa | aacactttga | gccctatggg | 420 |
| aaggtcacca  | acgtgcgtat | cagacgcaac | ttctcatttg | ttcagtttga | aacacaagag | 480 |
| gatgctacaa  | aagcccttga | agctactcaa | agaagcaaaa | tattggatag | ggttgtttcc | 540 |
| gtggagtatg  | cgttgaaaga | tgacgatgaa | agagatgatc | gaaatgggtg | tcgtagcccg | 600 |
| agaaggctct  | ttagtcctgt | gtatcgtagg | cgtcatgtaa | tgatgtactg | tcgttatttt | 660 |
| aaagaaaatt  | tggcaccttt | tgtataaaca | gaatttctta | tacctcgcag | tttgtgttta | 720 |

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..228  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Leu | Gly | Phe | Val | Phe | Arg | Phe | Phe | Ser | Asp | Cys | Ser | Glu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Arg | Ile | Lys | Ile | Lys | Met | Arg | Pro | Val | Phe | Val | Gly | Asn | Phe | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Glu | Thr | Arg | Gln | Ser | Asp | Leu | Glu | Arg | Leu | Phe | Asp | Lys | Tyr | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Val | Asp | Arg | Val | Asp | Met | Lys | Ser | Gly | Tyr | Ala | Phe | Val | Tyr | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Asp | Glu | Arg | Asp | Ala | Glu | Asp | Ala | Ile | Arg | Lys | Leu | Asp | Asn | Phe |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Phe | Gly | Tyr | Glu | Lys | Arg | Arg | Leu | Ser | Val | Glu | Trp | Ala | Lys | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Arg | Gly | Arg | Pro | Arg | Gly | Asp | Ala | Lys | Ala | Pro | Ser | Asn | Leu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Thr | Lys | Thr | Leu | Phe | Val | Ile | Asn | Phe | Asp | Pro | Ile | Arg | Thr | Lys |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Glu | His | Asp | Ile | Glu | Lys | His | Phe | Glu | Pro | Tyr | Gly | Lys | Val | Thr | Asn |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Val | Arg | Ile | Arg | Arg | Asn | Phe | Ser | Phe | Val | Gln | Phe | Glu | Thr | Gln | Glu |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Ala | Thr | Lys | Ala | Leu | Glu | Ala | Thr | Gln | Arg | Ser | Lys | Ile | Leu | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Val | Val | Ser | Val | Glu | Tyr | Ala | Leu | Lys | Asp | Asp | Asp | Glu | Arg | Asp |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Asp | Arg | Asn | Gly | Gly | Arg | Ser | Pro | Arg | Arg | Ser | Leu | Ser | Pro | Val | Tyr |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Arg | Arg | His | Val | Met | Met | Tyr | Cys | Arg | Tyr | Phe | Lys | Glu | Asn | Leu |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Ala | Pro | Phe | Val |     |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1498182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Pro | Val | Phe | Val | Gly | Asn | Phe | Glu | Tyr | Glu | Thr | Arg | Gln | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Leu | Glu | Arg | Leu | Phe | Asp | Lys | Tyr | Gly | Arg | Val | Asp | Arg | Val | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Lys | Ser | Gly | Tyr | Ala | Phe | Val | Tyr | Phe | Glu | Asp | Glu | Arg | Asp | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Asp | Ala | Ile | Arg | Lys | Leu | Asp | Asn | Phe | Pro | Phe | Gly | Tyr | Glu | Lys |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Arg | Leu | Ser | Val | Glu | Trp | Ala | Lys | Gly | Glu | Arg | Gly | Arg | Pro | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Asp | Ala | Lys | Ala | Pro | Ser | Asn | Leu | Lys | Pro | Thr | Lys | Thr | Leu | Phe |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Ile | Asn | Phe | Asp | Pro | Ile | Arg | Thr | Lys | Glu | His | Asp | Ile | Glu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Phe | Glu | Pro | Tyr | Gly | Lys | Val | Thr | Asn | Val | Arg | Ile | Arg | Arg | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Ser | Phe | Val | Gln | Phe | Glu | Thr | Gln | Glu | Asp | Ala | Thr | Lys | Ala | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ala | Thr | Gln | Arg | Ser | Lys | Ile | Leu | Asp | Arg | Val | Val | Ser | Val | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Ala | Leu | Lys | Asp | Asp | Asp | Glu | Arg | Asp | Asp | Arg | Asn | Gly | Gly | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ser | Pro | Arg | Arg | Ser | Leu | Ser | Pro | Val | Tyr | Arg | Arg | Arg | His | Val | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Tyr | Cys | Arg | Tyr | Phe | Lys | Glu | Asn | Leu | Ala | Pro | Phe | Val |     |     |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 174 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..174  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498183  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:  
Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Ala  
1 5 10 15  
Glu Asp Ala Ile Arg Lys Leu Asp Asn Phe Pro Phe Gly Tyr Glu Lys  
20 25 30  
Arg Arg Leu Ser Val Glu Trp Ala Lys Gly Glu Arg Gly Arg Pro Arg  
35 40 45  
Gly Asp Ala Lys Ala Pro Ser Asn Leu Lys Pro Thr Lys Thr Leu Phe  
50 55 60  
Val Ile Asn Phe Asp Pro Ile Arg Thr Lys Glu His Asp Ile Glu Lys  
65 70 75 80  
His Phe Glu Pro Tyr Gly Lys Val Thr Asn Val Arg Ile Arg Arg Asn  
85 90 95  
Phe Ser Phe Val Gln Phe Glu Thr Gln Glu Asp Ala Thr Lys Ala Leu  
100 105 110  
Glu Ala Thr Gln Arg Ser Lys Ile Leu Asp Arg Val Val Ser Val Glu  
115 120 125  
Tyr Ala Leu Lys Asp Asp Asp Glu Arg Asp Asp Arg Asn Gly Gly Arg  
130 135 140  
Ser Pro Arg Arg Ser Leu Ser Pro Val Tyr Arg Arg Arg His Val Met  
145 150 155 160  
Met Tyr Cys Arg Tyr Phe Lys Glu Asn Leu Ala Pro Phe Val  
165 170

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1051 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1051

(D) OTHER INFORMATION: / Ceres Seq. ID 1498190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

|            |             |            |            |             |            |      |
|------------|-------------|------------|------------|-------------|------------|------|
| aaaaaacaga | aaaaattcgt  | ggaaacgcca | ttaacgagat | ctagcacaaa  | ctcgtagtgt | 60   |
| ggtgtagaag | aagacaaaag  | caaggagctt | cataataaaa | ccctagagat  | atttgtttct | 120  |
| ccaatttcaa | aagacgagac  | gtgaagaaga | cgatcgaaga | tgaacatttt  | cagattagct | 180  |
| ggtgatatga | ctcacctagc  | cagtgttctt | gtcttgcttc | tcaagatcca  | caccatcaaa | 240  |
| tcctgcgctg | gtgttttcatt | gaagactcaa | gaactctatg | ccattgtctt  | tgcgacgcgt | 300  |
| tatttgata  | ttttcacgag  | ttttgtgtct | ctgtacaaca | cctctatgaa  | gttggtgttc | 360  |
| ttaggaagtt | ctttttcgat  | tgtgtggtac | atgaagtatc | ataaggccgt  | ccacaggact | 420  |
| tacgacagag | agcaagatac  | gtttcgtcat | tggttccttg | tgcttccttg  | ctttctctta | 480  |
| gctcttctga | ttcatgaaaa  | gtttaccttt | cttgaggat  | tgtggacgtt  | ttcattgtac | 540  |
| ttggaggctg | ttgccatatt  | acctcagctt | gtcttggtgc | aaaggactag  | aatatttgac | 600  |
| aacttgaccg | gacaatatat  | atttctcctt | ggggggtacc | gtggattata  | catcctcaac | 660  |
| tggatctacc | gttacttcac  | tgagccgcac | tttgttcact | ggataacatg  | gatcgccggg | 720  |
| tttgttcaaa | cactgtctta  | tgccgacttc | ttctattatt | atttcctaag  | ctggaagaac | 780  |
| aacaaaaagc | tccaattacc  | agcttaattt | ctaaagtttc | aatgctcggg  | aaccctacgg | 840  |
| attcgatttg | gtgcccagaca | aaacatctac | cggaatgtta | ccaatttact  | ctgttggtgg | 900  |
| ttattagagg | agaacgagca  | tagatgtgta | aactccagca | atctaactta  | ttacactttc | 960  |
| tttagacttt | ctcgtctctc  | atcttttttt | ttggctgact | tagtggttact | aatattttcg | 1020 |

acgcgacagt aatatattca ccacaattcg c

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ile | Phe | Arg | Leu | Ala | Gly | Asp | Met | Thr | His | Leu | Ala | Ser | Val |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Leu | Leu | Leu | Lys | Ile | His | Thr | Ile | Lys | Ser | Cys | Ala | Gly | Val |
|     |     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |
| Ser | Leu | Lys | Thr | Gln | Glu | Leu | Tyr | Ala | Ile | Val | Phe | Ala | Thr | Arg | Tyr |
|     |     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |
| Leu | Asp | Ile | Phe | Thr | Ser | Phe | Val | Ser | Leu | Tyr | Asn | Thr | Ser | Met | Lys |
|     |     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |
| Leu | Val | Phe | Leu | Gly | Ser | Phe | Ser | Ile | Val | Trp | Tyr | Met | Lys | Tyr |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| His | Lys | Ala | Val | His | Arg | Thr | Tyr | Asp | Arg | Glu | Gln | Asp | Thr | Phe | Arg |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| His | Trp | Phe | Leu | Val | Leu | Pro | Cys | Phe | Leu | Leu | Ala | Leu | Leu | Ile | His |
|     |     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |
| Glu | Lys | Phe | Thr | Phe | Leu | Glu | Val | Leu | Trp | Thr | Phe | Ser | Leu | Tyr | Leu |
|     |     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |
| Glu | Ala | Val | Ala | Ile | Leu | Pro | Gln | Leu | Val | Leu | Leu | Gln | Arg | Thr | Arg |
|     |     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |
| Asn | Ile | Asp | Asn | Leu | Thr | Gly | Gln | Tyr | Ile | Phe | Leu | Leu | Gly | Gly | Tyr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Arg | Gly | Leu | Tyr | Ile | Leu | Asn | Trp | Ile | Tyr | Arg | Tyr | Phe | Thr | Glu | Pro |
|     |     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Phe | Val | His | Trp | Ile | Thr | Trp | Ile | Ala | Gly | Phe | Val | Gln | Thr | Leu |
|     |     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |
| Leu | Tyr | Ala | Asp | Phe | Phe | Tyr | Tyr | Tyr | Phe | Leu | Ser | Trp | Lys | Asn | Asn |
|     |     |     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |
| Lys | Lys | Leu | Gln | Leu | Pro | Ala |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 210 |     |     |     | 215 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | His | Leu | Ala | Ser | Val | Leu | Val | Leu | Leu | Leu | Lys | Ile | His | Thr |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Lys | Ser | Cys | Ala | Gly | Val | Ser | Leu | Lys | Thr | Gln | Glu | Leu | Tyr | Ala |
|     |     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |
| Ile | Val | Phe | Ala | Thr | Arg | Tyr | Leu | Asp | Ile | Phe | Thr | Ser | Phe | Val | Ser |
|     |     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |
| Leu | Tyr | Asn | Thr | Ser | Met | Lys | Leu | Val | Phe | Leu | Gly | Ser | Ser | Phe | Ser |
|     |     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Val | Trp | Tyr | Met | Lys | Tyr | His | Lys | Ala | Val | His | Arg | Thr | Tyr | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Glu | Gln | Asp | Thr | Phe | Arg | His | Trp | Phe | Leu | Val | Leu | Pro | Cys | Phe |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Leu | Ala | Leu | Leu | Ile | His | Glu | Lys | Phe | Thr | Phe | Leu | Glu | Val | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Trp | Thr | Phe | Ser | Leu | Tyr | Leu | Glu | Ala | Val | Ala | Ile | Leu | Pro | Gln | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Leu | Leu | Gln | Arg | Thr | Arg | Asn | Ile | Asp | Asn | Leu | Thr | Gly | Gln | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Phe | Leu | Leu | Gly | Gly | Tyr | Arg | Gly | Leu | Tyr | Ile | Leu | Asn | Trp | Ile |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Arg | Tyr | Phe | Thr | Glu | Pro | His | Phe | Val | His | Trp | Ile | Thr | Trp | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Gly | Phe | Val | Gln | Thr | Leu | Leu | Tyr | Ala | Asp | Phe | Phe | Tyr | Tyr | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Leu | Ser | Trp | Lys | Asn | Asn | Lys | Lys | Leu | Gln | Leu | Pro | Ala |     |     |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Leu | Val | Phe | Leu | Gly | Ser | Ser | Phe | Ser | Ile | Val | Trp | Tyr | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Tyr | His | Lys | Ala | Val | His | Arg | Thr | Tyr | Asp | Arg | Glu | Gln | Asp | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Arg | His | Trp | Phe | Leu | Val | Leu | Pro | Cys | Phe | Leu | Leu | Ala | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | His | Glu | Lys | Phe | Thr | Phe | Leu | Glu | Val | Leu | Trp | Thr | Phe | Ser | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Leu | Glu | Ala | Val | Ala | Ile | Leu | Pro | Gln | Leu | Val | Leu | Leu | Gln | Arg |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Arg | Asn | Ile | Asp | Asn | Leu | Thr | Gly | Gln | Tyr | Ile | Phe | Leu | Leu | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Tyr | Arg | Gly | Leu | Tyr | Ile | Leu | Asn | Trp | Ile | Tyr | Arg | Tyr | Phe | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Pro | His | Phe | Val | His | Trp | Ile | Thr | Trp | Ile | Ala | Gly | Phe | Val | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Leu | Leu | Tyr | Ala | Asp | Phe | Phe | Tyr | Tyr | Tyr | Phe | Leu | Ser | Trp | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Asn | Lys | Lys | Leu | Gln | Leu | Pro | Ala |     |     |     |     |     |     |     |
| 145 |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..947
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

|            |             |             |             |            |             |     |
|------------|-------------|-------------|-------------|------------|-------------|-----|
| aatgttgctt | taaaaccaat  | gctcctcttc  | ttgtttcttca | tataaaccac | atatcctctc  | 60  |
| ctccatatct | taacaatttc  | atagcaaacc  | ctaaaattga  | gaaagagata | gagagagaaa  | 120 |
| gatgggtaga | ggaaagatcg  | agataaagag  | gatagagaac  | gcaaacaaca | gagtgggtgac | 180 |
| gttctcaaag | aggaggaatg  | gattgggtgaa | gaaggctaaa  | gagatcacag | ttctttgtga  | 240 |
| tgcaaaagtt | gccctcataa  | tctttgcaag  | taatggtaag  | atgattgatt | actgttgtcc  | 300 |
| ttccatggat | cttgggtgcta | tgttggacca  | ataccagaag  | ttatctggca | agaaactatg  | 360 |
| ggatgctaag | catgagaacc  | ttagcaatga  | gattgatagg  | atcaagaaag | agaatgatag  | 420 |
| cttacaactg | gagctcaggc  | at ttgaagg  | agaagatata  | cagtctctca | acttgaaaaa  | 480 |
| tctgatggct | gtcgagcacg  | ccattgaaca  | tggcctcgac  | aaagtccgag | accaccagat  | 540 |
| ggagatcctt | atatcaaaga  | ggagaaatga  | gaagatgatg  | gcggaggagc | aacggcaact  | 600 |
| cactttccag | ctgcaacaac  | aggagatggc  | tatagcaagc  | aacgcaagag | gaatgatgat  | 660 |
| gagagatcat | gatgggcagt  | ttggatatag  | agtgcaaccg  | attcagccaa | atcttcagga  | 720 |
| aaagattatg | tctttggtca  | tcgattgatc  | atcgagattt  | tataatctca | tcctgatcaa  | 780 |
| ctcctatcta | taatatcgtg  | gtcctttagtt | tgtctttatc  | aatctgtgtg | tcttaatctc  | 840 |
| gagcaacata | tatactcgct  | atcagacttt  | ttacttaagc  | tatatgtgtg | ttgtttgctt  | 900 |
| atgacctcta | tgtattggtt  | gtgttgtgtg  | cttaaactgt  | tcgmact    |             |     |

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1498195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Arg | Gly | Lys | Ile | Glu | Ile | Lys | Arg | Ile | Glu | Asn | Ala | Asn | Asn |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg | Val | Val | Thr | Phe | Ser | Lys | Arg | Arg | Asn | Gly | Leu | Val | Lys | Lys | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Glu | Ile | Thr | Val | Leu | Cys | Asp | Ala | Lys | Val | Ala | Leu | Ile | Ile | Phe |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Ala | Ser | Asn | Gly | Lys | Met | Ile | Asp | Tyr | Cys | Cys | Pro | Ser | Met | Asp | Leu |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Gly | Ala | Met | Leu | Asp | Gln | Tyr | Gln | Lys | Leu | Ser | Gly | Lys | Lys | Leu | Trp |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Asp | Ala | Lys | His | Glu | Asn | Leu | Ser | Asn | Glu | Ile | Asp | Arg | Ile | Lys | Lys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Glu | Asn | Asp | Ser | Leu | Gln | Leu | Glu | Leu | Arg | His | Leu | Lys | Gly | Glu | Asp |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Gln | Ser | Leu | Asn | Leu | Lys | Asn | Leu | Met | Ala | Val | Glu | His | Ala | Ile |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     |     | 125 |     |     |  |
| Glu | His | Gly | Leu | Asp | Lys | Val | Arg | Asp | His | Gln | Met | Glu | Ile | Leu | Ile |  |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |
| Ser | Lys | Arg | Arg | Asn | Glu | Lys | Met | Met | Ala | Glu | Glu | Gln | Arg | Gln | Leu |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Thr | Phe | Gln | Leu | Gln | Gln | Glu | Met | Ala | Ile | Ala | Ser | Asn | Ala | Arg |     |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Gly | Met | Met | Met | Arg | Asp | His | Asp | Gly | Gln | Phe | Gly | Tyr | Arg | Val | Gln |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Pro | Ile | Gln | Pro | Asn | Leu | Gln | Glu | Lys | Ile | Met | Ser | Leu | Val | Ile | Asp |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

```

 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..155
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498196
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Asp | Tyr | Cys | Cys | Pro | Ser | Met | Asp | Leu | Gly | Ala | Met | Leu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Tyr | Gln | Lys | Leu | Ser | Gly | Lys | Lys | Leu | Trp | Asp | Ala | Lys | His | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Leu | Ser | Asn | Glu | Ile | Asp | Arg | Ile | Lys | Lys | Glu | Asn | Asp | Ser | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gln | Leu | Glu | Leu | Arg | His | Leu | Lys | Gly | Glu | Asp | Ile | Gln | Ser | Leu | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Lys | Asn | Leu | Met | Ala | Val | Glu | His | Ala | Ile | Glu | His | Gly | Leu | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Val | Arg | Asp | His | Gln | Met | Glu | Ile | Leu | Ile | Ser | Lys | Arg | Arg | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Glu | Lys | Met | Met | Ala | Glu | Glu | Gln | Arg | Gln | Leu | Thr | Phe | Gln | Leu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Gln | Glu | Met | Ala | Ile | Ala | Ser | Asn | Ala | Arg | Gly | Met | Met | Met | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | His | Asp | Gly | Gln | Phe | Gly | Tyr | Arg | Val | Gln | Pro | Ile | Gln | Pro | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Gln | Glu | Lys | Ile | Met | Ser | Leu | Val | Ile | Asp |     |     |     |     |     |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..147
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1498197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

[illegible]

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1145 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1145  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498198  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

```
atttcaaacc acacattcaa actaactctg caaaagaaaa aaaaactcag agcagaggag 60
atcgagagag acaaagagag acaaagagag agagagagag agagagagag agagagagag 120
agagatcttc aacaagcaat gtctatatcc atggcggtat tctctccgcc gatctcttcc 180
tcacttcaaa accctaattc catccccaag atctcaacct ctcttctctc caccaaacgt 240
ttctctctaa tctccgtccc tagagcttcc tccgacaatg gtacgacttc ccccgctcgtg 300
aaaattccga agcctgcgtc tgtagctgta gaggaagttc cggttaaadc tccggcggaa 360
agctcctccg cttctgaaaa cggcgccggt ggaggtgaag cgactgattc gagtactgag 420
acggtaatac aatatcaaaa tgcgaagtgg gttaatggaa cttgggatct gaaacagttc 480
gagaaagatg gcaaaactga ttgggattct gttatcgttt ctgaggcaaa gaggagaaaa 540
tggcttgaag ataaccggga aacaacgagt aacgacgagc ttgttgtctt cgataacttcg 600
attattccat ggtgggcatg gatgaagaga taccatctac ctgaagctga acttctcaat 660
ggtcgtgctg cgatgatagg gttcttcatt gcttactttg ttgatagtct taccggagta 720
ggacttggtg atcaaatggg gaatttcttc tgcaaaacac tcttgtttgt ggctgtagct 780
ggagttctct tcatccgtaa gaatgaagat ttagacaaac ttaaggatct gttcgtatgag 840
actacgttat atgacaaaca atggcaagct gcatggaaaag agccagattc atcaacagtt 900
tcttcaaaga agtgaacaag ttcttacaat ctttcatttt cttttttttg ttatgaata 960
atctgtgaat cagtgaaggt ttatctctac tgaactactg atcttcagat tttgtaattc 1020
ttctgcttta aaaatctcta tgaagtagt tcaaaagataa tgtatcgaag gtctttgact 1080
tgtaaagcag acctatttcg ttttgacgct tgataattta atcaataaga gatttttttt 1140
ttaat
```

- (2) INFORMATION FOR SEQ ID NO:265:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 304 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..304  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498199  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```
Ile Ser Asn His Thr Phe Lys Leu Thr Leu Gln Lys Lys Lys Lys Leu
1 5 10 15
Arg Ala Glu Glu Ile Glu Arg Asp Lys Glu Arg Gln Arg Glu Arg Glu
20 25 30
Arg Glu Arg Glu Arg Glu Arg Glu Arg Asp Leu Gln Gln Ala Met Ser
35 40 45
Ile Ser Met Ala Leu Phe Ser Pro Pro Ile Ser Ser Ser Leu Gln Asn
50 55 60
Pro Asn Leu Ile Pro Lys Ile Ser Thr Ser Leu Leu Ser Thr Lys Arg
65 70 75 80
Phe Ser Leu Ile Ser Val Pro Arg Ala Ser Ser Asp Asn Gly Thr Thr
85 90 95
Ser Pro Val Val Lys Ile Pro Lys Pro Ala Ser Val Ala Val Glu Glu
100 105 110
Val Pro Val Lys Ser Pro Ala Glu Ser Ser Ser Ala Ser Glu Asn Gly
115 120 125
Ala Val Gly Gly Glu Ala Thr Asp Ser Ser Thr Glu Thr Val Ile Lys
130 135 140
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Gln | Asn | Ala | Lys | Trp | Val | Asn | Gly | Thr | Trp | Asp | Leu | Lys | Gln | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Lys | Asp | Gly | Lys | Thr | Asp | Trp | Asp | Ser | Val | Ile | Val | Ser | Glu | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Arg | Arg | Lys | Trp | Leu | Glu | Asp | Asn | Pro | Glu | Thr | Thr | Ser | Asn | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Leu | Val | Val | Phe | Asp | Thr | Ser | Ile | Ile | Pro | Trp | Trp | Ala | Trp | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Arg | Tyr | His | Leu | Pro | Glu | Ala | Glu | Leu | Leu | Asn | Gly | Arg | Ala | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Met | Ile | Gly | Phe | Phe | Met | Ala | Tyr | Phe | Val | Asp | Ser | Leu | Thr | Gly | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Leu | Val | Asp | Gln | Met | Gly | Asn | Phe | Phe | Cys | Lys | Thr | Leu | Leu | Phe |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Ala | Val | Ala | Gly | Val | Leu | Phe | Ile | Arg | Lys | Asn | Glu | Asp | Leu | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Leu | Lys | Asp | Leu | Phe | Asp | Glu | Thr | Thr | Leu | Tyr | Asp | Lys | Gln | Trp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gln | Ala | Ala | Trp | Lys | Glu | Pro | Asp | Ser | Ser | Thr | Val | Ser | Ser | Lys | Lys |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..258
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ile | Ser | Met | Ala | Leu | Phe | Ser | Pro | Pro | Ile | Ser | Ser | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Asn | Pro | Asn | Leu | Ile | Pro | Lys | Ile | Ser | Thr | Ser | Leu | Leu | Ser | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Arg | Phe | Ser | Leu | Ile | Ser | Val | Pro | Arg | Ala | Ser | Ser | Asp | Asn | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Thr | Thr | Ser | Pro | Val | Val | Lys | Ile | Pro | Lys | Pro | Ala | Ser | Val | Ala | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Glu | Val | Pro | Val | Lys | Ser | Pro | Ala | Glu | Ser | Ser | Ser | Ala | Ser | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Gly | Ala | Val | Gly | Gly | Glu | Ala | Thr | Asp | Ser | Ser | Thr | Glu | Thr | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Lys | Tyr | Gln | Asn | Ala | Lys | Trp | Val | Asn | Gly | Thr | Trp | Asp | Leu | Lys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Gln | Phe | Glu | Lys | Asp | Gly | Lys | Thr | Asp | Trp | Asp | Ser | Val | Ile | Val | Ser |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Glu | Ala | Lys | Arg | Arg | Lys | Trp | Leu | Glu | Asp | Asn | Pro | Glu | Thr | Thr | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Asn | Asp | Glu | Leu | Val | Val | Phe | Asp | Thr | Ser | Ile | Ile | Pro | Trp | Trp | Ala |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Trp | Met | Lys | Arg | Tyr | His | Leu | Pro | Glu | Ala | Glu | Leu | Leu | Asn | Gly | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ala | Ala | Met | Ile | Gly | Phe | Phe | Met | Ala | Tyr | Phe | Val | Asp | Ser | Leu | Thr |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Gly | Val | Gly | Leu | Val | Asp | Gln | Met | Gly | Asn | Phe | Phe | Cys | Lys | Thr | Leu |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Leu | Phe | Val | Ala | Val | Ala | Gly | Val | Leu | Phe | Ile | Arg | Lys | Asn | Glu | Asp |

(2) INFORMATION FOR SEQ ID NO:267:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1498201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..790



(D) OTHER INFORMATION: / Ceres Seq. ID 1498202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaaaaagttt | ctgagagatt | gattaaaata | tttatttgat | tacagatctg | ctctgctgct | 60  |
| atagaattgc | ggattctagt | gcaaatagaa | gggaagttgt | cggcgaaagg | tcacatttta | 120 |
| ttattgacaa | gatgattcaa | atggacggtg | gagataggct | gagagtgcg  | ttattagatc | 180 |
| gaatgtcaac | ggtggagaat | ggccggagct | cagtgacttt | agaagatatt | ctgatggctg | 240 |
| aaacgagcag | tttccgatct | cttactacgc | cgacaactcc | ggtgaggaat | cactctagta | 300 |
| gtagtttact | tgacgtgatg | agaagagagc | gtcgccgtga | taaaaccgct | tggaaatctc | 360 |
| tccgggata  | gctcyktctt | aaacgcaccg | ctactggttg | gatctcgtct | aatcctatcc | 420 |
| ctaccttgg  | taatcatatt | cttactccgg | ataacgatag | ccaccgattt | aaccgccttg | 480 |
| gattcctcct | tactaactcg | gagacaaacc | ggagcagtcg | tgacgtcagc | gacgcagcag | 540 |
| aggaagtggc | ggagcgagaa | ggaaggctcc | ggctaggcac | cgtgttggcg | gcggagagag | 600 |
| aggaaatgca | accaccgagg | atgtctctaa | tggagtgtgt | ggagccaccg | tctcaaccac | 660 |
| cgcccattaa | gcattctcgt | aataagtttt | aattactttg | gtgatttgta | tgagcgagct | 720 |
| ctctttgcgc | tgctgactct | ctctatttat | ctctgcttct | tgcttgtaaa | taaaatgcgt | 780 |
| tctattgagc |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1498203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Gln | Met | Asp | Gly | Gly | Asp | Arg | Leu | Arg | Val | Thr | Leu | Leu | Asp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Met | Ser | Thr | Val | Glu | Asn | Gly | Arg | Ser | Ser | Val | Thr | Leu | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Leu | Met | Ala | Glu | Thr | Ser | Ser | Phe | Arg | Ser | Leu | Thr | Thr | Pro | Thr |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Thr | Pro | Val | Arg | Asn | His | Ser | Ser | Ser | Ser | Leu | Leu | Asp | Val | Met | Arg |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Arg | Glu | Arg | Arg | Arg | Asp | Lys | Thr | Ala | Trp | Lys | Ser | Leu | Arg | Asp | Xaa |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Xaa | Leu | Lys | Arg | Thr | Ala | Thr | Gly | Trp | Ile | Ser | Ser | Asn | Pro | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Pro | Thr | Leu | Asp | Asn | His | Ile | Leu | Thr | Pro | Asp | Asn | Asp | Ser | His | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Asn | Arg | Leu | Gly | Phe | Leu | Leu | Thr | Asn | Ser | Glu | Thr | Asn | Arg | Ser |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Ser | Arg | Asp | Val | Ser | Asp | Ala | Ala | Glu | Glu | Val | Ala | Glu | Arg | Glu | Gly |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Arg | Leu | Arg | Leu | Gly | Thr | Val | Leu | Ala | Ala | Glu | Arg | Glu | Glu | Met | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Pro | Arg | Met | Ser | Leu | Met | Glu | Leu | Leu | Glu | Pro | Pro | Ser | Gln | Pro |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Pro | Pro | Ile | Lys | His | Leu | Val | Asn | Lys | Phe |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1498204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

```
Met Asp Gly Gly Asp Arg Leu Arg Val Thr Leu Leu Asp Arg Met Ser
1 5 10 15
Thr Val Glu Asn Gly Arg Ser Ser Val Thr Leu Glu Asp Ile Leu Met
20 25 30
Ala Glu Thr Ser Ser Phe Arg Ser Leu Thr Thr Pro Thr Thr Pro Val
35 40 45
Arg Asn His Ser Ser Ser Ser Leu Leu Asp Val Met Arg Arg Glu Arg
50 55 60
Arg Arg Asp Lys Thr Ala Trp Lys Ser Leu Arg Asp Xaa Leu Xaa Leu
65 70 75 80
Lys Arg Thr Ala Thr Gly Trp Ile Ser Ser Asn Pro Ile Pro Thr Leu
85 90 95
Asp Asn His Ile Leu Thr Pro Asp Asn Asp Ser His Arg Phe Asn Arg
100 105 110
Leu Gly Phe Leu Leu Thr Asn Ser Glu Thr Asn Arg Ser Ser Arg Asp
115 120 125
Val Ser Asp Ala Ala Glu Glu Val Ala Glu Arg Glu Gly Arg Leu Arg
130 135 140
Leu Gly Thr Val Leu Ala Ala Glu Arg Glu Glu Met Gln Pro Pro Arg
145 150 155 160
Met Ser Leu Met Glu Leu Leu Glu Pro Pro Ser Gln Pro Pro Pro Ile
165 170 175
Lys His Leu Val Asn Lys Phe
180
```

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1498205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```
Met Ser Thr Val Glu Asn Gly Arg Ser Ser Val Thr Leu Glu Asp Ile
1 5 10 15
Leu Met Ala Glu Thr Ser Ser Phe Arg Ser Leu Thr Thr Pro Thr Thr
20 25 30
Pro Val Arg Asn His Ser Ser Ser Ser Leu Leu Asp Val Met Arg Arg
35 40 45
Glu Arg Arg Arg Asp Lys Thr Ala Trp Lys Ser Leu Arg Asp Xaa Leu
50 55 60
Xaa Leu Lys Arg Thr Ala Thr Gly Trp Ile Ser Ser Asn Pro Ile Pro
65 70 75 80
Thr Leu Asp Asn His Ile Leu Thr Pro Asp Asn Asp Ser His Arg Phe
85 90 95
Asn Arg Leu Gly Phe Leu Leu Thr Asn Ser Glu Thr Asn Arg Ser Ser
100 105 110
Arg Asp Val Ser Asp Ala Ala Glu Glu Val Ala Glu Arg Glu Gly Arg
115 120 125
Leu Arg Leu Gly Thr Val Leu Ala Ala Glu Arg Glu Glu Met Gln Pro
130 135 140
Pro Arg Met Ser Leu Met Glu Leu Leu Glu Pro Pro Ser Gln Pro Pro
145 150 155 160
Pro Ile Lys His Leu Val Asn Lys Phe
165
```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1609
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```
ccatagttcc agttctgaaa tctcactttc acagtttgtg tctgtgcatg aatggccatg 60
gcagagctct caacccccaa aacgacgtcg ccttttctca actcttcgtc tcggcttcgt 120
ctctcttcaa aattgcacct ttcaaaccac ttctgccatc ttcttcttcc acctctccac 180
acaacaactc ccaactccaa aatctcttgc tccgtttctc aaaatagcca agctcctggt 240
gctgtgcaag aaaatggatt ggtgaagacg aagaaagagt gttatggagt gttctgcctc 300
acctatgata ttaaagctga agaagagaca agatcatgga agaagttaat taatattgca 360
gtttcagggt ctgcaggaat gatttctaac catcttctct tcaaaacttg ttcaggggaa 420
gtatttggtc cagatcaacc cattgcattg aaactgctag gatcagagag atcaattcaa 480
gctcttgaag gtgttgcaat ggaactggag gattcattgt tcccattggt gagagaagtt 540
attataggaa cagatccaaa tgaagtgttc caagatgtgg agtgggctat tctgattgga 600
gcaaaacctc gaggccctgg aatggaacgt gctgacttgt tggacatcaa tggccaaatc 660
tttgctgagc agggcaaagc tctgaacaaa gctgcctctc ctaacgtcaa gggtcttgta 720
gtgggaaacc cttgcaacac caatgccttg atttgtctta aaaatgctcc caacattcct 780
gcaaagaact tccatgccct cacgagggtta gacgaaaatc gtgccaaatg ccagcttgct 840
cttaaagccg gtgtttttct tgacaaaagt tctaatatga ccatatgggg aaatcaactc 900
acgactcagg tgcagactt cttaaagtcc agaattaatg gcctgcctgt gaaggagggt 960
attacagata ccaaatgggt agaagagggg ttcactgaga gtgtgcagaa gagagggtgg 1020
ttattaattc agaaatgggg tcatcttctc gctgcttcta ctgctgtttc cattgttgat 1080
gctataaagt ctcttgtrac tctactcct gaggktgatt ggtttttcgac tgggggtgtac 1140
acggatggaa atccttatgg tattgaagag ggccttgtct tcagtatgcc atgccggctc 1200
aaggagatg gagattatga acttgtcaag gatgtagaaa ttgatgacta ccttcgccaa 1260
cgaatcgcca agtcggaagc ggaactgttg gctgagaaga gatgtgttgc acacctcaact 1320
ggagagggga ttgcctactg tgatcttggt ccggtagata ctatgcttcc tgggggaagtt 1380
tgattttttc aggcgtttga acatctcaag taagcattct cttccggggt gttagctgta 1440
cagagcacag ccacattact tatgatgatt gttcagaata agaaaatgaa actcttattt 1500
cttattttaca tgcattctgta tgtgattttt cttgagcaat gtcctaaaag tcatatacag 1560
tagtatttgt aaacacttga aacgtttcta tgctttattc cagtttcag
```

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```
Met Ala Met Ala Glu Leu Ser Thr Pro Lys Thr Thr Ser Pro Phe Leu
1 5 10 15
Asn Ser Ser Ser Arg Leu Arg Leu Ser Ser Lys Leu His Leu Ser Asn
20 25 30
His Phe Arg His Leu Leu Leu Pro Leu His Thr Thr Thr Pro Asn
35 40 45
Ser Lys Ile Ser Cys Ser Val Ser Gln Asn Ser Gln Ala Pro Val Ala
50 55 60
Val Gln Glu Asn Gly Leu Val Lys Thr Lys Lys Glu Cys Tyr Gly Val
65 70 75 80
```

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Phe        | Cys        | Leu        | Thr        | Tyr<br>85  | Asp        | Leu        | Lys        | Ala        | Glu<br>90  | Glu        | Glu        | Thr        | Arg        | Ser<br>95  | Trp        |
| Lys        | Lys        | Leu        | Ile<br>100 | Asn        | Ile        | Ala        | Val        | Ser<br>105 | Gly        | Ala        | Ala        | Gly        | Met<br>110 | Ile        | Ser        |
| Asn        | His        | Leu        | Leu<br>115 | Phe        | Lys        | Leu        | Ala<br>120 | Ser        | Gly        | Glu        | Val        | Phe<br>125 | Gly        | Pro        | Asp        |
| Gln        | Pro<br>130 | Ile        | Ala        | Leu        | Lys        | Leu<br>135 | Leu        | Gly        | Ser        | Glu        | Arg<br>140 | Ser        | Ile        | Gln        | Ala        |
| Leu<br>145 | Glu        | Gly        | Val        | Ala        | Met<br>150 | Glu        | Leu        | Glu        | Asp        | Ser        | Leu        | Phe        | Pro        | Leu        | Leu<br>160 |
| Arg        | Glu        | Val        | Asp        | Ile<br>165 | Gly        | Thr        | Asp        | Pro        | Asn<br>170 | Glu        | Val        | Phe        | Gln        | Asp<br>175 | Val        |
| Glu        | Trp        | Ala        | Ile<br>180 | Leu        | Ile        | Gly        | Ala<br>185 | Lys        | Pro        | Arg        | Gly        | Pro        | Gly<br>190 | Met        | Glu        |
| Arg        | Ala        | Asp<br>195 | Leu        | Leu        | Asp        | Ile        | Asn<br>200 | Gly        | Gln        | Ile        | Phe        | Ala<br>205 | Glu        | Gln        | Gly        |
| Lys        | Ala<br>210 | Leu        | Asn        | Lys        | Ala        | Ala<br>215 | Ser        | Pro        | Asn        | Val        | Lys<br>220 | Val        | Leu        | Val        | Val        |
| Gly<br>225 | Asn        | Pro        | Cys        | Asn<br>230 | Thr        | Asn        | Ala        | Leu        | Ile        | Cys<br>235 | Leu        | Lys        | Asn        | Ala        | Pro<br>240 |
| Asn        | Ile        | Pro        | Ala        | Lys<br>245 | Asn        | Phe        | His        | Ala        | Leu<br>250 | Thr        | Arg        | Leu        | Asp<br>255 | Glu        | Asn        |
| Arg        | Ala        | Lys        | Cys<br>260 | Gln        | Leu        | Ala        | Leu        | Lys<br>265 | Ala        | Gly        | Val        | Phe        | Tyr<br>270 | Asp        | Lys        |
| Val        | Ser        | Asn<br>275 | Met        | Thr        | Ile        | Trp        | Gly<br>280 | Asn        | His        | Ser        | Thr        | Thr<br>285 | Gln        | Val        | Pro        |
| Asp        | Phe<br>290 | Leu        | Asn        | Ala        | Arg        | Ile<br>295 | Asn        | Gly        | Leu        | Pro        | Val<br>300 | Lys        | Glu        | Val        | Ile        |
| Thr<br>305 | Asp        | His        | Lys        | Trp        | Leu        | Glu<br>310 | Glu        | Gly        | Phe        | Thr<br>315 | Glu        | Ser        | Val        | Gln        | Lys<br>320 |
| Arg        | Gly        | Gly        | Leu<br>325 | Leu        | Ile        | Gln        | Lys        | Trp        | Gly<br>330 | Arg        | Ser        | Ser        | Ala        | Ala<br>335 | Ser        |
| Thr        | Ala        | Val        | Ser<br>340 | Ile        | Val        | Asp        | Ala        | Ile<br>345 | Lys        | Ser        | Leu        | Xaa        | Thr<br>350 | Pro        | Thr        |
| Pro        | Glu        | Xaa<br>355 | Asp        | Trp        | Phe        | Ser        | Thr<br>360 | Gly        | Val        | Tyr        | Thr        | Asp<br>365 | Gly        | Asn        | Pro        |
| Tyr        | Gly<br>370 | Ile        | Glu        | Glu        | Gly        | Leu<br>375 | Val        | Phe        | Ser        | Met        | Pro<br>380 | Cys        | Arg        | Ser        | Lys        |
| Gly<br>385 | Asp        | Gly        | Asp        | Tyr        | Glu<br>390 | Leu        | Val        | Lys        | Asp        | Val<br>395 | Glu        | Ile        | Asp        | Asp        | Tyr<br>400 |
| Leu        | Arg        | Gln        | Arg        | Ile<br>405 | Ala        | Lys        | Ser        | Glu        | Ala<br>410 | Glu        | Leu        | Leu        | Ala        | Glu<br>415 | Lys        |
| Arg        | Cys        | Val        | Ala<br>420 | His        | Leu        | Thr        | Gly        | Glu<br>425 | Gly        | Ile        | Ala        | Tyr        | Cys<br>430 | Asp        | Leu        |
| Gly        | Pro        | Val<br>435 | Asp        | Thr        | Met        | Leu        | Pro<br>440 | Gly        | Glu        | Val        |            |            |            |            |            |

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..441  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Ala Glu Leu Ser Thr Pro Lys Thr Thr Ser Pro Phe Leu Asn Ser  
1 5 10 15  
Ser Ser Arg Leu Arg Leu Ser Ser Lys Leu His Leu Ser Asn His Phe

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | His | Leu | Leu | Leu | Pro | Pro | Leu | His | Thr | Thr | Thr | Pro | Asn | Ser | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ile | Ser | Cys | Ser | Val | Ser | Gln | Asn | Ser | Gln | Ala | Pro | Val | Ala | Val | Gln |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu | Asn | Gly | Leu | Val | Lys | Thr | Lys | Lys | Glu | Cys | Tyr | Gly | Val | Phe | Cys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu | Thr | Tyr | Asp | Leu | Lys | Ala | Glu | Glu | Glu | Thr | Arg | Ser | Trp | Lys | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Ile | Asn | Ile | Ala | Val | Ser | Gly | Ala | Ala | Gly | Met | Ile | Ser | Asn | His |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Leu | Phe | Lys | Leu | Ala | Ser | Gly | Glu | Val | Phe | Gly | Pro | Asp | Gln | Pro |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ile | Ala | Leu | Lys | Leu | Leu | Gly | Ser | Glu | Arg | Ser | Ile | Gln | Ala | Leu | Glu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gly | Val | Ala | Met | Glu | Leu | Glu | Asp | Ser | Leu | Phe | Pro | Leu | Leu | Arg | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Val | Asp | Ile | Gly | Thr | Asp | Pro | Asn | Glu | Val | Phe | Gln | Asp | Val | Glu | Trp |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ala | Ile | Leu | Ile | Gly | Ala | Lys | Pro | Arg | Gly | Pro | Gly | Met | Glu | Arg | Ala |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Asp | Leu | Leu | Asp | Ile | Asn | Gly | Gln | Ile | Phe | Ala | Glu | Gln | Gly | Lys | Ala |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Leu | Asn | Lys | Ala | Ala | Ser | Pro | Asn | Val | Lys | Val | Leu | Val | Val | Gly | Asn |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Pro | Cys | Asn | Thr | Asn | Ala | Leu | Ile | Cys | Leu | Lys | Asn | Ala | Pro | Asn | Ile |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Pro | Ala | Lys | Asn | Phe | His | Ala | Leu | Thr | Arg | Leu | Asp | Glu | Asn | Arg | Ala |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Lys | Cys | Gln | Leu | Ala | Leu | Lys | Ala | Gly | Val | Phe | Tyr | Asp | Lys | Val | Ser |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Asn | Met | Thr | Ile | Trp | Gly | Asn | His | Ser | Thr | Thr | Gln | Val | Pro | Asp | Phe |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Leu | Asn | Ala | Arg | Ile | Asn | Gly | Leu | Pro | Val | Lys | Glu | Val | Ile | Thr | Asp |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| His | Lys | Trp | Leu | Glu | Glu | Gly | Phe | Thr | Glu | Ser | Val | Gln | Lys | Arg | Gly |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Gly | Leu | Leu | Ile | Gln | Lys | Trp | Gly | Arg | Ser | Ser | Ala | Ala | Ser | Thr | Ala |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Val | Ser | Ile | Val | Asp | Ala | Ile | Lys | Ser | Leu | Xaa | Thr | Pro | Thr | Pro | Glu |  |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Xaa | Asp | Trp | Phe | Ser | Thr | Gly | Val | Tyr | Thr | Asp | Gly | Asn | Pro | Tyr | Gly |  |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Ile | Glu | Glu | Gly | Leu | Val | Phe | Ser | Met | Pro | Cys | Arg | Ser | Lys | Gly | Asp |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
| Gly | Asp | Tyr | Glu | Leu | Val | Lys | Asp | Val | Glu | Ile | Asp | Asp | Tyr | Leu | Arg |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |
| Gln | Arg | Ile | Ala | Lys | Ser | Glu | Ala | Glu | Leu | Leu | Ala | Glu | Lys | Arg | Cys |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
| Val | Ala | His | Leu | Thr | Gly | Glu | Gly | Ile | Ala | Tyr | Cys | Asp | Leu | Gly | Pro |  |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |
| Val | Asp | Thr | Met | Leu | Pro | Gly | Glu | Val |     |     |     |     |     |     |     |  |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..334

(D) OTHER INFORMATION: / Ceres Seq. ID 1498209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```
Met Ile Ser Asn His Leu Leu Phe Lys Leu Ala Ser Gly Glu Val Phe
1 5 10 15
Gly Pro Asp Gln Pro Ile Ala Leu Lys Leu Leu Gly Ser Glu Arg Ser
20 25 30
Ile Gln Ala Leu Glu Gly Val Ala Met Glu Leu Glu Asp Ser Leu Phe
35 40 45
Pro Leu Leu Arg Glu Val Asp Ile Gly Thr Asp Pro Asn Glu Val Phe
50 55 60
Gln Asp Val Glu Trp Ala Ile Leu Ile Gly Ala Lys Pro Arg Gly Pro
65 70 75 80
Gly Met Glu Arg Ala Asp Leu Leu Asp Ile Asn Gly Gln Ile Phe Ala
85 90 95
Glu Gln Gly Lys Ala Leu Asn Lys Ala Ala Ser Pro Asn Val Lys Val
100 105 110
Leu Val Val Gly Asn Pro Cys Asn Thr Asn Ala Leu Ile Cys Leu Lys
115 120 125
Asn Ala Pro Asn Ile Pro Ala Lys Asn Phe His Ala Leu Thr Arg Leu
130 135 140
Asp Glu Asn Arg Ala Lys Cys Gln Leu Ala Leu Lys Ala Gly Val Phe
145 150 155 160
Tyr Asp Lys Val Ser Asn Met Thr Ile Trp Gly Asn His Ser Thr Thr
165 170 175
Gln Val Pro Asp Phe Leu Asn Ala Arg Ile Asn Gly Leu Pro Val Lys
180 185 190
Glu Val Ile Thr Asp His Lys Trp Leu Glu Glu Gly Phe Thr Glu Ser
195 200 205
Val Gln Lys Arg Gly Gly Leu Leu Ile Gln Lys Trp Gly Arg Ser Ser
210 215 220
Ala Ala Ser Thr Ala Val Ser Ile Val Asp Ala Ile Lys Ser Leu Xaa
225 230 235 240
Thr Pro Thr Pro Glu Xaa Asp Trp Phe Ser Thr Gly Val Tyr Thr Asp
245 250 255
Gly Asn Pro Tyr Gly Ile Glu Glu Gly Leu Val Phe Ser Met Pro Cys
260 265 270
Arg Ser Lys Gly Asp Gly Asp Tyr Glu Leu Val Lys Asp Val Glu Ile
275 280 285
Asp Asp Tyr Leu Arg Gln Arg Ile Ala Lys Ser Glu Ala Glu Leu Leu
290 295 300
Ala Glu Lys Arg Cys Val Ala His Leu Thr Gly Glu Gly Ile Ala Tyr
305 310 315 320
Cys Asp Leu Gly Pro Val Asp Thr Met Leu Pro Gly Glu Val
325 330
```

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1500 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1500

(D) OTHER INFORMATION: / Ceres Seq. ID 1498210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```
atctcttggt ctctccgccc atctctgctc tcttttatit tcccagaaag tttttttttt 60
tttcccgaat tccgttaatc tcattggggg ttccattgat agcaatggcg acggctttcg 120
ctcccactaa gctcactgcc acggttcctc tgcattggat ccatgagaat cgtctcttgc 180
```

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| tcccgatccg  | attggctcct  | ccttcttctt | tcctcggatc | cacccggttc  | ctctcccttc  | 240  |
| gcagactcaa  | tcactccaac  | gccaccgcgc | gatctcccgt | cgtctctgtc  | caggaagttg  | 300  |
| tcaaggagaa  | gcaatccacc  | aataatacca | gcctgttgat | aaccaaagag  | gaaggattgg  | 360  |
| agttgtatga  | agatatgata  | ctaggtagat | ctttcgaaga | catgtgtgct  | caaattgtatt | 420  |
| accgaggcaa  | gatgttttgt  | tttgttcact | tgtacaatgg | ccaagaggct  | gtttctactg  | 480  |
| gctttatcaa  | gctccttacc  | aagtctgact | ctgtcgttag | tacctaccgt  | gaccatgtcc  | 540  |
| atgccctcag  | caaaggtgtc  | tctgctcgtg | ctgttatgag | cgagctcttc  | ggcaagggtta | 600  |
| ctggatgctg  | cagaggccaa  | ggtggatcca | tgcacatgtt | ctccaaagaa  | cacaacatgc  | 660  |
| ttggtggctt  | tgtcttttatt | ggtgaaggca | ttcctgtcgc | cactgggtgct | gccttttagct | 720  |
| ccaagtacag  | gaggggaagt  | ttgaaacagg | attgtgatga | tgtaactgtc  | gccttttttcg | 780  |
| gagatggaac  | ttgtaacaac  | ggacagttct | tcgagtgtct | caacatggct  | gctctctata  | 840  |
| aactgcctat  | tatcttttgt  | gtcgagaata | acttggtggc | cattgggatg  | tctcacttga  | 900  |
| gagccacttc  | tgaccccgag  | atttggaaga | aaggtcctgc | atttgggatg  | cctgggtgttc | 960  |
| atgttgacgg  | tatggatgtc  | ttgaaggtca | gggaagtcgc | taaagaggct  | gtcactagag  | 1020 |
| ctagaagagg  | agaaggtcca  | accttggttg | aatgtgagac | ttatagattt  | agaggacact  | 1080 |
| ccttggtctga | tcccgatgag  | ctccgtgatg | ctgctgagaa | agccaaatac  | gcgggctagag | 1140 |
| acccaatcgc  | agcattgaag  | aagtatttga | tagagaacaa | gcttgcaaag  | gaagcagagc  | 1200 |
| taaagtcaat  | agagaaaaag  | atagacgagt | tggtggagga | agcgggttgag | tttgacagacg | 1260 |
| ctagtccaca  | gcccggctgc  | agtcagttgc | tagaagaatt | gtttgctgat  | ccaaaaggat  | 1320 |
| ttggaattgg  | acctgatgga  | cggtaacagt | gtgaggaccc | caagtttacc  | gaaggcacag  | 1380 |
| ctcaagtctg  | agaagacaag  | tttaaccata | agctgtctac | tgtctcttcg  | atgtatttcta | 1440 |
| tatatcttat  | taagttaaat  | gctacagaga | atcagtttga | atcatttgca  | ctttttgctg  | 1500 |

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..462

(D) OTHER INFORMATION: / Ceres Seq. ID 1498211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Phe | Ser | Pro | Pro | Ile | Ser | Ala | Leu | Phe | Tyr | Phe | Pro | Arg | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Phe | Phe | Phe | Ser | Arg | Ile | Pro | Leu | Ile | Ser | Leu | Gly | Phe | Pro | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ala | Met | Ala | Thr | Ala | Phe | Ala | Pro | Thr | Lys | Leu | Thr | Ala | Thr | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Leu | His | Gly | Ser | His | Glu | Asn | Arg | Leu | Leu | Leu | Pro | Ile | Arg | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Pro | Pro | Ser | Ser | Phe | Leu | Gly | Ser | Thr | Arg | Ser | Leu | Ser | Leu | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Leu | Asn | His | Ser | Asn | Ala | Thr | Arg | Arg | Ser | Pro | Val | Val | Ser | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Glu | Val | Val | Lys | Glu | Lys | Gln | Ser | Thr | Asn | Asn | Thr | Ser | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Thr | Lys | Glu | Glu | Gly | Leu | Glu | Leu | Tyr | Glu | Asp | Met | Ile | Leu | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Ser | Phe | Glu | Asp | Met | Cys | Ala | Gln | Met | Tyr | Tyr | Arg | Gly | Lys | Met |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Gly | Phe | Val | His | Leu | Tyr | Asn | Gly | Gln | Glu | Ala | Val | Ser | Thr | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Ile | Lys | Leu | Leu | Thr | Lys | Ser | Asp | Ser | Val | Val | Ser | Thr | Tyr | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | His | Val | His | Ala | Leu | Ser | Lys | Gly | Val | Ser | Ala | Arg | Ala | Val | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Glu | Leu | Phe | Gly | Lys | Val | Thr | Gly | Cys | Cys | Arg | Gly | Gln | Gly | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

Ser Met His Met Phe Ser Lys Glu His Asn Met Leu Gly Gly Phe Ala  
210 215 220  
Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala Ala Phe Ser Ser  
225 230 235 240  
Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp Asp Val Thr Val  
245 250 255  
Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln Phe Phe Glu Cys  
260 265 270  
Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile Phe Val Val Glu  
275 280 285  
Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg Ala Thr Ser Asp  
290 295 300  
Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met Pro Gly Val His  
305 310 315 320  
Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val Ala Lys Glu Ala  
325 330 335  
Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu Val Glu Cys Glu  
340 345 350  
Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro Asp Glu Leu Arg  
355 360 365  
Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp Pro Ile Ala Ala  
370 375 380  
Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys Glu Ala Glu Leu  
385 390 395 400  
Lys Ser Ile Glu Lys Lys Ile Asp Glu Leu Val Glu Glu Ala Val Glu  
405 410 415  
Phe Ala Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln Leu Leu Glu Asn  
420 425 430  
Val Phe Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro Asp Gly Arg Tyr  
435 440 445  
Arg Cys Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala Gln Val  
450 455 460

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Met Ala Thr Ala Phe Ala Pro Thr Lys Leu Thr Ala Thr Val Pro Leu  
1 5 10 15  
His Gly Ser His Glu Asn Arg Leu Leu Leu Pro Ile Arg Leu Ala Pro  
20 25 30  
Pro Ser Ser Phe Leu Gly Ser Thr Arg Ser Leu Ser Leu Arg Arg Leu  
35 40 45  
Asn His Ser Asn Ala Thr Arg Arg Ser Pro Val Val Ser Val Gln Glu  
50 55 60  
Val Val Lys Glu Lys Gln Ser Thr Asn Asn Thr Ser Leu Leu Ile Thr  
65 70 75 80  
Lys Glu Glu Gly Leu Glu Leu Tyr Glu Asp Met Ile Leu Gly Arg Ser  
85 90 95  
Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr Arg Gly Lys Met Phe Gly  
100 105 110  
Phe Val His Leu Tyr Asn Gly Gln Glu Ala Val Ser Thr Gly Phe Ile  
115 120 125  
Lys Leu Leu Thr Lys Ser Asp Ser Val Val Ser Thr Tyr Arg Asp His



(2) INFORMATION FOR SEQ ID NO:279:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:279:

Ile Leu Gly Arg Ser Phe Glu Asp Met Cys A

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |  |  |  |  |
| Arg | Gly | Lys | Met | Phe | Gly | Phe | Val | His | Leu | Tyr | Asn | Gly | Gln | Glu | Ala |  |  |  |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |  |  |  |
| Val | Ser | Thr | Gly | Phe | Ile | Lys | Leu | Thr | Lys | Ser | Asp | Ser | Val | Val |     |  |  |  |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |  |  |  |
| Ser | Thr | Tyr | Arg | Asp | His | Val | His | Ala | Leu | Ser | Lys | Gly | Val | Ser | Ala |  |  |  |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |  |  |  |  |
| Arg | Ala | Val | Met | Ser | Glu | Leu | Phe | Gly | Lys | Val | Thr | Gly | Cys | Cys | Arg |  |  |  |  |
|     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     |     | 80  |  |  |  |  |
| Gly | Gln | Gly | Gly | Ser | Met | His | Met | Phe | Ser | Lys | Glu | His | Asn | Met | Leu |  |  |  |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     | 95  |  |  |  |  |

Gly Gly Phe Ala Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala  
100 105 110  
Ala Phe Ser Ser Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp  
115 120 125  
Asp Val Thr Val Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln  
130 135 140  
Phe Phe Glu Cys Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile  
145 150 155 160  
Phe Val Val Glu Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg  
165 170 175  
Ala Thr Ser Asp Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met  
180 185 190  
Pro Gly Val His Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val  
195 200 205  
Ala Lys Glu Ala Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu  
210 215 220  
Val Glu Cys Glu Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro  
225 230 235 240  
Asp Glu Leu Arg Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp  
245 250 255  
Pro Ile Ala Ala Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys  
260 265 270  
Glu Ala Glu Leu Lys Ser Ile Glu Lys Lys Ile Asp Glu Leu Val Glu  
275 280 285  
Glu Ala Val Glu Phe Ala Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln  
290 295 300  
Leu Leu Glu Asn Val Phe Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro  
305 310 315 320  
Asp Gly Arg Tyr Arg Cys Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala  
325 330 335  
Gln Val

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

|            |             |             |             |             |            |      |
|------------|-------------|-------------|-------------|-------------|------------|------|
| aaaataattt | gaaaggaata  | tgaatattcc  | gttgaagaag  | acttgctcct  | gaaatccttt | 60   |
| ggaccgaaac | tcgtaaaatt  | atttcccttc  | aatttctctg  | aaatctattc  | accgtctcct | 120  |
| ttgtctcctc | ctccaaatcg  | atcgttcctc  | gtcgtcgtct  | gattttctct  | acgattgctt | 180  |
| tttctgtcta | gctcgataag  | aaaaaacaaa  | actaattttt  | gaagagtttt  | tttttttggg | 240  |
| tttgggagcg | atgggtcaag  | cttttcgtaa  | gctattcgat  | actttcttcg  | gcaatcaaga | 300  |
| aatgagggtc | gttatgctgg  | ggctggatgc  | tgctggcaaa  | acaactattc  | tctacaagct | 360  |
| tcatattggg | gaagttttgt  | ctactgttcc  | caccattgga  | ttcaatgttg  | agaaagttca | 420  |
| gtacaagaat | gtgatgttca  | cagtttgagg  | tggttggtggc | caagagaaac  | tgagacctct | 480  |
| ttggaggcat | tacttcaata  | atactgatgg  | acttatatac  | gtgggtggatt | ccttagatcg | 540  |
| agagaggatc | gggaaagcaa  | agcaagaatt  | tcaggagatc  | ataaaaagacc | cattcatgct | 600  |
| aaacagtatc | attctggtgt  | ttgcaaacaa  | acaggacatg  | agaggagcca  | tgtcaccgag | 660  |
| agaagtatgt | gaagggttag  | gcttatttga  | tctcaagaac  | aggaaatggc  | acatacaagg | 720  |
| tacttggtgt | cttcgtggag  | acgggcttta  | tgaaggcttg  | gactggttat  | catctactct | 780  |
| taaggatgtt | aaagccgctg  | gattcacatc  | ggttggccac  | tcgtttttaa  | tcttccaggt | 840  |
| atactttgat | atcaatggcc  | agtgtcttct  | tcttggtctt  | atcacgaaat  | cagaatctct | 900  |
| gaagactttt | tttgtttaagg | aaagaatgat  | cttctcattg  | tggcaatatt  | agactccatt | 960  |
| agactatttt | tgaattttga  | tcattgctgcc | atgaaagctt  | ctttgtatat  | tctgctgatg | 1020 |

aagagttgta tcacttgaaa aaccttctct ttgggggtcat ctttgtccga ttaagacttt 1080  
ggtagatgta tatacattcc ttcgaaatca tgatatattt ttttat

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Gln | Ala | Phe | Arg | Lys | Leu | Phe | Asp | Thr | Phe | Phe | Gly | Asn | Gln |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Met | Arg | Val | Val | Met | Leu | Gly | Leu | Asp | Ala | Ala | Gly | Lys | Thr | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Leu | Tyr | Lys | Leu | His | Ile | Gly | Glu | Val | Leu | Ser | Thr | Val | Pro | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Gly | Phe | Asn | Val | Glu | Lys | Val | Gln | Tyr | Lys | Asn | Val | Met | Phe | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Trp | Asp | Val | Gly | Gly | Gln | Glu | Lys | Leu | Arg | Pro | Leu | Trp | Arg | His |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Tyr | Phe | Asn | Asn | Thr | Asp | Gly | Leu | Ile | Tyr | Val | Val | Asp | Ser | Leu | Asp |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Glu | Arg | Ile | Gly | Lys | Ala | Lys | Gln | Glu | Phe | Gln | Glu | Ile | Ile | Lys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asp | Pro | Phe | Met | Leu | Asn | Ser | Ile | Leu | Val | Phe | Ala | Asn | Lys | Gln |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Asp | Met | Arg | Gly | Ala | Met | Ser | Pro | Arg | Glu | Val | Cys | Glu | Gly | Leu | Gly |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Phe | Asp | Leu | Lys | Asn | Arg | Lys | Trp | His | Ile | Gln | Gly | Thr | Cys | Ala |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Arg | Gly | Asp | Gly | Leu | Tyr | Glu | Gly | Leu | Asp | Trp | Leu | Ser | Ser | Thr |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Leu | Lys | Asp | Val | Lys | Ala | Ala | Gly | Phe | Thr | Ser | Val | Gly | His | Ser | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Val | Val | Met | Leu | Gly | Leu | Asp | Ala | Ala | Gly | Lys | Thr | Thr | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Tyr | Lys | Leu | His | Ile | Gly | Glu | Val | Leu | Ser | Thr | Val | Pro | Thr | Ile |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Gly | Phe | Asn | Val | Glu | Lys | Val | Gln | Tyr | Lys | Asn | Val | Met | Phe | Thr | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Trp | Asp | Val | Gly | Gly | Gln | Glu | Lys | Leu | Arg | Pro | Leu | Trp | Arg | His | Tyr |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Phe | Asn | Asn | Thr | Asp | Gly | Leu | Ile | Tyr | Val | Val | Asp | Ser | Leu | Asp | Arg |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Arg | Ile | Gly | Lys | Ala | Lys | Gln | Glu | Phe | Gln | Glu | Ile | Ile | Lys | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Phe | Met | Leu | Asn | Ser | Ile | Ile | Leu | Val | Phe | Ala | Asn | Lys | Gln | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Arg | Gly | Ala | Met | Ser | Pro | Arg | Glu | Val | Cys | Glu | Gly | Leu | Gly | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Asp | Leu | Lys | Asn | Arg | Lys | Trp | His | Ile | Gln | Gly | Thr | Cys | Ala | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Gly | Asp | Gly | Leu | Tyr | Glu | Gly | Leu | Asp | Trp | Leu | Ser | Ser | Thr | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Asp | Val | Lys | Ala | Ala | Gly | Phe | Thr | Ser | Val | Gly | His | Ser | Phe |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1498217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Leu | Asp | Ala | Ala | Gly | Lys | Thr | Thr | Ile | Leu | Tyr | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Ile | Gly | Glu | Val | Leu | Ser | Thr | Val | Pro | Thr | Ile | Gly | Phe | Asn | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Lys | Val | Gln | Tyr | Lys | Asn | Val | Met | Phe | Thr | Val | Trp | Asp | Val | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Gln | Glu | Lys | Leu | Arg | Pro | Leu | Trp | Arg | His | Tyr | Phe | Asn | Asn | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asp | Gly | Leu | Ile | Tyr | Val | Asp | Ser | Leu | Asp | Arg | Glu | Arg | Ile | Gly |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Ala | Lys | Gln | Glu | Phe | Gln | Glu | Ile | Ile | Lys | Asp | Pro | Phe | Met | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Ser | Ile | Ile | Leu | Val | Phe | Ala | Asn | Lys | Gln | Asp | Met | Arg | Gly | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Ser | Pro | Arg | Glu | Val | Cys | Glu | Gly | Leu | Gly | Leu | Phe | Asp | Leu | Lys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asn | Arg | Lys | Trp | His | Ile | Gln | Gly | Thr | Cys | Ala | Leu | Arg | Gly | Asp | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Tyr | Glu | Gly | Leu | Asp | Trp | Leu | Ser | Ser | Thr | Leu | Lys | Asp | Val | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ala | Gly | Phe | Thr | Ser | Val | Gly | His | Ser | Phe |     |     |     |     |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1056 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1056

(D) OTHER INFORMATION: / Ceres Seq. ID 1498218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaaaaaaaaa | accaaagcaa | aaaaatggct | ttgaaactca | cttctccgcc | ttcagttttc | 60  |
| tcacaatcaa | ggagattatc | ttcttcttcg | ttaattccga | taaggtcaaa | atccacattc | 120 |

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| accggatttc  | gacgagaac  | cggtgtttat | ttaagcaaaa | cgacggcgct | tcagtcgtct | 180  |
| acaaaaactga | gtgtggcggc | ggagagtcct | gcggcgacaa | ttgacgacga | tgattggggg | 240  |
| aaagtatcgg  | cggttctgtt | tgatatggac | ggtgtgcttt | gtaacagtga | agatctttct | 300  |
| agacgcgccg  | ccgtggatgt | ttttacggag | atgggagttg | aagtcactgt | ggacgatttc | 360  |
| gttcctttta  | tgggaacagg | tgaagccaag | tttttaggag | gtgttgcttc | agtcaaagaa | 420  |
| gttaaaggat  | ttgatccaga | tgcagctaaa | aagagattct | ttgaaatata | tctcgataag | 480  |
| tatgcgaagc  | cagaatctgg | gattggattt | ccaggagcat | tggagcttgt | tactgagtgt | 540  |
| aagaacaaa   | gccttaaagt | cgctgttgca | tctagtgtg  | accgtatcaa | agttgatgcg | 600  |
| aatctgaaa   | ctgctggttt | gtctttgacc | atgtttgatg | ccattgtttc | agcagatgcc | 660  |
| tttgagaatt  | tgaaccagc  | tccagatatt | ttcctggctg | ctgcaaagat | cttaggtgtg | 720  |
| cctaccagcg  | agtgtgttgt | tattgaagat | gcgcttgctg | gagtccaagc | cgcacaagct | 780  |
| gcgaacatga  | gatgtatagc | cgtaaaaact | actttatctg | aagcaattct | taaggatgct | 840  |
| ggctccttcaa | tgatacgaga | cgatattgga | aacatctcaa | tcaatgacat | tctcactggg | 900  |
| ggctcagatt  | ctaccagtat | gtagtctcaa | agaaattcga | tggaaaatat | cgttcttttc | 960  |
| atgtgtattt  | tatttcttgt | ttactccttt | tgaaaacttt | tgaataaagg | ggctttcttt | 1020 |
| gtaacgagat  | tacacattta | aaacaatctt | ttctgt     |            |            |      |

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..307

(D) OTHER INFORMATION: / Ceres Seq. ID 1498219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Lys | Asn | Gln | Ser | Lys | Lys | Met | Ala | Leu | Lys | Leu | Thr | Ser | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Ser | Val | Phe | Ser | Gln | Ser | Arg | Arg | Leu | Ser | Ser | Ser | Ser | Leu | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ile | Arg | Ser | Lys | Ser | Thr | Phe | Thr | Gly | Phe | Arg | Ser | Arg | Thr | Gly |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Val | Tyr | Leu | Ser | Lys | Thr | Thr | Ala | Leu | Gln | Ser | Ser | Thr | Lys | Leu | Ser |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Val | Ala | Ala | Glu | Ser | Pro | Ala | Ala | Thr | Ile | Ala | Thr | Asp | Asp | Trp | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Val | Ser | Ala | Val | Leu | Phe | Asp | Met | Asp | Gly | Val | Leu | Cys | Asn | Ser |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Asp | Leu | Ser | Arg | Arg | Ala | Ala | Val | Asp | Val | Phe | Thr | Glu | Met | Gly |
|     |     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |
| Val | Glu | Val | Thr | Val | Asp | Asp | Phe | Val | Pro | Phe | Met | Gly | Thr | Gly | Glu |
|     |     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |
| Ala | Lys | Phe | Leu | Gly | Gly | Val | Ala | Ser | Val | Lys | Glu | Val | Lys | Gly | Phe |
|     |     |     |     |     |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Asp | Pro | Asp | Ala | Ala | Lys | Lys | Arg | Phe | Phe | Glu | Ile | Tyr | Leu | Asp | Lys |
| 145 |     |     |     |     |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Ala | Lys | Pro | Glu | Ser | Gly | Ile | Gly | Phe | Pro | Gly | Ala | Leu | Glu | Leu |
|     |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |
| Val | Thr | Glu | Cys | Lys | Asn | Lys | Gly | Leu | Lys | Val | Ala | Val | Ala | Ser | Ser |
|     |     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |
| Ala | Asp | Arg | Ile | Lys | Val | Asp | Ala | Asn | Leu | Lys | Ala | Ala | Gly | Leu | Ser |
|     |     |     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |
| Leu | Thr | Met | Phe | Asp | Ala | Ile | Val | Ser | Ala | Asp | Ala | Phe | Glu | Asn | Leu |
|     |     |     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |
| Lys | Pro | Ala | Pro | Asp | Ile | Phe | Leu | Ala | Ala | Ala | Lys | Ile | Leu | Gly | Val |
| 225 |     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Pro | Thr | Ser | Glu | Cys | Val | Val | Ile | Glu | Asp | Ala | Leu | Ala | Gly | Val | Gln |
|     |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Ala | Ala | Gln | Ala | Ala | Asn | Met | Arg | Cys | Ile | Ala | Val | Lys | Thr | Thr | Leu |

260 265 270  
Ser Glu Ala Ile Leu Lys Asp Ala Gly Pro Ser Met Ile Arg Asp Asp  
275 280 285  
Ile Gly Asn Ile Ser Ile Asn Asp Ile Leu Thr Gly Gly Ser Asp Ser  
290 295 300  
Thr Ser Met  
305

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..299
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met Ala Leu Lys Leu Thr Ser Pro Pro Ser Val Phe Ser Gln Ser Arg  
1 5 10 15  
Arg Leu Ser Ser Ser Leu Ile Pro Ile Arg Ser Lys Ser Thr Phe  
20 25 30  
Thr Gly Phe Arg Ser Arg Thr Gly Val Tyr Leu Ser Lys Thr Thr Ala  
35 40 45  
Leu Gln Ser Ser Thr Lys Leu Ser Val Ala Ala Glu Ser Pro Ala Ala  
50 55 60  
Thr Ile Ala Thr Asp Asp Trp Gly Lys Val Ser Ala Val Leu Phe Asp  
65 70 75 80  
Met Asp Gly Val Leu Cys Asn Ser Glu Asp Leu Ser Arg Arg Ala Ala  
85 90 95  
Val Asp Val Phe Thr Glu Met Gly Val Glu Val Thr Val Asp Asp Phe  
100 105 110  
Val Pro Phe Met Gly Thr Gly Glu Ala Lys Phe Leu Gly Gly Val Ala  
115 120 125  
Ser Val Lys Glu Val Lys Gly Phe Asp Pro Asp Ala Ala Lys Lys Arg  
130 135 140  
Phe Phe Glu Ile Tyr Leu Asp Lys Tyr Ala Lys Pro Glu Ser Gly Ile  
145 150 155 160  
Gly Phe Pro Gly Ala Leu Glu Leu Val Thr Glu Cys Lys Asn Lys Gly  
165 170 175  
Leu Lys Val Ala Val Ala Ser Ser Ala Asp Arg Ile Lys Val Asp Ala  
180 185 190  
Asn Leu Lys Ala Ala Gly Leu Ser Leu Thr Met Phe Asp Ala Ile Val  
195 200 205  
Ser Ala Asp Ala Phe Glu Asn Leu Lys Pro Ala Pro Asp Ile Phe Leu  
210 215 220  
Ala Ala Ala Lys Ile Leu Gly Val Pro Thr Ser Glu Cys Val Val Ile  
225 230 235 240  
Glu Asp Ala Leu Ala Gly Val Gln Ala Ala Gln Ala Ala Asn Met Arg  
245 250 255  
Cys Ile Ala Val Lys Thr Thr Leu Ser Glu Ala Ile Leu Lys Asp Ala  
260 265 270  
Gly Pro Ser Met Ile Arg Asp Asp Ile Gly Asn Ile Ser Ile Asn Asp  
275 280 285  
Ile Leu Thr Gly Gly Ser Asp Ser Thr Ser Met  
290 295

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..219  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asp | Gly | Val | Leu | Cys | Asn | Ser | Glu | Asp | Leu | Ser | Arg | Arg | Ala | Ala |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Val | Asp | Val | Phe | Thr | Glu | Met | Gly | Val | Glu | Val | Thr | Val | Asp | Asp | Phe |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Val | Pro | Phe | Met | Gly | Thr | Gly | Glu | Ala | Lys | Phe | Leu | Gly | Gly | Val | Ala |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Ser | Val | Lys | Glu | Val | Lys | Gly | Phe | Asp | Pro | Asp | Ala | Ala | Lys | Lys | Arg |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Phe | Phe | Glu | Ile | Tyr | Leu | Asp | Lys | Tyr | Ala | Lys | Pro | Glu | Ser | Gly | Ile |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Gly | Phe | Pro | Gly | Ala | Leu | Glu | Leu | Val | Thr | Glu | Cys | Lys | Asn | Lys | Gly |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Leu | Lys | Val | Ala | Val | Ala | Ser | Ser | Ala | Asp | Arg | Ile | Lys | Val | Asp | Ala |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asn | Leu | Lys | Ala | Ala | Gly | Leu | Ser | Leu | Thr | Met | Phe | Asp | Ala | Ile | Val |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Ala | Asp | Ala | Phe | Glu | Asn | Leu | Lys | Pro | Ala | Pro | Asp | Ile | Phe | Leu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ala | Ala | Ala | Lys | Ile | Leu | Gly | Val | Pro | Thr | Ser | Glu | Cys | Val | Val | Ile |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Glu | Asp | Ala | Leu | Ala | Gly | Val | Gln | Ala | Ala | Gln | Ala | Ala | Asn | Met | Arg |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Cys | Ile | Ala | Val | Lys | Thr | Thr | Leu | Ser | Glu | Ala | Ile | Leu | Lys | Asp | Ala |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Gly | Pro | Ser | Met | Ile | Arg | Asp | Asp | Ile | Gly | Asn | Ile | Ser | Ile | Asn | Asp |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Ile | Leu | Thr | Gly | Gly | Ser | Asp | Ser | Thr | Ser | Met |     |     |     |     |     |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 643 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..643  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

|              |             |             |            |            |            |     |
|--------------|-------------|-------------|------------|------------|------------|-----|
| aaaaaaaaatca | aaccacccat  | tcaaacaaaa  | cacaaaaaca | aaaaaaaaaa | catttcccca | 60  |
| aaaaaaaaaaaa | aacagaggat  | gaaacaaaac  | cagagcaagt | ttttgagaat | aatctcaacg | 120 |
| cctctaagag   | ctttaggcaa  | ggcacgtgat  | ttctacgtga | gaagcatcac | cggttgcgca | 180 |
| gctcggactc   | aatattcctc  | ctccgcctcc  | gtctccgctc | cttttccaag | aagccggagc | 240 |
| tcctcctccg   | ccgccttctc  | ctcctccgca  | tcattcccga | gaaccaccga | tttcgggata | 300 |
| gatgaagatt   | acagcgagct  | agtgaagagct | gcgtcgggtg | ggagtttagg | gcacaagaat | 360 |
| gagatagaca   | tgttgataca  | agagaagctg  | caacagcaga | agcaacagaa | gcaaggaggg | 420 |
| ttgcctaaga   | gctcgagtgc  | tgggatggcg  | aggatagagg | aagaggaaga | aacagaggaa | 480 |
| ggatctgtga   | atccgaaggt  | gaagaagact  | aagaaagtct | ctgatctttt | gtatcctcgt | 540 |
| agcaaatctt   | acgccgttac  | tactagtacc  | cctatcttgt | aacttctctt | cttatttttt | 600 |
| cttcttctta   | atttttagtat | tttgtggatt  | gattatcatt | ttc        |            |     |

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..193
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498224
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Lys Lys Ile Lys Pro Thr Ile Gln Thr Lys His Lys Asn Lys Lys Lys  
1 5 10 15  
Asn Ile Ser Pro Lys Lys Lys Lys Gln Arg Met Lys Gln Asn Gln Ser  
20 25 30  
Lys Phe Leu Arg Ile Ile Ser Thr Pro Leu Arg Ala Leu Gly Lys Ala  
35 40 45  
Arg Asp Phe Tyr Val Arg Ser Ile Thr Gly Cys Ala Ala Arg Thr Gln  
50 55 60  
Tyr Ser Ser Ser Ala Ser Val Ser Ala Pro Phe Pro Arg Ser Arg Ser  
65 70 75 80  
Ser Ser Ser Ala Ala Phe Ser Ser Ser Ala Ser Ser Arg Arg Thr Thr  
85 90 95  
Asp Phe Gly Ile Asp Glu Asp Tyr Ser Glu Leu Val Arg Ala Ala Ser  
100 105 110  
Val Arg Ser Leu Gly His Lys Asn Glu Ile Asp Met Leu Ile Gln Glu  
115 120 125  
Lys Leu Gln Gln Gln Lys Gln Gln Lys Gln Gly Gly Leu Pro Lys Ser  
130 135 140  
Ser Ser Ala Gly Met Ala Arg Ile Glu Glu Glu Glu Thr Glu Glu  
145 150 155 160  
Gly Ser Val Asn Pro Lys Val Lys Lys Thr Lys Lys Val Ser Asp Leu  
165 170 175  
Leu Tyr Pro Arg Ser Lys Ser Tyr Ala Val Thr Thr Ser Thr Pro Ile  
180 185 190  
Leu

(2) INFORMATION FOR SEQ ID NO:290:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 167 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..167
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Met Lys Gln Asn Gln Ser Lys Phe Leu Arg Ile Ile Ser Thr Pro Leu  
1 5 10 15  
Arg Ala Leu Gly Lys Ala Arg Asp Phe Tyr Val Arg Ser Ile Thr Gly  
20 25 30  
Cys Ala Ala Arg Thr Gln Tyr Ser Ser Ser Ala Ser Val Ser Ala Pro  
35 40 45  
Phe Pro Arg Ser Arg Ser Ser Ser Ser Ala Ala Phe Ser Ser Ser Ala  
50 55 60  
Ser Ser Arg Arg Thr Thr Asp Phe Gly Ile Asp Glu Asp Tyr Ser Glu  
65 70 75 80  
Leu Val Arg Ala Ala Ser Val Arg Ser Leu Gly His Lys Asn Glu Ile  
85 90 95  
Asp Met Leu Ile Gln Glu Lys Leu Gln Gln Gln Lys Gln Gln Lys Gln



100 105 110  
Gly Gly Leu Pro Lys Ser Ser Ser Ala Gly Met Ala Arg Ile Glu Glu  
115 120 125  
Glu Glu Glu Thr Glu Glu Gly Ser Val Asn Pro Lys Val Lys Lys Thr  
130 135 140  
Lys Lys Val Ser Asp Leu Leu Tyr Pro Arg Ser Lys Ser Tyr Ala Val  
145 150 155 160  
Thr Thr Ser Thr Pro Ile Leu  
165

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| attacttctc  | cactgaatgc | atttactctc  | ctaattgcata | tcgtgggttt | gcccgtgagt | 60  |
| tcatacaaaga | tttggaaaga | ataaggccaa  | gggcgattct  | ggacatcata | aagctcgtgt | 120 |
| aagatttttag | aattgcaaca | accacaaaga  | tgccctgagca | agggacgtgt | gagcgatgcg | 180 |
| ggtatatattc | tagccagaaa | tggtgtaaaag | cttggtgttt  | gctggaagga | ctgaaccgtg | 240 |
| gtttgcctaa  | gatgggtatt | ggaagacctc  | gaggcgtaaa  | tggtgatcat | aataaggaaa | 300 |
| caaagaagcc  | tggatctgta | gcaaaatcta  | tagagagcaa  | acaatgtgga | tctctggatt | 360 |
| tctaaaattt  | tgagaaaaaa | gctacaaaat  | cgtatgagtc  | atagtgaatg | atttgattat | 420 |
| atagaaaaag  | aaaagatttt | ttttttcctt  | tcataaaactt | cttgtagaac | ttaattgtac | 480 |
| ttttggtttt  | cttttttggt | t           |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Phe | Ser | Thr | Glu | Cys | Ile | Tyr | Ser | Pro | Asn | Ala | Tyr | Arg | Gly | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Arg | Glu | Phe | Ile | Lys | Asp | Leu | Glu | Arg | Ile | Arg | Pro | Arg | Ala | Ile |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Asp | Ile | Ile | Lys | Ser | Gly | Glu | Asp | Phe | Arg | Ile | Ala | Thr | Thr | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Lys | Met | Pro | Glu | Gln | Gly | Thr | Cys | Glu | Arg | Cys | Gly | Tyr | Ile | Ser | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Lys | Trp | Cys | Lys | Ala | Cys | Val | Leu | Leu | Glu | Gly | Leu | Asn | Arg | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Pro | Lys | Met | Gly | Ile | Gly | Arg | Pro | Arg | Gly | Val | Asn | Gly | Asp | His |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Lys | Glu | Thr | Lys | Lys | Pro | Gly | Ser | Val | Ala | Lys | Ser | Ile | Glu | Ser |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Gln | Cys | Gly | Ser | Leu | Asp | Phe |     |     |     |     |     |     |     |     |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..71
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Glu | Gln | Gly | Thr | Cys | Glu | Arg | Cys | Gly | Tyr | Ile | Ser | Ser | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Trp | Cys | Lys | Ala | Cys | Val | Leu | Leu | Glu | Gly | Leu | Asn | Arg | Gly | Leu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Lys | Met | Gly | Ile | Gly | Arg | Pro | Arg | Gly | Val | Asn | Gly | Asp | His | Asn |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Glu | Thr | Lys | Lys | Pro | Gly | Ser | Val | Ala | Lys | Ser | Ile | Glu | Ser | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Cys | Gly | Ser | Leu | Asp | Phe |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..567
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| aaaaacacaa | caaaatggga  | aacttcatat | gcgtaacgga | aaaaacgacg | acgtcgtggn  | 60  |
| tcaggagacg | ataatggatc  | atataacaag | agaaggagaa | gaagaagatc | caccgtgggt  | 120 |
| cacgacgaca | acgacgacgg  | agagaagctg | ctcggagaaa | caagcaacgt | tacgtcaaca  | 180 |
| agttcgtcat | cgtcttctga  | gagaagagag | attaagataa | ggataacgaa | aaaggaactt  | 240 |
| gaagatctca | tgagaaacat  | tggtttgaag | agtttaacgg | cggaagagat | tcttttctaag | 300 |
| ttaattttcg | aagggtggaga | ccaaatcgga | ttctctgcgg | tcgatgtgac | gaatcaccac  | 360 |
| caaccatgga | aaccgggtgtt | gcaaagcata | ccggagatgg | attagtgtta | ttttttttat  | 420 |
| ttttcttata | aaaaaataga  | taaaaaaatc | tgagtgatgc | gtgtgtctaa | acttgaccct  | 480 |
| ctcgacaggt | gatttttagct | tttaaaaagt | atgtacatgt | ttggttttgt | aattaatttt  | 540 |
| tttattgaaa | tttttattga  | aattttt    |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Gln | Gln | Asn | Gly | Lys | Leu | His | Met | Arg | Asn | Gly | Lys | Asn | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | Val | Val | Xaa | Gln | Glu | Thr | Ile | Met | Asp | His | Ile | Thr | Arg | Glu | Gly |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Glu | Glu | Glu | Asp | Pro | Pro | Trp | Phe | Thr | Thr | Thr | Thr | Thr | Thr | Glu | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Cys | Ser | Glu | Lys | Gln | Ala | Thr | Leu | Arg | Gln | Gln | Val | Arg | His | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Leu Leu Arg Glu Glu Arg Leu Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1498246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```
Met Arg Asn Gly Lys Asn Asp Asp Val Val Xaa Gln Glu Thr Ile Met
1 5 10 15
Asp His Ile Thr Arg Glu Gly Glu Glu Asp Pro Pro Trp Phe Thr
 20 25 30
Thr Thr Thr Thr Thr Glu Arg Ser Cys Ser Glu Lys Gln Ala Thr Leu
 35 40 45
Arg Gln Gln Val Arg His Arg Leu Leu Arg Glu Glu Arg Leu Arg
 50 55 60
```

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1498247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```
Met Arg Asn Ile Gly Leu Lys Ser Leu Thr Ala Glu Glu Ile Leu Ser
1 5 10 15
Lys Leu Ile Phe Glu Gly Gly Asp Gln Ile Gly Phe Ser Ala Val Asp
 20 25 30
Val Thr Asn His His Gln Pro Trp Lys Pro Val Leu Gln Ser Ile Pro
 35 40 45
Glu Met Asp
 50
```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1632
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```
tcttctctct acacacacac acacacacac acacacaaaa tggattcttc gaatgttgaa 60
gaaaacctaa acccagaaac aaaatccgca gaagaacaaa acccacttgc cattttccat 120
tcttctctac caatgcgcatc tcttctctctg accttggttc catcctcgac tcaatttctc 180
aaattgtttg ctcatcatcc aaacaagggtt aagatcccta cgcaggcttc ttctctcact 240
catctctctc tttcttctgt ctctcctttt ccttcttcca gaatctcttt caaatccacc 300
atcgctgcta accctcttca atcccccttc tccatcgctc ctcgctcgcc cgttgatcct 360
tcctccgccg ccgctctccg ccgtgctgct gtcgctctggt tccgcaatga cctccgtgtc 420
```



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Val | Tyr | Ala | His | Arg | Glu | Val | Ser | His | Asp | Glu | Val | Lys | Ala | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Lys | Ile | Glu | Thr | Ala | Met | Lys | Glu | Glu | Gly | Val | Glu | Val | Lys | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Trp | Gly | Ser | Thr | Leu | Tyr | His | Leu | Asp | Asp | Leu | Pro | Phe | Lys | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Asp | Leu | Pro | Ser | Asn | Tyr | Gly | Ala | Phe | Lys | Asp | Lys | Val | Gln | Lys |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Glu | Ile | Arg | Lys | Thr | Ile | Ala | Ala | Leu | Asp | Gln | Leu | Lys | Ser | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | Ser | Arg | Gly | Asp | Val | Glu | Leu | Gly | Asp | Ile | Pro | Ser | Leu | Leu | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Gly | Ile | Ser | Pro | Thr | Pro | Arg | Thr | Ser | Gln | Glu | Gly | Lys | Pro | Thr |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Met | Val | Gly | Gly | Glu | Thr | Glu | Ala | Leu | Thr | Arg | Leu | Lys | Ser | Phe | Ala |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Asp | Cys | Gln | Ala | Arg | Leu | Ser | Lys | Gly | Asn | Gln | Lys | Gly | Gly | Asn |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asn | Ser | Val | Phe | Gly | Ala | Asn | Phe | Ser | Cys | Lys | Ile | Ser | Pro | Trp | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Met | Gly | Ser | Ile | Ser | Pro | Arg | Ser | Met | Phe | Asp | Glu | Leu | Lys | Lys |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Thr | Ile | Ser | Ala | Ser | Thr | Thr | Ser | Thr | Thr | Pro | Arg | Asn | Gly | Pro | Gly |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asp | Thr | Gly | Leu | Asn | Trp | Leu | Met | Tyr | Glu | Leu | Leu | Trp | Arg | Asp | Phe |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Phe | Arg | Phe | Ile | Thr | Lys | Lys | Tyr | Ser | Ser | Ala | Lys | Thr | Gln | Val | Glu |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Ala | Gly | Pro | Ala | Thr | Ala | Cys | Thr | Gly | Ala | Phe | Ala |     |     |     |     |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..447
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ser | Ser | Asn | Val | Glu | Glu | Asn | Leu | Asn | Pro | Glu | Thr | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Glu | Glu | Gln | Asn | Pro | Leu | Ala | Ile | Phe | His | Ser | Ser | Leu | Pro | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ser | Leu | Ser | Leu | Thr | Leu | Phe | Pro | Ser | Ser | Thr | Gln | Phe | Leu | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Leu | Phe | Ala | His | His | Pro | Asn | Lys | Val | Lys | Ile | Pro | Thr | Gln | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Thr | His | Leu | Ser | Leu | Ser | Ser | Val | Ser | Pro | Phe | Pro | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Ile | Ser | Phe | Lys | Ser | Thr | Ile | Ala | Ala | Asn | Pro | Leu | Gln | Ser | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Ser | Ile | Val | Pro | Arg | Arg | Pro | Val | Asp | Pro | Ser | Ser | Ala | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Arg | Arg | Ala | Ala | Val | Val | Trp | Phe | Arg | Asn | Asp | Leu | Arg | Val | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Asn | Glu | Cys | Leu | Asn | Ser | Ala | Asn | Asp | Glu | Cys | Val | Ser | Val | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Val | Tyr | Cys | Phe | Asp | Pro | Arg | Asp | Tyr | Gly | Lys | Ser | Ser | Ser | Gly |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Asp | Lys | Thr | Gly | Pro | Phe | Arg | Ala | Gln | Phe | Leu | Ile | Glu | Ser | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Glu | Leu | Arg | Lys | Asn | Leu | Gln | Ala | Arg | Gly | Ser | Asn | Leu | Val | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Val | Gly | Lys | Pro | Glu | Ala | Val | Leu | Val | Glu | Leu | Ala | Lys | Glu | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Ala | Asp | Ala | Val | Tyr | Ala | His | Arg | Glu | Val | Ser | His | Asp | Glu | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Ala | Glu | Gly | Lys | Ile | Glu | Thr | Ala | Met | Lys | Glu | Glu | Gly | Val | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Val | Lys | Tyr | Phe | Trp | Gly | Ser | Thr | Leu | Tyr | His | Leu | Asp | Asp | Leu | Pro |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Phe | Lys | Ile | Glu | Asp | Leu | Pro | Ser | Asn | Tyr | Gly | Ala | Phe | Lys | Asp | Lys |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Gln | Lys | Leu | Glu | Ile | Arg | Lys | Thr | Ile | Ala | Ala | Leu | Asp | Gln | Leu |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Lys | Ser | Leu | Pro | Ser | Arg | Gly | Asp | Val | Glu | Leu | Gly | Asp | Ile | Pro | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Leu | Asp | Leu | Gly | Ile | Ser | Pro | Thr | Pro | Arg | Thr | Ser | Gln | Glu | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Pro | Thr | Met | Val | Gly | Gly | Glu | Thr | Glu | Ala | Leu | Thr | Arg | Leu | Lys |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Phe | Ala | Ala | Asp | Cys | Gln | Ala | Arg | Leu | Ser | Lys | Gly | Asn | Gln | Lys |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Gly | Asn | Asn | Ser | Val | Phe | Gly | Ala | Asn | Phe | Ser | Cys | Lys | Ile | Ser |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Pro | Trp | Leu | Ala | Met | Gly | Ser | Ile | Ser | Pro | Arg | Ser | Met | Phe | Asp | Glu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Leu | Lys | Lys | Thr | Ile | Ser | Ala | Ser | Thr | Thr | Ser | Thr | Thr | Pro | Arg | Asn |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Gly | Pro | Gly | Asp | Thr | Gly | Leu | Asn | Trp | Leu | Met | Tyr | Glu | Leu | Leu | Trp |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |     | 415 |     |
| Arg | Asp | Phe | Phe | Arg | Phe | Ile | Thr | Lys | Lys | Tyr | Ser | Ser | Ala | Lys | Thr |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Gln | Val | Glu | Ala | Gly | Pro | Ala | Thr | Ala | Cys | Thr | Gly | Ala | Phe | Ala |     |
|     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..859
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

|             |             |            |             |            |             |     |
|-------------|-------------|------------|-------------|------------|-------------|-----|
| atcgatttaa  | aaataaaaag  | cctctctttt | tttrtctcag  | tgagacaatc | gacttttctaa | 60  |
| aatcgatggc  | gactgagaaa  | ccgattacga | cggagactgt  | tgctctcact | gagaagaaaa  | 120 |
| tggaacatctc | tttagatgag  | attatcaaga | tggaagagag  | caataccaat | gtgaataagg  | 180 |
| gcaagaaaca  | gagagtattg  | aataaaaagg | agaaatttag  | tggtgctgcg | aagaatagtg  | 240 |
| cggtgaaagc  | acagcggttat | atggactctc | gggtctgatgt | tagacagggg | gcttttgcta  | 300 |
| agaagagggtc | taattttccaa | ggaaaccagt | ttcctgtaac  | aaaacaaccg | ttgctcgtaa  | 360 |
| agccgcttct  | gctactccgc  | gtggtagacc | ttataatggt  | ggaaggatga | ctaatacgaa  | 420 |
| tcaatcaagg  | tttattgctc  | caccagctca | gaatagagct  | tcacaaagag | ggtttgctgc  | 480 |
| aaagcagcag  | cagcagcaaa  | gggagaagat | agtgcagcag  | caggcaaatg | gaggaggagg  | 540 |
| agggcaagag  | caatggcctc  | agacactgga | ttctcgggtt  | gcaaacaatg | aggaagagag  | 600 |
| aatgagaatg  | agaaggtttg  | cagacaatag | aagcaatgta  | ggcaacaatg | gagctggatc  | 660 |
| gcacacagcag | cagcggttcga | tggtcccgtg | ggtgagaaga  | gctacaagat | tccccaactg  | 720 |

atttatgacc tgcagaatag tcttggttca agggtagggg gaacatattt gctacttatg 780  
tagtttggtt tggattcatt gtatcaagtg tagaacattc gtatgtgaag ctctaaaacc 840  
ttgaatcttt ttcttggcc

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1498255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Arg Ile Lys Asn Lys Lys Pro Leu Phe Phe Xaa Leu Ser Glu Thr Ile  
1 5 10 15  
Asp Phe Leu Lys Ser Met Ala Thr Glu Lys Pro Ile Thr Thr Glu Thr  
20 25 30  
Val Ala Leu Thr Glu Lys Lys Met Asp Ile Ser Leu Asp Glu Ile Ile  
35 40 45  
Lys Met Glu Lys Ser Asn Thr Asn Val Asn Lys Gly Lys Lys Gln Arg  
50 55 60  
Val Leu Asn Lys Lys Glu Lys Phe Ser Gly Ala Ala Lys Asn Ser Ala  
65 70 75 80  
Val Lys Ala Gln Arg Tyr Met Asp Ser Arg Ser Asp Val Arg Gln Gly  
85 90 95  
Ala Phe Ala Lys Lys Arg Ser Asn Phe Gln Gly Asn Gln Phe Pro Val  
100 105 110  
Thr Lys Gln Pro Leu Leu Val Lys Pro Leu Leu Leu Leu Arg Val Val  
115 120 125  
Asp Leu Ile Met Val Glu Gly  
130 135

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1498256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Met Ala Thr Glu Lys Pro Ile Thr Thr Glu Thr Val Ala Leu Thr Glu  
1 5 10 15  
Lys Lys Met Asp Ile Ser Leu Asp Glu Ile Ile Lys Met Glu Lys Ser  
20 25 30  
Asn Thr Asn Val Asn Lys Gly Lys Lys Gln Arg Val Leu Asn Lys Lys  
35 40 45  
Glu Lys Phe Ser Gly Ala Ala Lys Asn Ser Ala Val Lys Ala Gln Arg  
50 55 60  
Tyr Met Asp Ser Arg Ser Asp Val Arg Gln Gly Ala Phe Ala Lys Lys  
65 70 75 80  
Arg Ser Asn Phe Gln Gly Asn Gln Phe Pro Val Thr Lys Gln Pro Leu  
85 90 95  
Leu Val Lys Pro Leu Leu Leu Leu Arg Val Val Asp Leu Ile Met Val  
100 105 110  
Glu Gly

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met Thr Asn Thr Asn Gln Ser Arg Phe Ile Ala Pro Pro Ala Gln Asn  
1 5 10 15  
Arg Ala Ser Gln Arg Gly Phe Val Ala Lys Gln Gln Gln Gln Arg  
20 25 30  
Glu Lys Ile Val Gln Gln Gln Ala Asn Gly Gly Gly Gly Gly Gln Arg  
35 40 45  
Gln Trp Pro Gln Thr Leu Asp Ser Arg Phe Ala Asn Met Lys Glu Glu  
50 55 60  
Arg Met Arg Met Arg Arg Phe Ala Asp Asn Arg Ser Asn Val Gly Asn  
65 70 75 80  
Asn Gly Ala Gly Ser His Gln Gln Gln Arg Ser Met Val Pro Trp Val  
85 90 95  
Arg Arg Ala Thr Arg Phe Pro Asn  
100

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..988
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

aaaagaagac ttttgtaagg aaataaacac acaactaaag agatgtcgtc aaccttgagc 60  
aacgaagagt caggactcgg tgattcaa at cggttcgacgg aagtagatag cggcgacgga 120  
ggaaacttca cggcttacga gtctcgattc cagtcgcagc ggtttgactc ttccttctct 180  
aattttgact cccaaccgga gaaagagtca gacttaccag gcggcgattc atctcctcga 240  
cccgaaactc aatctccgcc gtcgataaat agtttcgatg atacaaacgg ttcgatcttg 300  
ccgccaccat cggccatgga gaaagaggaa ggtttcgctc ttagagagtg gcgaaggcta 360  
aatgctctga gattggaaga gaaagaaaag gaagagaaag aaatggttca acaaattcta 420  
gaagcagcag agcaatataa ggctgagttc tatagcaagc gtaacgttac tattgaaaac 480  
aacaagaaac taaaccgcga gaaagagaag ttttttttgg agaatacaaga aaagttttac 540  
gctgaagctg acaaaaaaaa ttggaaggcg attgcagaac tcattcctcg tgaagtgcc 600  
gttatagaga atagagggaa caagaagaaa acagcaacca taactgtaat ccagggacca 660  
aagccaggga agcccactga tctgtgctcg tatgctgtaa gtgctcacga aactcaagca 720  
caatccgccca actcatatga agccaaaact gccctacca tctggagctg acccgaatgt 780  
gagtggtgagt gaacagggtca cagttacaga gaagttgtag ttgtgtatgt gacaagttaa 840  
cttcttcttg attgatgtta aaccgtcttt actttgttag cttccctcat gttcagttc 900  
gactattgtt tgttttgatt tcgtctttgg tcttaccatt gttggtttcc cacacagttt 960  
tctactttga tgtatatata atatattc

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1498262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Ser | Thr | Leu | Ser | Asn | Glu | Glu | Ser | Gly | Leu | Gly | Asp | Ser | Asn |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg | Ser | Thr | Glu | Val | Asp | Ser | Gly | Asp | Gly | Gly | Asn | Phe | Thr | Ala | Tyr |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |  |
| Glu | Ser | Arg | Phe | Gln | Ser | Gln | Arg | Phe | Asp | Ser | Ser | Phe | Ser | Asn | Phe |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Asp | Ser | Gln | Pro | Glu | Lys | Glu | Ser | Asp | Leu | Pro | Gly | Gly | Asp | Ser | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Pro | Arg | Pro | Glu | Thr | Gln | Ser | Pro | Pro | Ser | Ile | Asn | Ser | Phe | Asp | Asp |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Thr | Asn | Gly | Ser | Ile | Leu | Pro | Pro | Pro | Ser | Ala | Met | Glu | Lys | Glu | Glu |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Gly | Phe | Ala | Leu | Arg | Glu | Trp | Arg | Arg | Leu | Asn | Ala | Leu | Arg | Leu | Glu |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Lys | Glu | Lys | Glu | Glu | Lys | Glu | Met | Val | Gln | Gln | Ile | Leu | Glu | Ala |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala | Glu | Gln | Tyr | Lys | Ala | Glu | Phe | Tyr | Ser | Lys | Arg | Asn | Val | Thr | Ile |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Asn | Asn | Lys | Lys | Leu | Asn | Arg | Glu | Lys | Glu | Lys | Phe | Phe | Leu | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Asn | Gln | Glu | Lys | Phe | Tyr | Ala | Glu | Ala | Asp | Lys | Asn | Asn | Trp | Lys | Ala |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ile | Ala | Glu | Leu | Ile | Pro | Arg | Glu | Val | Pro | Val | Ile | Glu | Asn | Arg | Gly |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Asn | Lys | Lys | Lys | Thr | Ala | Thr | Ile | Thr | Val | Ile | Gln | Gly | Pro | Lys | Pro |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Gly | Lys | Pro | Thr | Asp | Leu | Cys | Ser | Tyr | Ala | Ser | Ser | Ala | His | Glu | Thr |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Gln | Ala | Gln | Ser | Ala | Asn | Ser | Tyr | Glu | Ala | Lys | Thr | Ala | Leu | Thr | Ile |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Trp | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1498263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Lys | Glu | Glu | Gly | Phe | Ala | Leu | Arg | Glu | Trp | Arg | Arg | Leu | Asn |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ala | Leu | Arg | Leu | Glu | Glu | Lys | Glu | Lys | Glu | Glu | Lys | Glu | Met | Val | Gln |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |  |
| Gln | Ile | Leu | Glu | Ala | Ala | Glu | Gln | Tyr | Lys | Ala | Glu | Phe | Tyr | Ser | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Arg | Asn | Val | Thr | Ile | Glu | Asn | Asn | Lys | Lys | Leu | Asn | Arg | Glu | Lys | Glu |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Lys | Phe | Phe | Leu | Glu | Asn | Gln | Glu | Lys | Phe | Tyr | Ala | Glu | Ala | Asp | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Asn | Asn | Trp | Lys | Ala | Ile | Ala | Glu | Leu | Ile | Pro | Arg | Glu | Val | Pro | Val |  |

85 90 95  
Ile Glu Asn Arg Gly Asn Lys Lys Lys Thr Ala Thr Ile Thr Val Ile  
100 105 110  
Gln Gly Pro Lys Pro Gly Lys Pro Thr Asp Leu Cys Ser Tyr Ala Ser  
115 120 125  
Ser Ala His Glu Thr Gln Ala Gln Ser Ala Asn Ser Tyr Glu Ala Lys  
130 135 140  
Thr Ala Leu Thr Ile Trp Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1498264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Val Gln Gln Ile Leu Glu Ala Ala Glu Gln Tyr Lys Ala Glu Phe  
1 5 10 15  
Tyr Ser Lys Arg Asn Val Thr Ile Glu Asn Asn Lys Lys Leu Asn Arg  
20 25 30  
Glu Lys Glu Lys Phe Phe Leu Glu Asn Gln Glu Lys Phe Tyr Ala Glu  
35 40 45  
Ala Asp Lys Asn Asn Trp Lys Ala Ile Ala Glu Leu Ile Pro Arg Glu  
50 55 60  
Val Pro Val Ile Glu Asn Arg Gly Asn Lys Lys Lys Thr Ala Thr Ile  
65 70 75 80  
Thr Val Ile Gln Gly Pro Lys Pro Gly Lys Pro Thr Asp Leu Cys Ser  
85 90 95  
Tyr Ala Ser Ser Ala His Glu Thr Gln Ala Gln Ser Ala Asn Ser Tyr  
100 105 110  
Glu Ala Lys Thr Ala Leu Thr Ile Trp Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..601

(D) OTHER INFORMATION: / Ceres Seq. ID 1498268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

ttccaacaaa cctcgatgaa gaaatatcgt ctcttcctgg atggaccgtc gaatcgaacc 60  
gagcagtagc gtttattgac tcagaccatt tctcgggtccc cgaggggaag cgagctttgg 120  
aactttttatc gggcaaagaa ggcataatct ctcaaattgg tgagacaaag gcgaacattc 180  
cgtacaagat gtctttctct ttgggacacg caggggacaa gtgtaaggaa cctttggctg 240  
taatggcttt tgctggagat caagcacaga actttcatta tatggcgcaa gcaaactcga 300  
gtttcgaaaag atcggagttg aacttcactg cgaaagctga acgtacgagg atcgcttct 360  
acagcattta ttacaatacg aggacggacg atatgacttc attgtgtgga cctgtgattg 420  
atgacgttaa ggtttggttc tccgggtcta gtagaattgg atttagtttt ccgcttttta 480  
ttcttctttc tttggttttc atctagattg ttccggttca gaaattgtat tggtagaccg 540  
ggaattaaga cgggattcca cgttgtatga tgtatcgttg tatgatggat cggttcaagg 600  
t

(2) INFORMATION FOR SEQ ID NO:310:

```
(i) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..167
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498269
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:
```

(2) INFORMATION FOR SEQ ID NO:311:

```
(i) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..116
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498270
```

[illegible]

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Phe | Ser | Leu | Gly | His | Ala | Gly | Asp | Lys | Cys | Lys | Glu | Pro | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Val | Met | Ala | Phe | Ala | Gly | Asp | Gln | Ala | Gln | Asn | Phe | His | Tyr | Met |
|     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |
| Ala | Gln | Ala | Asn | Ser | Ser | Phe | Glu | Arg | Ser | Glu | Leu | Asn | Phe | Thr | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Ala | Glu | Arg | Thr | Arg | Ile | Ala | Phe | Tyr | Ser | Ile | Tyr | Tyr | Asn | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Arg | Thr | Asp | Asp | Met | Thr | Ser | Leu | Cys | Gly | Pro | Val | Ile | Asp | Asp | Val |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Lys | Val | Trp | Phe | Ser | Gly | Ser | Ser | Arg | Ile | Gly | Phe | Ser | Phe | Pro | Leu |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Ile | Leu | Leu | Ser | Leu | Val | Phe | Ile |     |     |     |     |     |     |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

|             |            |            |            |             |             |      |
|-------------|------------|------------|------------|-------------|-------------|------|
| aacccccaaaa | atagacctca | cctctctcgt | cttctctatt | ctctccgctc  | cttaattttcc | 60   |
| aattccaacc  | ttctctgttt | tgccttgatg | gaaaagatag | ctccggagct  | cttcctcgtc  | 120  |
| gccggtaacc  | cggactcttt | cgtcgtcgac | gacctcctcg | acttctctaa  | cgacgacggc  | 180  |
| gaagttgacg  | acggcttaaa | cactcttccc | gattcttcaa | cactctccac  | cggcactctc  | 240  |
| accgacagtt  | ccaactcctc | ctcgcctttc | accgacggca | ctggcttctc  | cgacctatat  | 300  |
| attccgaatg  | acgatatagc | agaattagaa | tggttatcaa | atthttgtgga | agaatcattc  | 360  |
| gcaggagaa   | accaagasaa | gcktcactta | ttttccggkt | taaaaaaccc  | tcaaaccamc  | 420  |
| gggtcgaccc  | tgaccactt  | aattaaaccc | gaasccgaac | ttgatcatca  | attcatcgac  | 480  |
| atcgatgaat  | ccaacgtcgc | cgttcctgcc | aagsccagaa | scaagagatc  | mcgttytgca  | 540  |
| gcctccacgt  | gggcttcccc | tyttttatcc | ttagccgatt | ccgacgaaac  | caatcccaag  | 600  |
| aagaaacaac  | gaagagtga  | agaacaagac | ttcgccggag | atatggacgt  | ggattgcgga  | 660  |
| gaaagcggag  | gaggacgacg | ttgtttgac  | tgcgcgacgg | agaagacgcc  | gcaatggagg  | 720  |
| acgggaccta  | tgggtccgaa | gacgctttgt | aacgcttgcg | gagtgaggta  | caaatacagg  | 780  |
| aggctcgtgc  | cggagtata  | accggcgctc | agtccgacgt | tcgtgatggc  | gaggcactcg  | 840  |
| aactctcacc  | ggaaagtgat | ggagctccgg | cgacagaagg | agatgagaga  | cgagcatttg  | 900  |
| ctgagtcagc  | ttaggtgtga | gaatctactg | atggatatca | gatccaacgg  | tgaagatttc  | 960  |
| ttaatgcata  | ataatactaa | ccacgtggct | cctgatttta | gacacttaat  | ctagttttct  | 1020 |
| atttccacgt  | ggataatttc | gcaataattt | gttcggttgc | tttagcttta  | tttttttttt  | 1080 |
| tttctttttt  | aacatttggt | tttcattttc | tgcagactac | ttctagtact  | attgatatat  | 1140 |
| ttg         |            |            |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..337  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Pro | Lys | Asn | Arg | Pro | His | Leu | Ser | Arg | Leu | Leu | Tyr | Ser | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Ile | Ser | Asn | Ser | Asn | Leu | Leu | Cys | Phe | Ala | Leu | Met | Glu | Lys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Ala | Pro | Glu | Leu | Phe | Leu | Val | Ala | Gly | Asn | Pro | Asp | Ser | Phe | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Asp | Asp | Leu | Leu | Asp | Phe | Ser | Asn | Asp | Asp | Gly | Glu | Val | Asp | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Leu | Asn | Thr | Leu | Pro | Asp | Ser | Ser | Thr | Leu | Ser | Thr | Gly | Thr | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Asp | Ser | Ser | Asn | Ser | Ser | Ser | Leu | Phe | Thr | Asp | Gly | Thr | Gly | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Asp | Leu | Tyr | Ile | Pro | Asn | Asp | Asp | Ile | Ala | Glu | Leu | Glu | Trp | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Asn | Phe | Val | Glu | Glu | Ser | Phe | Ala | Gly | Glu | Asp | Gln | Xaa | Lys | Xaa |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Leu | Phe | Ser | Xaa | Leu | Lys | Asn | Pro | Gln | Thr | Xaa | Gly | Ser | Thr | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | His | Leu | Ile | Lys | Pro | Glu | Xaa | Glu | Leu | Asp | His | Gln | Phe | Ile | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Asp | Glu | Ser | Asn | Val | Ala | Val | Pro | Ala | Lys | Xaa | Arg | Xaa | Lys | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Xaa | Arg | Xaa | Ala | Ala | Ser | Thr | Trp | Ala | Ser | Arg | Xaa | Leu | Ser | Leu | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Asp | Ser | Asp | Glu | Thr | Asn | Pro | Lys | Lys | Lys | Gln | Arg | Arg | Val | Lys | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Asp | Phe | Ala | Gly | Asp | Met | Asp | Val | Asp | Cys | Gly | Glu | Ser | Gly | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Arg | Arg | Cys | Leu | His | Cys | Ala | Thr | Glu | Lys | Thr | Pro | Gln | Trp | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Thr | Gly | Pro | Met | Gly | Pro | Lys | Thr | Leu | Cys | Asn | Ala | Cys | Gly | Val | Arg |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Tyr | Lys | Ser | Gly | Arg | Leu | Val | Pro | Glu | Tyr | Arg | Pro | Ala | Ser | Ser | Pro |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Phe | Val | Met | Ala | Arg | His | Ser | Asn | Ser | His | Arg | Lys | Val | Met | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Arg | Arg | Gln | Lys | Glu | Met | Arg | Asp | Glu | His | Leu | Leu | Ser | Gln | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Cys | Glu | Asn | Leu | Leu | Met | Asp | Ile | Arg | Ser | Asn | Gly | Glu | Asp | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Leu | Met | His | Asn | Asn | Thr | Asn | His | Val | Ala | Pro | Asp | Phe | Arg | His | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |

Ile

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 308 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..308

(D) OTHER INFORMATION: / Ceres Seq. ID 1498274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Met Glu Lys Ile Ala Pro Glu Leu Phe Leu Val Ala Gly Asn Pro Asp  
1 5 10 15  
Ser Phe Val Val Asp Asp Leu Leu Asp Phe Ser Asn Asp Asp Gly Glu  
20 25 30  
Val Asp Asp Gly Leu Asn Thr Leu Pro Asp Ser Ser Thr Leu Ser Thr  
35 40 45  
Gly Thr Leu Thr Asp Ser Ser Asn Ser Ser Ser Leu Phe Thr Asp Gly  
50 55 60  
Thr Gly Phe Ser Asp Leu Tyr Ile Pro Asn Asp Ile Ala Glu Leu  
65 70 75 80  
Glu Trp Leu Ser Asn Phe Val Glu Glu Ser Phe Ala Gly Glu Asp Gln  
85 90 95  
Xaa Lys Xaa His Leu Phe Ser Xaa Leu Lys Asn Pro Gln Thr Xaa Gly  
100 105 110  
Ser Thr Leu Thr His Leu Ile Lys Pro Glu Xaa Glu Leu Asp His Gln  
115 120 125  
Phe Ile Asp Ile Asp Glu Ser Asn Val Ala Val Pro Ala Lys Xaa Arg  
130 135 140  
Xaa Lys Arg Xaa Arg Xaa Ala Ala Ser Thr Trp Ala Ser Arg Xaa Leu  
145 150 155 160  
Ser Leu Ala Asp Ser Asp Glu Thr Asn Pro Lys Lys Lys Gln Arg Arg  
165 170 175  
Val Lys Glu Gln Asp Phe Ala Gly Asp Met Asp Val Asp Cys Gly Glu  
180 185 190  
Ser Gly Gly Gly Arg Arg Cys Leu His Cys Ala Thr Glu Lys Thr Pro  
195 200 205  
Gln Trp Arg Thr Gly Pro Met Gly Pro Lys Thr Leu Cys Asn Ala Cys  
210 215 220  
Gly Val Arg Tyr Lys Ser Gly Arg Leu Val Pro Glu Tyr Arg Pro Ala  
225 230 235 240  
Ser Ser Pro Thr Phe Val Met Ala Arg His Ser Asn Ser His Arg Lys  
245 250 255  
Val Met Glu Leu Arg Arg Gln Lys Glu Met Arg Asp Glu His Leu Leu  
260 265 270  
Ser Gln Leu Arg Cys Glu Asn Leu Leu Met Asp Ile Arg Ser Asn Gly  
275 280 285  
Glu Asp Phe Leu Met His Asn Asn Thr Asn His Val Ala Pro Asp Phe  
290 295 300  
Arg His Leu Ile  
305

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1661 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1661

(D) OTHER INFORMATION: / Ceres Seq. ID 1498279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aatcaaaccc | aaaagcccaa | aaccagaaaa | agaaaaatct | ctcttttgaa | aattctcctt | 60  |
| ttgcaaatca | ttcaagtga  | gcagaatcat | ctccttcttc | ttcttctoca | gcttcatcaa | 120 |
| tctcttctaa | actttttgcg | tttacctgaa | aaactgtttt | gatcggaaga | atctgattgc | 180 |
| ttcgatgtcg | ctgtcgaa   | agattcccg  | ttactctcga | tgacctctg  | catcttcttc | 240 |
| cacttttttt | ccccagtttt | ctgataactt | ttctcagatg | agaagttcta | cgttacttct | 300 |

```
tctcaagttc ttctttcttct tcttcaatct gacttcgctt gagtatcaag ttgatggagc 360
atttggttga acatatggga taaattatgg aaggatagct gacaacatac catctccgga 420
gaaagtagtt ttactttctaa agcaagctaa aattcgggaat gtgcgtatat acgatgtaga 480
tcacactggt cttgaagcgt ttagtggaac tgggttagac cttggtggtg gacttcctaa 540
tgggttttta aaagagatga gttcaaatgc tgatcatgct ttcacttggg ttaaagaaaa 600
tatccagtct ttcttaccga agactcggat tcgcgggtatc gctataggta acgaagttct 660
tggaggcggg gattctgagc tcgcgggagc tttacttggt gctgctaaaa atgtgtacaa 720
tgcgttgaag aaaatgaatc tggaggacac tgtgcagatc actacggctc attcacaggc 780
tgtgttttct gattcctacc cgccttcgtc ttgtgtgttt aaagagaatg ttgttcagtt 840
catgaagcca ttgttggagt tttttcagca gattgggtct cctttttgtt tgaatgctta 900
cccttttttg gcgtacactt ataatccgaa ggagattgat atcaactatg ctcttttcaa 960
gccaacggaa gggatatatg acccgaaaaac cgatttgcac tacgataaca tgcttgatgc 1020
tcagattgat gctgcttaca tggcgttgca agatgctggg ttaagaaga tggaggttat 1080
gatcactgaa actgggtggg cttctaaagg ggattcagat gaacctgcag caacaccaga 1140
gaacgcaaga acgtataact ataacctcag gaagaggcgt gctaagaaga aagggacacc 1200
tcttagacca aaaacggtgc ttaaagccta tatctttgca ttgttcaatg aaaactcaaa 1260
accgggcaag agttctgaga cacactttgg actttttaaa cctgatggaa ccataatcata 1320
tgacattgga ttcaacagtc taaagtctga ttctcccaag tcaactatct catcatcaaa 1380
gtcagctcgt tactatgtgg cattggtcat ctctgtctcg gctttcctct tgatgatata 1440
aatgcggaat tgggtgtgagc ttgacgatc ctgcgatttg gtcgtacatt cgtagcacta 1500
taatatatat tactagggtt gggacgctaa cgaaatggta ggagcacaaa tttactgcaa 1560
ttctcatata ttagccaag agatatccag aaaagatata accagacact atcatatata 1620
cacatcttat gtaaaacaaa tctaatacat aaatttgggc c
```

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..387

(D) OTHER INFORMATION: / Ceres Seq. ID 1498280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

```
Met Arg Ser Ser Thr Leu Leu Leu Lys Phe Phe Phe Phe Phe Phe
1 5 10 15
Asn Leu Thr Ser Leu Glu Tyr Gln Val Asp Gly Ala Phe Val Gly Thr
20 25 30
Tyr Gly Ile Asn Tyr Gly Arg Ile Ala Asp Asn Ile Pro Ser Pro Glu
35 40 45
Lys Val Val Leu Leu Leu Lys Gln Ala Lys Ile Arg Asn Val Arg Ile
50 55 60
Tyr Asp Val Asp His Thr Val Leu Glu Ala Phe Ser Gly Thr Gly Leu
65 70 75 80
Asp Leu Val Val Gly Leu Pro Asn Gly Phe Leu Lys Glu Met Ser Ser
85 90 95
Asn Ala Asp His Ala Phe Thr Trp Val Lys Glu Asn Ile Gln Ser Phe
100 105 110
Leu Pro Lys Thr Arg Ile Arg Gly Ile Ala Ile Gly Asn Glu Val Leu
115 120 125
Gly Gly Gly Asp Ser Glu Leu Ala Gly Ala Leu Leu Gly Ala Ala Lys
130 135 140
Asn Val Tyr Asn Ala Leu Lys Lys Met Asn Leu Glu Asp Thr Val Gln
145 150 155 160
Ile Thr Thr Ala His Ser Gln Ala Val Phe Ser Asp Ser Tyr Pro Pro
165 170 175
Ser Ser Cys Val Phe Lys Glu Asn Val Val Gln Phe Met Lys Pro Leu
180 185 190
Leu Glu Phe Phe Gln Gln Ile Gly Ser Pro Phe Cys Leu Asn Ala Tyr
195 200 205
```

Pro Phe Leu Ala Tyr Thr Tyr Asn Pro Lys Glu Ile Asp Ile Asn Tyr  
210 215 220  
Ala Leu Phe Lys Pro Thr Glu Gly Ile Tyr Asp Pro Lys Thr Asp Leu  
225 230 235 240  
His Tyr Asp Asn Met Leu Asp Ala Gln Ile Asp Ala Ala Tyr Met Ala  
245 250 255  
Leu Gln Asp Ala Gly Phe Lys Lys Met Glu Val Met Ile Thr Glu Thr  
260 265 270  
Gly Trp Ala Ser Lys Gly Asp Ser Asp Glu Pro Ala Ala Thr Pro Glu  
275 280 285  
Asn Ala Arg Thr Tyr Asn Tyr Asn Leu Arg Lys Arg Leu Ala Lys Lys  
290 295 300  
Lys Gly Thr Pro Leu Arg Pro Lys Thr Val Leu Lys Ala Tyr Ile Phe  
305 310 315 320  
Ala Leu Phe Asn Glu Asn Ser Lys Pro Gly Lys Ser Ser Glu Thr His  
325 330 335  
Phe Gly Leu Phe Lys Pro Asp Gly Thr Ile Ser Tyr Asp Ile Gly Phe  
340 345 350  
Asn Ser Leu Lys Ser Asp Ser Pro Lys Ser Leu Ile Ser Ser Ser Lys  
355 360 365  
Ser Ala Arg Tyr Tyr Val Ala Leu Val Ile Ser Val Ser Ala Phe Leu  
370 375 380  
Leu Met Ile  
385

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1498281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met Ser Ser Asn Ala Asp His Ala Phe Thr Trp Val Lys Glu Asn Ile  
1 5 10 15  
Gln Ser Phe Leu Pro Lys Thr Arg Ile Arg Gly Ile Ala Ile Gly Asn  
20 25 30  
Glu Val Leu Gly Gly Gly Asp Ser Glu Leu Ala Gly Ala Leu Leu Gly  
35 40 45  
Ala Ala Lys Asn Val Tyr Asn Ala Leu Lys Lys Met Asn Leu Glu Asp  
50 55 60  
Thr Val Gln Ile Thr Thr Ala His Ser Gln Ala Val Phe Ser Asp Ser  
65 70 75 80  
Tyr Pro Pro Ser Ser Cys Val Phe Lys Glu Asn Val Val Gln Phe Met  
85 90 95  
Lys Pro Leu Leu Glu Phe Phe Gln Gln Ile Gly Ser Pro Phe Cys Leu  
100 105 110  
Asn Ala Tyr Pro Phe Leu Ala Tyr Thr Tyr Asn Pro Lys Glu Ile Asp  
115 120 125  
Ile Asn Tyr Ala Leu Phe Lys Pro Thr Glu Gly Ile Tyr Asp Pro Lys  
130 135 140  
Thr Asp Leu His Tyr Asp Asn Met Leu Asp Ala Gln Ile Asp Ala Ala  
145 150 155 160  
Tyr Met Ala Leu Gln Asp Ala Gly Phe Lys Lys Met Glu Val Met Ile  
165 170 175  
Thr Glu Thr Gly Trp Ala Ser Lys Gly Asp Ser Asp Glu Pro Ala Ala  
180 185 190  
Thr Pro Glu Asn Ala Arg Thr Tyr Asn Tyr Asn Leu Arg Lys Arg Leu



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 195                                                             | 200 | 205 |
| Ala Lys Lys Lys Gly Thr Pro Leu Arg Pro Lys Thr Val Leu Lys Ala |     |     |
| 210                                                             | 215 | 220 |
| Tyr Ile Phe Ala Leu Phe Asn Glu Asn Ser Lys Pro Gly Lys Ser Ser |     |     |
| 225                                                             | 230 | 235 |
| Glu Thr His Phe Gly Leu Phe Lys Pro Asp Gly Thr Ile Ser Tyr Asp |     |     |
| 245                                                             | 250 | 255 |
| Ile Gly Phe Asn Ser Leu Lys Ser Asp Ser Pro Lys Ser Leu Ile Ser |     |     |
| 260                                                             | 265 | 270 |
| Ser Ser Lys Ser Ala Arg Tyr Tyr Val Ala Leu Val Ile Ser Val Ser |     |     |
| 275                                                             | 280 | 285 |
| Ala Phe Leu Leu Met Ile                                         |     |     |
| 290                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..235
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Asn Leu Glu Asp Thr Val Gln Ile Thr Thr Ala His Ser Gln Ala |     |     |
| 1                                                               | 5   | 10  |
| Val Phe Ser Asp Ser Tyr Pro Pro Ser Ser Cys Val Phe Lys Glu Asn |     |     |
| 20                                                              | 25  | 30  |
| Val Val Gln Phe Met Lys Pro Leu Leu Glu Phe Phe Gln Gln Ile Gly |     |     |
| 35                                                              | 40  | 45  |
| Ser Pro Phe Cys Leu Asn Ala Tyr Pro Phe Leu Ala Tyr Thr Tyr Asn |     |     |
| 50                                                              | 55  | 60  |
| Pro Lys Glu Ile Asp Ile Asn Tyr Ala Leu Phe Lys Pro Thr Glu Gly |     |     |
| 65                                                              | 70  | 75  |
| Ile Tyr Asp Pro Lys Thr Asp Leu His Tyr Asp Asn Met Leu Asp Ala |     |     |
| 85                                                              | 90  | 95  |
| Gln Ile Asp Ala Ala Tyr Met Ala Leu Gln Asp Ala Gly Phe Lys Lys |     |     |
| 100                                                             | 105 | 110 |
| Met Glu Val Met Ile Thr Glu Thr Gly Trp Ala Ser Lys Gly Asp Ser |     |     |
| 115                                                             | 120 | 125 |
| Asp Glu Pro Ala Ala Thr Pro Glu Asn Ala Arg Thr Tyr Asn Tyr Asn |     |     |
| 130                                                             | 135 | 140 |
| Leu Arg Lys Arg Leu Ala Lys Lys Lys Gly Thr Pro Leu Arg Pro Lys |     |     |
| 145                                                             | 150 | 155 |
| Thr Val Leu Lys Ala Tyr Ile Phe Ala Leu Phe Asn Glu Asn Ser Lys |     |     |
| 165                                                             | 170 | 175 |
| Pro Gly Lys Ser Ser Glu Thr His Phe Gly Leu Phe Lys Pro Asp Gly |     |     |
| 180                                                             | 185 | 190 |
| Thr Ile Ser Tyr Asp Ile Gly Phe Asn Ser Leu Lys Ser Asp Ser Pro |     |     |
| 195                                                             | 200 | 205 |
| Lys Ser Leu Ile Ser Ser Ser Lys Ser Ala Arg Tyr Tyr Val Ala Leu |     |     |
| 210                                                             | 215 | 220 |
| Val Ile Ser Val Ser Ala Phe Leu Leu Met Ile                     |     |     |
| 225                                                             | 230 | 235 |

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..690

(D) OTHER INFORMATION: / Ceres Seq. ID 1498283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| aaaatcgctcg | ctctctgcct | ctctcgcac   | tccaaatcga | aatcgctctc | cgtctccgct | 60  |
| tccgtctccg  | tctccgtctc | cgtctccgct  | tccgtctccg | tctccatctc | tctctccggt | 120 |
| aagtcactga  | aagatggggc | gtgttagaac  | caagacggtg | aagaaatctt | cacgtcragt | 180 |
| cattgagaag  | tactactctc | gcattgactct | tgactttcac | actaacaaga | agatccttga | 240 |
| agagggttgc  | atcatcccat | caaagagact  | ccgcaacaag | attgctggat | tctccaccca | 300 |
| cttgatgaaa  | cgtatccaga | akkgaccagt  | ccgtggmatc | tactcaagc  | ttcaagaaga | 360 |
| agagcgtgaa  | cgccgtatgg | actttgttcc  | cgatgagtct | gctatcaaga | ctgatgagat | 420 |
| caaggctcga  | aaagagactc | ttgagatgct  | tgcttctcta | ggaatgtctg | acactctcgg | 480 |
| catctctgca  | gtcgacccac | aacaagctat  | ggcaccaatc | cctgctttcg | gcggcggcag | 540 |
| ggcaccacaga | agatactaag | atggacgatt  | ggctctcttt | tttcacagtt | agggacaaga | 600 |
| aagacttttg  | tggttggtta | ttgtttcttt  | tgattatgtc | ttaaactcaa | tgtgagactc | 660 |
| tttcgtatta  | atgggttttg | agttatgtgg  |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1498284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Arg | Val | Arg | Thr | Lys | Thr | Val | Lys | Lys | Ser | Ser | Arg | Xaa | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Glu | Lys | Tyr | Tyr | Ser | Arg | Met | Thr | Leu | Asp | Phe | His | Thr | Asn | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ile | Leu | Glu | Glu | Val | Ala | Ile | Pro | Ser | Lys | Arg | Ile | Leu | Arg | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ile | Ala | Gly | Phe | Ser | Thr | His | Leu | Met | Lys | Arg | Ile | Gln | Xaa | Xaa |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Val | Arg | Xaa | Ile | Ser | Leu | Lys | Leu | Gln | Glu | Glu | Glu | Arg | Glu | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Met | Asp | Phe | Val | Pro | Asp | Glu | Ser | Ala | Ile | Lys | Thr | Asp | Glu | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Val | Asp | Lys | Glu | Thr | Leu | Glu | Met | Leu | Ala | Ser | Leu | Gly | Met | Ser |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asp | Thr | Leu | Gly | Ile | Ser | Ala | Val | Asp | Pro | Gln | Gln | Ala | Met | Ala | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Pro | Ala | Phe | Gly | Gly | Gly | Arg | Ala | Pro | Arg | Arg | Tyr |     |     |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1498285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Met Thr Leu Asp Phe His Thr Asn Lys Lys Ile Leu Glu Glu Val Ala

```

1 5 10 15
Ile Ile Pro Ser Lys Arg Leu Arg Asn Lys Ile Ala Gly Phe Ser Thr
 20 25 30
His Leu Met Lys Arg Ile Gln Xaa Xaa Pro Val Arg Xaa Ile Ser Leu
 35 40 45
Lys Leu Gln Glu Glu Glu Arg Glu Arg Arg Met Asp Phe Val Pro Asp
 50 55 60
Glu Ser Ala Ile Lys Thr Asp Glu Ile Lys Val Asp Lys Glu Thr Leu
65 70 75 80
Glu Met Leu Ala Ser Leu Gly Met Ser Asp Thr Leu Gly Ile Ser Ala
 85 90 95
Val Asp Pro Gln Ala Met Ala Pro Ile Pro Ala Phe Gly Gly Gly
 100 105 110
Arg Ala Pro Arg Arg Tyr
 115
```

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1498286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

```

Met Lys Arg Ile Gln Xaa Xaa Pro Val Arg Xaa Ile Ser Leu Lys Leu
1 5 10 15
Gln Glu Glu Glu Arg Glu Arg Arg Met Asp Phe Val Pro Asp Glu Ser
 20 25 30
Ala Ile Lys Thr Asp Glu Ile Lys Val Asp Lys Glu Thr Leu Glu Met
 35 40 45
Leu Ala Ser Leu Gly Met Ser Asp Thr Leu Gly Ile Ser Ala Val Asp
50 55 60
Pro Gln Gln Ala Met Ala Pro Ile Pro Ala Phe Gly Gly Gly Arg Ala
65 70 75 80
Pro Arg Arg Tyr
```

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1264

(D) OTHER INFORMATION: / Ceres Seq. ID 1498291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```

attatgagaa agaatctcac ctaatgatgt tctaggtaat ggtctcttta tgcgacagct 60
acgagactat accacctaac atctccgaga aagaagctgc gtggctaagg tccttctacg 120
cagcgggaga ggaggaaaaa gagcgtagaa cgcattgcaat tgcggttgct gccgcgacag 180
ctgctgcagc tgacgcagcg gttgcggcgg ctaaagcggc tgctgcggtt gttatgctcc 240
aaggtcaagg caagagtggc ccgttaggag gtggcaaaaag ccgtgagcat cgtgctgcta 300
tgcagatcca atgtgccttt agaggctact tggcgagaaa agcgttgaga gcgttgagag 360
gagtgggtgaa gattcaagct ttagtgagag gtttttggt acggaatcaa gcggcggcga 420
ctctccggag tatggaagca cttgttagag ctcaaaaaac tgtaagatt caaagagctc 480
tccgtcgtaa cggaatgct gctccggcga gaaaatccac ggaaagattc tccggatctt 540
tggagaatcg aaacaacggc gaagagacag ctaagatagt ggaggtagat acagggaccc 600
```

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| gaccCGggac | ttacagaatc  | cgagcaccCG | ttttatccgG | gtcggatttc | ttagacaacc  | 660  |
| cgtttcgacg | tacgctttct  | tcaccgctct | cgggtcGagt | cccaccgCGt | ctatcaatgc  | 720  |
| ctaaacctga | atgggaagag  | tgcagtagca | agttcccgac | ggcgagagc  | acacctcgtt  | 780  |
| tttctgggtg | gtctccggcg  | aggagcgtgt | gctgctctgg | tggcggagta | gaggcggagg  | 840  |
| tggatacaga | ggctgatgct  | aaccggttct | gtttcttgtc | gggggaattt | aactcgggtt  | 900  |
| acatggcgga | tacaacgtcg  | tttagggcga | aactgaggtc | gcatagtgc  | ccgagacaga  | 960  |
| gaccagagag | taatgcttca  | gctggcggat | ggaggaggag | tatcggcggc | ggtggtgtta  | 1020 |
| ggatgcagag | acagtcgtgt  | tcgggtgtca | gagaagctgt | ggtcgggaat | atcgagaggc  | 1080 |
| gtaggatgcg | ttgggtgattc | ttatttccat | aattattatc | cgtttagttt | tgggttaatta | 1140 |
| ggggagtaat | gttattaatt  | taatatagtt | tgatattatt | atagttttct | aagtttctact | 1200 |
| gacaaaattt | aaaattgttg  | tttcttgtat | gctacatatt | ctatttctat | gtaagttttt  | 1260 |
| tgcc       |             |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..352
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Ser | Leu | Cys | Asp | Ser | Tyr | Glu | Thr | Ile | Pro | Pro | Asn | Ile | Ser |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Glu | Lys | Glu | Ala | Ala | Trp | Leu | Arg | Ser | Phe | Tyr | Ala | Ala | Gly | Glu | Glu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Lys | Glu | Arg | Arg | Thr | His | Ala | Ile | Ala | Val | Ala | Ala | Ala | Thr | Ala |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Ala | Ala | Asp | Ala | Ala | Val | Ala | Ala | Ala | Lys | Ala | Ala | Ala | Ala | Val |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Val | Met | Leu | Gln | Gly | Gln | Gly | Lys | Ser | Gly | Pro | Leu | Gly | Gly | Gly | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ser | Arg | Glu | His | Arg | Ala | Ala | Met | Gln | Ile | Gln | Cys | Ala | Phe | Arg | Gly |  |
|     |     |     | 85  |     |     |     |     |     |     | 90  |     |     |     | 95  |     |  |
| Tyr | Leu | Ala | Arg | Lys | Ala | Leu | Arg | Ala | Leu | Arg | Gly | Val | Val | Lys | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gln | Ala | Leu | Val | Arg | Gly | Phe | Leu | Val | Arg | Asn | Gln | Ala | Ala | Ala | Thr |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Arg | Ser | Met | Glu | Ala | Leu | Val | Arg | Ala | Gln | Lys | Thr | Val | Lys | Ile |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Gln | Arg | Ala | Leu | Arg | Arg | Asn | Gly | Asn | Ala | Ala | Pro | Ala | Arg | Lys | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Thr | Glu | Arg | Phe | Ser | Gly | Ser | Leu | Glu | Asn | Arg | Asn | Asn | Gly | Glu | Glu |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Thr | Ala | Lys | Ile | Val | Glu | Val | Asp | Thr | Gly | Thr | Arg | Pro | Gly | Thr | Tyr |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Arg | Ile | Arg | Ala | Pro | Val | Leu | Ser | Gly | Ser | Asp | Phe | Leu | Asp | Asn | Pro |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Phe | Arg | Arg | Thr | Leu | Ser | Ser | Pro | Leu | Ser | Gly | Arg | Val | Pro | Pro | Arg |  |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |  |
| Leu | Ser | Met | Pro | Lys | Pro | Glu | Trp | Glu | Glu | Cys | Ser | Ser | Lys | Phe | Pro |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Thr | Ala | Gln | Ser | Thr | Pro | Arg | Phe | Ser | Gly | Gly | Ser | Pro | Ala | Arg | Ser |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Val | Cys | Cys | Ser | Gly | Gly | Gly | Val | Glu | Ala | Glu | Val | Asp | Thr | Glu | Ala |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Asp | Ala | Asn | Arg | Phe | Cys | Phe | Leu | Ser | Gly | Glu | Phe | Asn | Ser | Gly | Tyr |  |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Met | Ala | Asp | Thr | Thr | Ser | Phe | Arg | Ala | Lys | Leu | Arg | Ser | His | Ser | Ala |  |

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| 290                                                             |     | 295 |     | 300 |
| Pro Arg Gln Arg Pro Glu Ser Asn Ala Ser Ala Gly Gly Trp Arg Arg |     |     |     |     |
| 305                                                             |     | 310 |     | 315 |
| Ser Ile Gly Gly Gly Gly Val Arg Met Gln Arg Gln Ser Cys Ser Gly |     |     |     | 320 |
|                                                                 |     | 325 |     | 330 |
| Val Arg Glu Ala Val Val Gly Asn Ile Glu Arg Arg Arg Met Arg Trp |     |     |     | 335 |
|                                                                 | 340 |     | 345 | 350 |

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..287

(D) OTHER INFORMATION: / Ceres Seq. ID 1498293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gln | Gly | Gln | Gly | Lys | Ser | Gly | Pro | Leu | Gly | Gly | Gly | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Glu | His | Arg | Ala | Ala | Met | Gln | Ile | Gln | Cys | Ala | Phe | Arg | Gly | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ala | Arg | Lys | Ala | Leu | Arg | Ala | Leu | Arg | Gly | Val | Val | Lys | Ile | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Val | Arg | Gly | Phe | Leu | Val | Arg | Asn | Gln | Ala | Ala | Ala | Thr | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Ser | Met | Glu | Ala | Leu | Val | Arg | Ala | Gln | Lys | Thr | Val | Lys | Ile | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ala | Leu | Arg | Arg | Asn | Gly | Asn | Ala | Ala | Pro | Ala | Arg | Lys | Ser | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Arg | Phe | Ser | Gly | Ser | Leu | Glu | Asn | Arg | Asn | Asn | Gly | Glu | Glu | Thr |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Lys | Ile | Val | Glu | Val | Asp | Thr | Gly | Thr | Arg | Pro | Gly | Thr | Tyr | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Arg | Ala | Pro | Val | Leu | Ser | Gly | Ser | Asp | Phe | Leu | Asp | Asn | Pro | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Arg | Thr | Leu | Ser | Ser | Pro | Leu | Ser | Gly | Arg | Val | Pro | Pro | Arg | Leu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Met | Pro | Lys | Pro | Glu | Trp | Glu | Glu | Cys | Ser | Ser | Lys | Phe | Pro | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Gln | Ser | Thr | Pro | Arg | Phe | Ser | Gly | Gly | Ser | Pro | Ala | Arg | Ser | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Cys | Cys | Ser | Gly | Gly | Gly | Val | Glu | Ala | Glu | Val | Asp | Thr | Glu | Ala | Asp |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ala | Asn | Arg | Phe | Cys | Phe | Leu | Ser | Gly | Glu | Phe | Asn | Ser | Gly | Tyr | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Asp | Thr | Thr | Ser | Phe | Arg | Ala | Lys | Leu | Arg | Ser | His | Ser | Ala | Pro |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Arg | Gln | Arg | Pro | Glu | Ser | Asn | Ala | Ser | Ala | Gly | Gly | Trp | Arg | Arg | Ser |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Ile | Gly | Gly | Gly | Gly | Val | Arg | Met | Gln | Arg | Gln | Ser | Cys | Ser | Gly | Val |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Glu | Ala | Val | Val | Gly | Asn | Ile | Glu | Arg | Arg | Arg | Met | Arg | Trp |     |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..265  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498294  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Met Gln Ile Gln Cys Ala Phe Arg Gly Tyr Leu Ala Arg Lys Ala Leu  
1 5 10 15  
Arg Ala Leu Arg Gly Val Val Lys Ile Gln Ala Leu Val Arg Gly Phe  
20 25 30  
Leu Val Arg Asn Gln Ala Ala Ala Thr Leu Arg Ser Met Glu Ala Leu  
35 40 45  
Val Arg Ala Gln Lys Thr Val Lys Ile Gln Arg Ala Leu Arg Arg Asn  
50 55 60  
Gly Asn Ala Ala Pro Ala Arg Lys Ser Thr Glu Arg Phe Ser Gly Ser  
65 70 75 80  
Leu Glu Asn Arg Asn Asn Gly Glu Glu Thr Ala Lys Ile Val Glu Val  
85 90 95  
Asp Thr Gly Thr Arg Pro Gly Thr Tyr Arg Ile Arg Ala Pro Val Leu  
100 105 110  
Ser Gly Ser Asp Phe Leu Asp Asn Pro Phe Arg Arg Thr Leu Ser Ser  
115 120 125  
Pro Leu Ser Gly Arg Val Pro Pro Arg Leu Ser Met Pro Lys Pro Glu  
130 135 140  
Trp Glu Glu Cys Ser Ser Lys Phe Pro Thr Ala Gln Ser Thr Pro Arg  
145 150 155 160  
Phe Ser Gly Gly Ser Pro Ala Arg Ser Val Cys Cys Ser Gly Gly Gly  
165 170 175  
Val Glu Ala Glu Val Asp Thr Glu Ala Asp Ala Asn Arg Phe Cys Phe  
180 185 190  
Leu Ser Gly Glu Phe Asn Ser Gly Tyr Met Ala Asp Thr Thr Ser Phe  
195 200 205  
Arg Ala Lys Leu Arg Ser His Ser Ala Pro Arg Gln Arg Pro Glu Ser  
210 215 220  
Asn Ala Ser Ala Gly Gly Trp Arg Arg Ser Ile Gly Gly Gly Gly Val  
225 230 235 240  
Arg Met Gln Arg Gln Ser Cys Ser Gly Val Arg Glu Ala Val Val Gly  
245 250 255  
Asn Ile Glu Arg Arg Arg Met Arg Trp  
260 265

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 727 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..727  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

|             |            |             |             |             |            |     |
|-------------|------------|-------------|-------------|-------------|------------|-----|
| aagtaggagg  | aagacgatgg | cgttagagaa  | gcacatagag  | aagggtactct | tcagcgatga | 60  |
| agtaattgcg  | caccgggtga | atcagcttgg  | aatcgatatt  | acttctgatt  | tctccggtga | 120 |
| ctcggaggaa  | actcctat   | ttgtcggcgt  | agccactggg  | gcttgccctct | tcttggccga | 180 |
| tctcgttagg  | cgaattgact | tgccaatagc  | tatagatttc  | attagagctg  | agtcttacgg | 240 |
| ctctgggtact | gtatccagt  | gagttcccag  | agtatcattt  | gacttaaagc  | ttgacatcac | 300 |
| gaacaagcac  | gttgcttgg  | tcgaggacat  | tgtggatact  | ggcaatacac  | ttagctgcct | 360 |
| gattgagcac  | atgaaagcaa | aaaaggcgctc | atctgttttcg | gtttgcactc  | tcctcgacaa | 420 |

gccatcgaga agaaagggttc attataagct ggttggaaag gggaaattct acagtgggtt 480  
tgaatgtcca gatgaatttg tcgtgggcta tggcatggat tttgcagaac aataccgcaa 540  
cctatcttac attggcgtat tgaagcctga atattacatg tgacaatatt gcatgaactg 600  
gtcaatcatg acatcttttg atgacttgca cctctgttag gtgttcaaag cagtagcacc 660  
aatgttatac tacaatttga cagtgtattct gatgtaaaag ctaatgcaaa ttggtgtatg 720  
atatgtt

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Ser Arg Arg Lys Thr Met Ala Leu Glu Lys His Ile Glu Lys Val Leu  
1 5 10 15  
Phe Ser Asp Glu Val Ile Ala His Arg Val Asn Gln Leu Gly Ile Asp  
20 25 30  
Ile Thr Ser Asp Phe Ser Gly Asp Ser Glu Glu Thr Pro Ile Phe Val  
35 40 45  
Gly Val Ala Thr Gly Ala Cys Leu Phe Leu Ala Asp Leu Val Arg Arg  
50 55 60  
Ile Asp Leu Pro Ile Ala Ile Asp Phe Ile Arg Ala Glu Ser Tyr Gly  
65 70 75 80  
Ser Gly Thr Val Ser Ser Gly Val Pro Arg Val Ser Phe Asp Leu Lys  
85 90 95  
Leu Asp Ile Thr Asn Lys His Val Val Leu Val Glu Asp Ile Val Asp  
100 105 110  
Thr Gly Asn Thr Leu Ser Cys Leu Ile Glu His Met Lys Ala Lys Lys  
115 120 125  
Ala Ser Ser Val Ser Val Cys Thr Leu Leu Asp Lys Pro Ser Arg Arg  
130 135 140  
Lys Val His Tyr Lys Leu Val Gly Lys Gly Lys Phe Tyr Ser Gly Phe  
145 150 155 160  
Glu Cys Pro Asp Glu Phe Val Val Gly Tyr Gly Met Asp Phe Ala Glu  
165 170 175  
Gln Tyr Arg Asn Leu Ser Tyr Ile Gly Val Leu Lys Pro Glu Tyr Tyr  
180 185 190  
Met

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Met Ala Leu Glu Lys His Ile Glu Lys Val Leu Phe Ser Asp Glu Val  
1 5 10 15  
Ile Ala His Arg Val Asn Gln Leu Gly Ile Asp Ile Thr Ser Asp Phe  
20 25 30  
Ser Gly Asp Ser Glu Glu Thr Pro Ile Phe Val Gly Val Ala Thr Gly

|                         |                     |                     |
|-------------------------|---------------------|---------------------|
| 35                      | 40                  | 45                  |
| Ala Cys Leu Phe Leu Ala | Asp Leu Val Arg Arg | Ile Asp Leu Pro Ile |
| 50                      | 55                  | 60                  |
| Ala Ile Asp Phe Ile Arg | Ala Glu Ser Tyr Gly | Ser Gly Thr Val Ser |
| 65                      | 70                  | 75                  |
| Ser Gly Val Pro Arg Val | Ser Phe Asp Leu Lys | Leu Asp Ile Thr Asn |
| 85                      | 90                  | 95                  |
| Lys His Val Val Leu Val | Glu Asp Ile Val Asp | Thr Gly Asn Thr Leu |
| 100                     | 105                 | 110                 |
| Ser Cys Leu Ile Glu His | Met Lys Ala Lys Lys | Ala Ser Val Ser     |
| 115                     | 120                 | 125                 |
| Val Cys Thr Leu Leu Asp | Lys Pro Ser Arg Arg | Lys Val His Tyr Lys |
| 130                     | 135                 | 140                 |
| Leu Val Gly Lys Gly Lys | Phe Tyr Ser Gly Phe | Glu Cys Pro Asp Glu |
| 145                     | 150                 | 155                 |
| Phe Val Val Gly Tyr Gly | Met Asp Phe Ala Glu | Gln Tyr Arg Asn Leu |
| 165                     | 170                 | 175                 |
| Ser Tyr Ile Gly Val Leu | Lys Pro Glu Tyr Tyr | Met                 |
| 180                     | 185                 |                     |

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1795
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| aaaataactta | ggaaagaaaa  | gagtcctcagc | agcatcagct  | cgtccttaaa | tctgatccat | 60   |
| catcgtcact  | ttctcccggc  | gaattccggt  | ttatcgattt  | aagtaacgag | atttgtgcaa | 120  |
| agatgactca  | ggacgtggag  | atgaaagata  | ataacacccc  | ttctcaatcg | attatctctt | 180  |
| cttcgacctc  | tactatgcag  | aatttgaagg  | agattgcagc  | actcatcgat | actgggtctt | 240  |
| acacgaagga  | ggttcgtcgt  | attgctcgtg  | ctgtgcgtct  | cactataggc | cttaggcaga | 300  |
| aactcacggg  | ctctgtgctc  | tcttccttcc  | tggattttgc  | tttggttcca | ggatccgaag | 360  |
| ctcactctcg  | cctctcttcc  | tttgttccta  | aggggtgatga | acatgacatg | gaagttgata | 420  |
| ctgcctcatc  | ggccacacaa  | gctgctcctt  | ctaagcatct  | acctgcagag | ctcgagatct | 480  |
| actgctactt  | cattgtttctt | ctttttctga  | ttgatcagaa  | gaagtacaac | gaggctaaag | 540  |
| cttggttcttc | agcaagcatt  | gctcgtctca  | agaacgtcaa  | ccgaaggacc | attgatgtga | 600  |
| tagcatcaac  | actctacttt  | tactattctt  | tgagttatga  | gcaaaccggt | gatcttgctg | 660  |
| aaattcgcgg  | tactcttctt  | gcgttgcatc  | attctgcaac  | gctaaggcac | gatgagctgg | 720  |
| gtcaggaaac  | ccttctgaac  | ctggtgctac  | gtaactatct  | gcattacaac | ctctatgatc | 780  |
| aggcagagaa  | gctaagatca  | aaggcacctc  | gctttgaggc  | tcattcaaac | caacagtttt | 840  |
| gtaggtacct  | tttctatctc  | gggaagattc  | gtactattca  | gctcgaatat | acggacgcaa | 900  |
| aagagagcct  | tcttcaggcg  | gccaggaaaag | cccctatagc  | agctttgggc | ttcaggatcc | 960  |
| aatgtaataa  | atgggcaatt  | ctggttcgtc  | tactgctggg  | tgagatacca | gagcgttcta | 1020 |
| tcttcactca  | aaagggtatg  | gagaaggccc  | tcagacccta  | cttcgagcta | acaaatgcgg | 1080 |
| ttaggattgg  | ggacttgagg  | ttgttttaga  | cagtccagga  | gaagttcttg | gacacatttg | 1140 |
| ctcaagacag  | aacgcacaat  | ctcatcgtgc  | gactccgcca  | caatgtcatc | aggactggac | 1200 |
| tgcggaacat  | aagtatctcc  | tactcgagaa  | tctctttacc  | cgatgttgcc | aaaaagctga | 1260 |
| ggctcaactc  | tgaaaaccct  | ggctgatgcg  | gaaagcatcg  | tggcaaaggc | catacgcgac | 1320 |
| ggagctatcg  | atgctacaat  | cgatcacaaa  | aacggatgca  | tggtctccaa | agaaactggg | 1380 |
| gacatctact  | cgacgaatga  | gccacaaaact | gcgttcaact  | caagaattgc | tttctgcctc | 1440 |
| aacatgcata  | acgaagctgt  | cagagcattg  | aggtttcctc  | ctaacactca | caaggagaaa | 1500 |
| gaaagcgatg  | agaagaggag  | agagaggaag  | caacaggaag  | aagagcttgc | taagcatatg | 1560 |
| gctgaggaag  | acgatgatga  | cttttagaca  | aagggtcatct | atttcttata | agagttgact | 1620 |
| ctccatctgt  | ctcacttttt  | ttatgttcac  | aagtttactt  | ggtactcttc | tcacgtcttc | 1680 |
| taagtgtttc  | tttattgagg  | atttttatcc  | tcaggaacct  | ttttattact | ctggtttcac | 1740 |
| tttaggaaaa  | gatatttatc  | ttgttggttt  | cagaagatca  | aattcaagtt | cgttt      |      |



(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..387

(D) OTHER INFORMATION: / Ceres Seq. ID 1498310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Gln | Asp | Val | Glu | Met | Lys | Asp | Asn | Asn | Thr | Pro | Ser | Gln | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Ile | Ser | Ser | Ser | Thr | Ser | Thr | Met | Gln | Asn | Leu | Lys | Glu | Ile | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ile | Asp | Thr | Gly | Ser | Tyr | Thr | Lys | Glu | Val | Arg | Arg | Ile | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Ala | Val | Arg | Leu | Thr | Ile | Gly | Leu | Arg | Gln | Lys | Leu | Thr | Gly | Ser |
|     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | Ser | Ser | Phe | Leu | Asp | Phe | Ala | Leu | Val | Pro | Gly | Ser | Glu | Ala |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Ser | Arg | Leu | Ser | Ser | Phe | Val | Pro | Lys | Gly | Asp | Glu | His | Asp | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Val | Asp | Thr | Ala | Ser | Ser | Ala | Thr | Gln | Ala | Ala | Pro | Ser | Lys | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Pro | Ala | Glu | Leu | Glu | Ile | Tyr | Cys | Tyr | Phe | Ile | Val | Leu | Leu | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ile | Asp | Gln | Lys | Lys | Tyr | Asn | Glu | Ala | Lys | Ala | Cys | Ser | Ser | Ala |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Ile | Ala | Arg | Leu | Lys | Asn | Val | Asn | Arg | Arg | Thr | Ile | Asp | Val | Ile |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ser | Arg | Leu | Tyr | Phe | Tyr | Tyr | Ser | Leu | Ser | Tyr | Glu | Gln | Thr | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Leu | Ala | Glu | Ile | Arg | Gly | Thr | Leu | Leu | Ala | Leu | His | His | Ser | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Leu | Arg | His | Asp | Glu | Leu | Gly | Gln | Glu | Thr | Leu | Leu | Asn | Leu | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Arg | Asn | Tyr | Leu | His | Tyr | Asn | Leu | Tyr | Asp | Gln | Ala | Glu | Lys | Leu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Ser | Lys | Ala | Pro | Arg | Phe | Glu | Ala | His | Ser | Asn | Gln | Gln | Phe | Cys |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Tyr | Leu | Phe | Tyr | Leu | Gly | Lys | Ile | Arg | Thr | Ile | Gln | Leu | Glu | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Asp | Ala | Lys | Glu | Ser | Leu | Leu | Gln | Ala | Ala | Arg | Lys | Ala | Pro | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Ala | Leu | Gly | Phe | Arg | Ile | Gln | Cys | Asn | Lys | Trp | Ala | Ile | Leu | Val |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Leu | Leu | Leu | Gly | Glu | Ile | Pro | Glu | Arg | Ser | Ile | Phe | Thr | Gln | Lys |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Met | Glu | Lys | Ala | Leu | Arg | Pro | Tyr | Phe | Glu | Leu | Thr | Asn | Ala | Val |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |
| Arg | Ile | Gly | Asp | Leu | Glu | Leu | Phe | Arg | Thr | Val | Gln | Glu | Lys | Phe | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Thr | Phe | Ala | Gln | Asp | Arg | Thr | His | Asn | Leu | Ile | Val | Arg | Leu | Arg |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| His | Asn | Val | Ile |     |     |     |     |     |     |     |     |     |     |     |     |

385

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1498311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asp | Asn | Asn | Thr | Pro | Ser | Gln | Ser | Ile | Ile | Ser | Ser | Ser | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Thr | Met | Gln | Asn | Leu | Lys | Glu | Ile | Ala | Ala | Leu | Ile | Asp | Thr | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Tyr | Thr | Lys | Glu | Val | Arg | Arg | Ile | Ala | Arg | Ala | Val | Arg | Leu | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Gly | Leu | Arg | Gln | Lys | Leu | Thr | Gly | Ser | Val | Leu | Ser | Ser | Phe | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Phe | Ala | Leu | Val | Pro | Gly | Ser | Glu | Ala | His | Ser | Arg | Leu | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Val | Pro | Lys | Gly | Asp | Glu | His | Asp | Met | Glu | Val | Asp | Thr | Ala | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ala | Thr | Gln | Ala | Ala | Pro | Ser | Lys | His | Leu | Pro | Ala | Glu | Leu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Tyr | Cys | Tyr | Phe | Ile | Val | Leu | Phe | Leu | Ile | Asp | Gln | Lys | Lys |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Tyr | Asn | Glu | Ala | Lys | Ala | Cys | Ser | Ser | Ala | Ser | Ile | Ala | Arg | Leu | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Val | Asn | Arg | Arg | Thr | Ile | Asp | Val | Ile | Ala | Ser | Arg | Leu | Tyr | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Tyr | Ser | Leu | Ser | Tyr | Glu | Gln | Thr | Gly | Asp | Leu | Ala | Glu | Ile | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Thr | Leu | Leu | Ala | Leu | His | His | Ser | Ala | Thr | Leu | Arg | His | Asp | Glu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Gly | Gln | Glu | Thr | Leu | Leu | Asn | Leu | Leu | Leu | Arg | Asn | Tyr | Leu | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Asn | Leu | Tyr | Asp | Gln | Ala | Glu | Lys | Leu | Arg | Ser | Lys | Ala | Pro | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Glu | Ala | His | Ser | Asn | Gln | Gln | Phe | Cys | Arg | Tyr | Leu | Phe | Tyr | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Lys | Ile | Arg | Thr | Ile | Gln | Leu | Glu | Tyr | Thr | Asp | Ala | Lys | Glu | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Leu | Gln | Ala | Ala | Arg | Lys | Ala | Pro | Ile | Ala | Ala | Leu | Gly | Phe | Arg |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ile | Gln | Cys | Asn | Lys | Trp | Ala | Ile | Leu | Val | Arg | Leu | Leu | Leu | Gly | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Pro | Glu | Arg | Ser | Ile | Phe | Thr | Gln | Lys | Gly | Met | Glu | Lys | Ala | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Pro | Tyr | Phe | Glu | Leu | Thr | Asn | Ala | Val | Arg | Ile | Gly | Asp | Leu | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Phe | Arg | Thr | Val | Gln | Glu | Lys | Phe | Leu | Asp | Thr | Phe | Ala | Gln | Asp |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | Thr | His | Asn | Leu | Ile | Val | Arg | Leu | Arg | His | Asn | Val | Ile | Arg | Thr |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Leu | Arg | Asn | Ile | Ser | Ile | Ser | Tyr | Ser | Arg | Ile | Ser | Leu | Pro | Asp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Val | Ala | Lys | Lys | Leu | Arg | Leu | Asn | Ser | Glu | Asn | Pro | Gly |     |     |     |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Asn | Leu | Lys | Glu | Ile | Ala | Ala | Leu | Ile | Asp | Thr | Gly | Ser | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Lys | Glu | Val | Arg | Arg | Ile | Ala | Arg | Ala | Val | Arg | Leu | Thr | Ile | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Arg | Gln | Lys | Leu | Thr | Gly | Ser | Val | Leu | Ser | Ser | Phe | Leu | Asp | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Val | Pro | Gly | Ser | Glu | Ala | His | Ser | Arg | Leu | Ser | Ser | Phe | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Lys | Gly | Asp | Glu | His | Asp | Met | Glu | Val | Asp | Thr | Ala | Ser | Ser | Ala |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Gln | Ala | Ala | Pro | Ser | Lys | His | Leu | Pro | Ala | Glu | Leu | Glu | Ile | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Tyr | Phe | Ile | Val | Leu | Leu | Phe | Leu | Ile | Asp | Gln | Lys | Lys | Tyr | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ala | Lys | Ala | Cys | Ser | Ser | Ala | Ser | Ile | Ala | Arg | Leu | Lys | Asn | Val |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Arg | Arg | Thr | Ile | Asp | Val | Ile | Ala | Ser | Arg | Leu | Tyr | Phe | Tyr | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Leu | Ser | Tyr | Glu | Gln | Thr | Gly | Asp | Leu | Ala | Glu | Ile | Arg | Gly | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Leu | Ala | Leu | His | His | Ser | Ala | Thr | Leu | Arg | His | Asp | Glu | Leu | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Gln | Glu | Thr | Leu | Leu | Asn | Leu | Leu | Leu | Arg | Asn | Tyr | Leu | His | Tyr | Asn |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Tyr | Asp | Gln | Ala | Glu | Lys | Leu | Arg | Ser | Lys | Ala | Pro | Arg | Phe | Glu |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ala | His | Ser | Asn | Gln | Gln | Phe | Cys | Arg | Tyr | Leu | Phe | Tyr | Leu | Gly | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Arg | Thr | Ile | Gln | Leu | Glu | Tyr | Thr | Asp | Ala | Lys | Glu | Ser | Leu | Leu |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Gln | Ala | Ala | Arg | Lys | Ala | Pro | Ile | Ala | Ala | Leu | Gly | Phe | Arg | Ile | Gln |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Cys | Asn | Lys | Trp | Ala | Ile | Leu | Val | Arg | Leu | Leu | Leu | Gly | Glu | Ile | Pro |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Arg | Ser | Ile | Phe | Thr | Gln | Lys | Gly | Met | Glu | Lys | Ala | Leu | Arg | Pro |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Tyr | Phe | Glu | Leu | Thr | Asn | Ala | Val | Arg | Ile | Gly | Asp | Leu | Glu | Leu | Phe |
|     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Arg | Thr | Val | Gln | Glu | Lys | Phe | Leu | Asp | Thr | Phe | Ala | Gln | Asp | Arg | Thr |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| His | Asn | Leu | Ile | Val | Arg | Leu | Arg | His | Asn | Val | Ile | Arg | Thr | Gly | Leu |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Arg | Asn | Ile | Ser | Ile | Ser | Tyr | Ser | Arg | Ile | Ser | Leu | Pro | Asp | Val | Ala |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Lys | Lys | Leu | Arg | Leu | Asn | Ser | Glu | Asn | Pro | Gly |     |     |     |     |     |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1905 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1905  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

```
acactgttac tctctctctc tcttcttctt cttcttcttc ttctgcatct catcgacatc 60
atccttttccc atggctgatg catacgagcc ttatcatgtt cttcaacaaa gccggcgaga 120
caaacttctgt attccatctc tcgattccca cttccacttt caccctcctc ctccctcctc 180
ctccggcggc ggaggtggcg tctttcctct cgctgattcc gatttcctcg cagccggtgg 240
ctttcactcc aacaacaaca acaaccacat atctaaccct agctacagta atttcatggg 300
atttctcggt ggcccttctt cttcttcata caccgcagtc gccgtcgccg gagatcattc 360
ctttaacgcc ggactttctt ccggagacgt tcttgtcttc aaacccgagc ctctatctct 420
atctttgtcc tctcacccta gactcgctta cgatctagtc gttcccgggtg ttgttaactc 480
cggattctgt agatctgccg gtgaagccaa cgccgccgcc gtcaccatcg cgtctagaag 540
ctctggtoct ctcggaacct tcacgggcta cgcgtcgatt cttaaaggat caaggttctt 600
gaaaccagca cagatgcttc ttgatgagtt ttgtaatgtg ggctcgtggga tttacaccga 660
caaagtcata gacgacgatg attcttctct gctttttgat ccgacggttg agaatctctg 720
cgggtgttct gatggcggcg gaggagataa tggaaagaaa aaatcaaaac tcatctccat 780
gctcgacgag gtttacaaga ggtataagca atactatgag cagctacaag ctgtgatggg 840
atcattcgaa tgcgttgacg gtctcgggca cgctgctccg tacgctaact tagccttgaa 900
agcgttgtct aagcatttca agtgtttgaa gaatgctata acggaccagc ttcaattcag 960
ccacaacaac aagatccaac aacaacaaca atgtggtcat ccgatgaact ctgagaataa 1020
gactgattct ttaagatttg gaggaagtga tagttctaga ggcttatgtt ctgctgggtca 1080
aagacatgga tttcctgatc atcatgctcc tgtttgagga ccgcaccgtg gcoctaccga 1140
acgtgctgtt actgttctaa gggcttggct cttcgatcat ttcttgcatc cttatccaac 1200
agatacagac aaactcatgc tggctaagca gacaggtctc tccagaaatc aggtatcgaa 1260
ttgggttcata aacgcaagag ttagggtttg gaagccgatg gtggaagaga ttcacatgct 1320
ggagactcga caatctcaga gatcttcttc ttcctcttgg agagacgaac gtactagcac 1380
cacggtcttc cctgacaaca acaacaacaa cccatcttcg tctcgggcac agcaaagacc 1440
taacaactca tctccgccta gacgggcacg aaacgacgac gttcatggca caaacaacaa 1500
caacagctat gtaaacagtg ggagcggcgg cggtagtgcg gttggtttct cgtatggaat 1560
tgggtcgtcg aatgtgccgg tgatgaatag cagcacaaac ggaggagtgt ctttgacgtt 1620
agggcttcat catcagattg ggttaccgga gccttttccg atgacaactg ctcagagggt 1680
tgggcttgat ggtggtagtg gcgatggtgg tgggtgggtat gaagggcaaa atcgtcagtt 1740
tgggagagat tttattggtg gtagtaatca tcagtttcta catgattttg taggttgaga 1800
ttatttgtgt ggaaaggaaa aaatatgttt gacgtttggg tatgtataag aagatatggg 1860
ggaattgaaa tgcataatgat gtgtatatta gaatgtttct tcttc
```

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 598 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..598  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

```
His Cys Tyr Ser Leu Ser Leu Phe Phe Phe Phe Phe Phe Cys Ile
1 5 10 15
Ser Ser Thr Ser Ser Phe Pro Met Ala Asp Ala Tyr Glu Pro Tyr His
20 25 30
Val Leu Gln Gln Ser Arg Arg Asp Lys Leu Arg Ile Pro Ser Leu Asp
35 40 45
Ser His Phe His Phe His Pro Pro Pro Pro Pro Ser Ser Gly Gly Gly
50 55 60
```

|        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly 65 | Gly | Val | Phe | Pro | Leu | Ala | Asp | Ser | Asp | Phe | Leu | Ala | Ala | Gly | Gly |
| Phe    | His | Ser | Asn | Asn | Asn | Asn | Asn | His | Ile | Ser | Asn | Pro | Ser | Tyr | Ser |
|        |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn    | Phe | Met | Gly | Phe | Leu | Gly | Gly | Pro | Ser | Ser | Ser | Ser | Ser | Thr | Ala |
|        |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Val    | Ala | Val | Ala | Gly | Asp | His | Ser | Phe | Asn | Ala | Gly | Leu | Ser | Ser | Gly |
|        |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Asp    | Val | Leu | Val | Phe | Lys | Pro | Glu | Pro | Leu | Ser | Leu | Ser | Leu | Ser | Ser |
|        |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |
| His    | Pro | Arg | Leu | Ala | Tyr | Asp | Leu | Val | Val | Pro | Gly | Val | Val | Asn | Ser |
| 145    |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly    | Phe | Cys | Arg | Ser | Ala | Gly | Glu | Ala | Asn | Ala | Ala | Ala | Ala | Val | Thr |
|        |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |
| Ala    | Ser | Arg | Ser | Ser | Gly | Pro | Leu | Gly | Pro | Phe | Thr | Gly | Tyr | Ala | Ser |
|        |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Ile    | Leu | Lys | Gly | Ser | Arg | Phe | Leu | Lys | Pro | Ala | Gln | Met | Leu | Leu | Asp |
|        |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Glu    | Phe | Cys | Asn | Val | Gly | Arg | Gly | Ile | Tyr | Thr | Asp | Lys | Val | Ile | Asp |
|        |     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |
| Asp    | Asp | Asp | Ser | Ser | Leu | Leu | Phe | Asp | Pro | Thr | Val | Glu | Asn | Leu | Cys |
| 225    |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly    | Val | Ser | Asp | Gly | Gly | Gly | Gly | Asp | Asn | Gly | Lys | Lys | Lys | Ser | Lys |
|        |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |
| Leu    | Ile | Ser | Met | Leu | Asp | Glu | Val | Tyr | Lys | Arg | Tyr | Lys | Gln | Tyr | Tyr |
|        |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Glu    | Gln | Leu | Gln | Ala | Val | Met | Gly | Ser | Phe | Glu | Cys | Val | Ala | Gly | Leu |
|        |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Gly    | His | Ala | Ala | Pro | Tyr | Ala | Asn | Leu | Ala | Leu | Lys | Ala | Leu | Ser | Lys |
|        |     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |
| His    | Phe | Lys | Cys | Leu | Lys | Asn | Ala | Ile | Thr | Asp | Gln | Leu | Gln | Phe | Ser |
| 305    |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| His    | Asn | Asn | Lys | Ile | Gln | Gln | Gln | Gln | Gln | Cys | Gly | His | Pro | Met | Asn |
|        |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |
| Ser    | Glu | Asn | Lys | Thr | Asp | Ser | Leu | Arg | Phe | Gly | Gly | Ser | Asp | Ser | Ser |
|        |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Arg    | Gly | Leu | Cys | Ser | Ala | Gly | Gln | Arg | His | Gly | Phe | Pro | Asp | His | His |
|        |     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |
| Ala    | Pro | Val | Trp | Arg | Pro | His | Arg | Gly | Leu | Pro | Glu | Arg | Ala | Val | Thr |
|        |     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |
| Val    | Leu | Arg | Ala | Trp | Leu | Phe | Asp | His | Phe | Leu | His | Pro | Tyr | Pro | Thr |
| 385    |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Asp    | Thr | Asp | Lys | Leu | Met | Leu | Ala | Lys | Gln | Thr | Gly | Leu | Ser | Arg | Asn |
|        |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |     | 415 |
| Gln    | Val | Ser | Asn | Trp | Phe | Ile | Asn | Ala | Arg | Val | Arg | Val | Trp | Lys | Pro |
|        |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Met    | Val | Glu | Glu | Ile | His | Met | Leu | Glu | Thr | Arg | Gln | Ser | Gln | Arg | Ser |
|        |     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Ser    | Ser | Ser | Ser | Trp | Arg | Asp | Glu | Arg | Thr | Ser | Thr | Thr | Val | Phe | Pro |
|        |     |     | 450 |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Asp    | Asn | Asn | Asn | Asn | Asn | Pro | Ser | Ser | Ser | Ser | Ala | Gln | Gln | Arg | Pro |
| 465    |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Asn    | Asn | Ser | Ser | Pro | Pro | Arg | Arg | Ala | Arg | Asn | Asp | Asp | Val | His | Gly |
|        |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Thr    | Asn | Asn | Asn | Asn | Ser | Tyr | Val | Asn | Ser | Gly | Ser | Gly | Gly | Gly | Ser |
|        |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Ala    | Val | Gly | Phe | Ser | Tyr | Gly | Ile | Gly | Ser | Ser | Asn | Val | Pro | Val | Met |
|        |     |     | 515 |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Asn    | Ser | Ser | Thr | Asn | Gly | Gly | Val | Ser | Leu | Thr | Leu | Gly | Leu | His | His |
|        |     |     | 530 |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Gln    | Ile | Gly | Leu | Pro | Glu | Pro | Phe | Pro | Met | Thr | Thr | Ala | Gln | Arg | Phe |

545                      550                      555                      560  
Gly Leu Asp Gly Gly Ser Gly Asp Gly Gly Gly Gly Tyr Glu Gly Gln  
                                 565                      570                      575  
Asn Arg Gln Phe Gly Arg Asp Phe Ile Gly Gly Ser Asn His Gln Phe  
                                 580                      585                      590  
Leu His Asp Phe Val Gly  
                                 595

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 575 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..575

(D) OTHER INFORMATION: / Ceres Seq. ID 1498315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Met Ala Asp Ala Tyr Glu Pro Tyr His Val Leu Gln Gln Ser Arg Arg  
1                      5                      10                      15  
Asp Lys Leu Arg Ile Pro Ser Leu Asp Ser His Phe His Phe His Pro  
                                 20                      25                      30  
Pro Pro Pro Pro Ser Ser Gly Gly Gly Gly Gly Val Phe Pro Leu Ala  
                                 35                      40                      45  
Asp Ser Asp Phe Leu Ala Ala Gly Gly Phe His Ser Asn Asn Asn Asn  
50                      55                      60  
Asn His Ile Ser Asn Pro Ser Tyr Ser Asn Phe Met Gly Phe Leu Gly  
65                      70                      75                      80  
Gly Pro Ser Ser Ser Ser Ser Thr Ala Val Ala Val Ala Gly Asp His  
                                 85                      90                      95  
Ser Phe Asn Ala Gly Leu Ser Ser Gly Asp Val Leu Val Phe Lys Pro  
                                 100                      105                      110  
Glu Pro Leu Ser Leu Ser Leu Ser His Pro Arg Leu Ala Tyr Asp  
                                 115                      120                      125  
Leu Val Val Pro Gly Val Val Asn Ser Gly Phe Cys Arg Ser Ala Gly  
130                      135                      140  
Glu Ala Asn Ala Ala Ala Val Thr Ile Ala Ser Arg Ser Ser Gly Pro  
145                      150                      155                      160  
Leu Gly Pro Phe Thr Gly Tyr Ala Ser Ile Leu Lys Gly Ser Arg Phe  
                                 165                      170                      175  
Leu Lys Pro Ala Gln Met Leu Leu Asp Glu Phe Cys Asn Val Gly Arg  
                                 180                      185                      190  
Gly Ile Tyr Thr Asp Lys Val Ile Asp Asp Asp Asp Ser Ser Leu Leu  
                                 195                      200                      205  
Phe Asp Pro Thr Val Glu Asn Leu Cys Gly Val Ser Asp Gly Gly Gly  
210                      215                      220  
Gly Asp Asn Gly Lys Lys Lys Ser Lys Leu Ile Ser Met Leu Asp Glu  
225                      230                      235                      240  
Val Tyr Lys Arg Tyr Lys Gln Tyr Tyr Glu Gln Leu Gln Ala Val Met  
                                 245                      250                      255  
Gly Ser Phe Glu Cys Val Ala Gly Leu Gly His Ala Ala Pro Tyr Ala  
                                 260                      265                      270  
Asn Leu Ala Leu Lys Ala Leu Ser Lys His Phe Lys Cys Leu Lys Asn  
275                      280                      285  
Ala Ile Thr Asp Gln Leu Gln Phe Ser His Asn Asn Lys Ile Gln Gln  
290                      295                      300  
Gln Gln Gln Cys Gly His Pro Met Asn Ser Glu Asn Lys Thr Asp Ser  
305                      310                      315                      320  
Leu Arg Phe Gly Gly Ser Asp Ser Ser Arg Gly Leu Cys Ser Ala Gly  
                                 325                      330                      335

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Arg | His | Gly | Phe | Pro | Asp | His | His | Ala | Pro | Val | Trp | Arg | Pro | His |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Arg | Gly | Leu | Pro | Glu | Arg | Ala | Val | Thr | Val | Leu | Arg | Ala | Trp | Leu | Phe |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asp | His | Phe | Leu | His | Pro | Tyr | Pro | Thr | Asp | Thr | Asp | Lys | Leu | Met | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Lys | Gln | Thr | Gly | Leu | Ser | Arg | Asn | Gln | Val | Ser | Asn | Trp | Phe | Ile |
|     | 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Asn | Ala | Arg | Val | Arg | Val | Trp | Lys | Pro | Met | Val | Glu | Glu | Ile | His | Met |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Leu | Glu | Thr | Arg | Gln | Ser | Gln | Arg | Ser | Ser | Ser | Ser | Ser | Trp | Arg | Asp |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Glu | Arg | Thr | Ser | Thr | Thr | Val | Phe | Pro | Asp | Asn | Asn | Asn | Asn | Asn | Pro |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |
| Ser | Ser | Ser | Ser | Ala | Gln | Gln | Arg | Pro | Asn | Asn | Ser | Ser | Pro | Pro | Arg |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Arg | Ala | Arg | Asn | Asp | Asp | Val | His | Gly | Thr | Asn | Asn | Asn | Asn | Ser | Tyr |
|     | 465 |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Val | Asn | Ser | Gly | Ser | Gly | Gly | Gly | Ser | Ala | Val | Gly | Phe | Ser | Tyr | Gly |
|     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Ile | Gly | Ser | Ser | Asn | Val | Pro | Val | Met | Asn | Ser | Ser | Thr | Asn | Gly | Gly |
|     |     | 500 |     |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Val | Ser | Leu | Thr | Leu | Gly | Leu | His | His | Gln | Ile | Gly | Leu | Pro | Glu | Pro |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Phe | Pro | Met | Thr | Thr | Ala | Gln | Arg | Phe | Gly | Leu | Asp | Gly | Gly | Ser | Gly |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Asp | Gly | Gly | Gly | Gly | Tyr | Glu | Gly | Gln | Asn | Arg | Gln | Phe | Gly | Arg | Asp |
|     | 545 |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Phe | Ile | Gly | Gly | Ser | Asn | His | Gln | Phe | Leu | His | Asp | Phe | Val | Gly |     |
|     |     |     | 565 |     |     |     |     | 570 |     |     |     |     |     | 575 |     |

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 500 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..500

(D) OTHER INFORMATION: / Ceres Seq. ID 1498316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Phe | Leu | Gly | Gly | Pro | Ser | Ser | Ser | Ser | Thr | Ala | Val | Ala |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Ala | Gly | Asp | His | Ser | Phe | Asn | Ala | Gly | Leu | Ser | Ser | Gly | Asp | Val |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Phe | Lys | Pro | Glu | Pro | Leu | Ser | Leu | Ser | Leu | Ser | Ser | His | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Leu | Ala | Tyr | Asp | Leu | Val | Val | Pro | Gly | Val | Val | Asn | Ser | Gly | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Arg | Ser | Ala | Gly | Glu | Ala | Asn | Ala | Ala | Ala | Val | Thr | Ile | Ala | Ser |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ser | Ser | Gly | Pro | Leu | Gly | Pro | Phe | Thr | Gly | Tyr | Ala | Ser | Ile | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Gly | Ser | Arg | Phe | Leu | Lys | Pro | Ala | Gln | Met | Leu | Leu | Asp | Glu | Phe |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Asn | Val | Gly | Arg | Gly | Ile | Tyr | Thr | Asp | Lys | Val | Ile | Asp | Asp | Asp |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ser | Ser | Leu | Leu | Phe | Asp | Pro | Thr | Val | Glu | Asn | Leu | Cys | Gly | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Asp | Gly | Gly | Gly | Gly | Asp | Asn | Gly | Lys | Lys | Lys | Ser | Lys | Leu | Ile |

(2) INFORMATION FOR SEQ ID NO:339:

(A) LENGTH: 755 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

```
(ix) FEATURE:
```

(A) NAM

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:339:

tcgtca agaaaaaaaaat tcgattttttt tgcgctctttt g

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| atggtctggc | gtggaaaaac | tcttggaatcc | ggtggggcg  | agaaagctac | atctcggagt  | 120 |
| agcaaagccg | gtcttcaatt | cccgggtggg  | cgtatcgctc | gtttcttaaa | agccggtataa | 180 |
| tacgccgaac | gtgttggtgc | cggtgctccg  | gtttatytgc | ccgccgttct | cgaatatattg | 240 |



(2) INFORMATION FOR SEO ID NO:340:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1498318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Val | Lys | Lys | Lys | Ile | Arg | Phe | Phe | Cys | Ala | Leu | Cys | Gly | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Leu | Lys | Met | Ala | Gly | Arg | Gly | Lys | Thr | Leu | Gly | Ser | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Lys | Lys | Ala | Thr | Ser | Arg | Ser | Ser | Lys | Ala | Gly | Leu | Gln | Phe | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Gly | Arg | Ile | Ala | Arg | Phe | Leu | Lys | Ala | Gly | Lys | Tyr | Ala | Glu | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Gly | Ala | Gly | Ala | Pro | Val | Tyr | Xaa | Ala | Ala | Val | Leu | Glu | Tyr | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Ala | Glu | Val | Leu | Glu | Leu | Ala | Gly | Asn | Ala | Ala | Arg | Asp | Asn | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Thr | Arg | Ile | Val | Val | Ser | Cys | Cys | Val | Ser | Ser |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:341:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1498319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

[illegible]

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1233  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498320  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

```
atccagaaaa aacaaaaaaa acaaaaaaat aataaaacaa aaaaatatct tttttttttc 60
taataaaaaa aaaaaaaata aataaatatg gaatacacaa atgtgtccat tttattaggc 120
atgttggtga tctttgtttc accaatggtg ttcgcagatg atttgacacc aatcccagag 180
ggcaaacccc aagtgggtgca gtggttcaat acccacgttg gtccattggt tcaacgtaaa 240
ggcttagatc ctgctctcgt agctgctgag gctgctccac gtatcatcaa cgtgaatcca 300
aagggaggtg aattcaaaac actaacagag gcaataaaga gcgttcctgc aggggaacaca 360
aagcgggtga tcataaagat ggctcctggt gagtacagag agaaggtcac tatcgacagg 420
aacaaccctt tcattacatt gatgggacaa cccaatgcc a tgctgttat cacctacgac 480
ggtaccgccg ccaagtatgg aaccgttgat agtgccctctc tcattatctt atccgactat 540
ttcatggccg ttaacatcgt cgtaaagaac actgcaccgg caccagatgg taaaactaag 600
ggagcacaag ccttatccat gagaatctcc ggaaactttg ctgctttcta caactgcaaa 660
ttctacggtt tccaagatac aatctgtgat gataccggaa accatttctt caaggattgt 720
tacgtcgaag gaacattcga tttcatcttc ggaagtggaa cctctatgta cttgggaaca 780
caattgcacg tggttggaga cgggtattaga gtgatcgag cgcatgcagg aaagagcgca 840
gaagaaaata gtggatactc tttcgtgcac tgcaaggtga ctggaactgg aggagtaatc 900
tatttgggaa gagcatggat gagccaccct aaggttgtct atgcctacac cgagatgacc 960
agcgttgtca accccaccgg atggcaagaa aacaagactc ccgcacatga caagaccgtg 1020
ttctacggag agtacaagtg ttcaggacca gggtcacaca aagccaagag agtgccattc 1080
acacaagaca tcgacgacaa agaagctaac cgtttcttat cctcggcta catccaagga 1140
tccaagtggc ttctcccacc acccgctttg taaattcttt aatatcaacc tattaaaatt 1200
aaaattaaaa cgtaaaacta aaattaaaac ttc
```

(2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 361 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..361  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498321  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```
Met Glu Tyr Thr Asn Val Ser Ile Leu Leu Gly Met Leu Val Ile Phe
1 5 10 15
Val Ser Pro Met Val Phe Ala Asp Asp Leu Thr Pro Ile Pro Glu Gly
20 25 30
Lys Pro Gln Val Val Gln Trp Phe Asn Thr His Val Gly Pro Leu Val
35 40 45
Gln Arg Lys Gly Leu Asp Pro Ala Leu Val Ala Ala Glu Ala Ala Pro
50 55 60
Arg Ile Ile Asn Val Asn Pro Lys Gly Gly Glu Phe Lys Thr Leu Thr
65 70 75 80
Asp Ala Ile Lys Ser Val Pro Ala Gly Asn Thr Lys Arg Val Ile Ile
85 90 95
Lys Met Ala Pro Gly Glu Tyr Arg Glu Lys Val Thr Ile Asp Arg Asn
100 105 110
Lys Pro Phe Ile Thr Leu Met Gly Gln Pro Asn Ala Met Pro Val Ile
115 120 125
Thr Tyr Asp Gly Thr Ala Ala Lys Tyr Gly Thr Val Asp Ser Ala Ser
130 135 140
```

```

Leu Ile Ile Leu Ser Asp Tyr Phe Met Ala Val Asn Ile Val Val Lys
145 150 155 160
Asn Thr Ala Pro Ala Pro Asp Gly Lys Thr Lys Gly Ala Gln Ala Leu
 165 170 175
Ser Met Arg Ile Ser Gly Asn Phe Ala Ala Phe Tyr Asn Cys Lys Phe
 180 185 190
Tyr Gly Phe Gln Asp Thr Ile Cys Asp Asp Thr Gly Asn His Phe Phe
 195 200 205
Lys Asp Cys Tyr Val Glu Gly Thr Phe Asp Phe Ile Phe Gly Ser Gly
 210 215 220
Thr Ser Met Tyr Leu Gly Thr Gln Leu His Val Val Gly Asp Gly Ile
225 230 235 240
Arg Val Ile Ala Ala His Ala Gly Lys Ser Ala Glu Glu Asn Ser Gly
 245 250 255
Tyr Ser Phe Val His Cys Lys Val Thr Gly Thr Gly Gly Val Ile Tyr
 260 265 270
Leu Gly Arg Ala Trp Met Ser His Pro Lys Val Val Tyr Ala Tyr Thr
 275 280 285
Glu Met Thr Ser Val Val Asn Pro Thr Gly Trp Gln Glu Asn Lys Thr
 290 295 300
Pro Ala His Asp Lys Thr Val Phe Tyr Gly Glu Tyr Lys Cys Ser Gly
305 310 315 320
Pro Gly Ser His Lys Ala Lys Arg Val Pro Phe Thr Gln Asp Ile Asp
 325 330 335
Asp Lys Glu Ala Asn Arg Phe Leu Ser Leu Gly Tyr Ile Gln Gly Ser
 340 345 350
Lys Trp Leu Leu Pro Pro Pro Ala Leu
 355 360

```

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..350
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```

Met Leu Val Ile Phe Val Ser Pro Met Val Phe Ala Asp Asp Leu Thr
1 5 10 15
Pro Ile Pro Glu Gly Lys Pro Gln Val Val Gln Trp Phe Asn Thr His
 20 25 30
Val Gly Pro Leu Val Gln Arg Lys Gly Leu Asp Pro Ala Leu Val Ala
 35 40 45
Ala Glu Ala Ala Pro Arg Ile Ile Asn Val Asn Pro Lys Gly Gly Glu
 50 55 60
Phe Lys Thr Leu Thr Asp Ala Ile Lys Ser Val Pro Ala Gly Asn Thr
65 70 75 80
Lys Arg Val Ile Ile Lys Met Ala Pro Gly Glu Tyr Arg Glu Lys Val
 85 90 95
Thr Ile Asp Arg Asn Lys Pro Phe Ile Thr Leu Met Gly Gln Pro Asn
 100 105 110
Ala Met Pro Val Ile Thr Tyr Asp Gly Thr Ala Ala Lys Tyr Gly Thr
 115 120 125
Val Asp Ser Ala Ser Leu Ile Ile Leu Ser Asp Tyr Phe Met Ala Val
 130 135 140
Asn Ile Val Val Lys Asn Thr Ala Pro Ala Pro Asp Gly Lys Thr Lys
145 150 155 160
Gly Ala Gln Ala Leu Ser Met Arg Ile Ser Gly Asn Phe Ala Ala Phe

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Asn | Cys | Lys | Phe | Tyr | Gly | Phe | Gln | Asp | Thr | Ile | Cys | Asp | Asp | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Asn | His | Phe | Phe | Lys | Asp | Cys | Tyr | Val | Glu | Gly | Thr | Phe | Asp | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Phe | Gly | Ser | Gly | Thr | Ser | Met | Tyr | Leu | Gly | Thr | Gln | Leu | His | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Gly | Asp | Gly | Ile | Arg | Val | Ile | Ala | Ala | His | Ala | Gly | Lys | Ser | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Glu | Asn | Ser | Gly | Tyr | Ser | Phe | Val | His | Cys | Lys | Val | Thr | Gly | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Gly | Val | Ile | Tyr | Leu | Gly | Arg | Ala | Trp | Met | Ser | His | Pro | Lys | Val |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Tyr | Ala | Tyr | Thr | Glu | Met | Thr | Ser | Val | Val | Asn | Pro | Thr | Gly | Trp |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gln | Glu | Asn | Lys | Thr | Pro | Ala | His | Asp | Lys | Thr | Val | Phe | Tyr | Gly | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Tyr | Lys | Cys | Ser | Gly | Pro | Gly | Ser | His | Lys | Ala | Lys | Arg | Val | Pro | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Gln | Asp | Ile | Asp | Asp | Lys | Glu | Ala | Asn | Arg | Phe | Leu | Ser | Leu | Gly |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Tyr | Ile | Gln | Gly | Ser | Lys | Trp | Leu | Leu | Pro | Pro | Pro | Ala | Leu |     |     |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1498323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Phe | Ala | Asp | Asp | Leu | Thr | Pro | Ile | Pro | Glu | Gly | Lys | Pro | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Gln | Trp | Phe | Asn | Thr | His | Val | Gly | Pro | Leu | Val | Gln | Arg | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Asp | Pro | Ala | Leu | Val | Ala | Glu | Ala | Ala | Pro | Arg | Ile | Ile |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asn | Val | Asn | Pro | Lys | Gly | Gly | Glu | Phe | Lys | Thr | Leu | Thr | Asp | Ala | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Ser | Val | Pro | Ala | Gly | Asn | Thr | Lys | Arg | Val | Ile | Ile | Lys | Met | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Gly | Glu | Tyr | Arg | Glu | Lys | Val | Thr | Ile | Asp | Arg | Asn | Lys | Pro | Phe |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Thr | Leu | Met | Gly | Gln | Pro | Asn | Ala | Met | Pro | Val | Ile | Thr | Tyr | Asp |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Thr | Ala | Ala | Lys | Tyr | Gly | Thr | Val | Asp | Ser | Ala | Ser | Leu | Ile | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Asp | Tyr | Phe | Met | Ala | Val | Asn | Ile | Val | Val | Lys | Asn | Thr | Ala |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Ala | Pro | Asp | Gly | Lys | Thr | Lys | Gly | Ala | Gln | Ala | Leu | Ser | Met | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Ser | Gly | Asn | Phe | Ala | Ala | Phe | Tyr | Asn | Cys | Lys | Phe | Tyr | Gly | Phe |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Asp | Thr | Ile | Cys | Asp | Asp | Thr | Gly | Asn | His | Phe | Phe | Lys | Asp | Cys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Val | Glu | Gly | Thr | Phe | Asp | Phe | Ile | Phe | Gly | Ser | Gly | Thr | Ser | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |

Tyr Leu Gly Thr Gln Leu His Val Val Gly Asp Gly Ile Arg Val Ile  
210 215 220  
Ala Ala His Ala Gly Lys Ser Ala Glu Glu Asn Ser Gly Tyr Ser Phe  
225 230 235 240  
Val His Cys Lys Val Thr Gly Thr Gly Gly Val Ile Tyr Leu Gly Arg  
245 250 255  
Ala Trp Met Ser His Pro Lys Val Val Tyr Ala Tyr Thr Glu Met Thr  
260 265 270  
Ser Val Val Asn Pro Thr Gly Trp Gln Glu Asn Lys Thr Pro Ala His  
275 280 285  
Asp Lys Thr Val Phe Tyr Gly Glu Tyr Lys Cys Ser Gly Pro Gly Ser  
290 295 300  
His Lys Ala Lys Arg Val Pro Phe Thr Gln Asp Ile Asp Asp Lys Glu  
305 310 315 320  
Ala Asn Arg Phe Leu Ser Leu Gly Tyr Ile Gln Gly Ser Lys Trp Leu  
325 330 335  
Leu Pro Pro Pro Ala Leu  
340

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1415
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cctttctacc catttcgtct ccttcatttt gacgttttct ttagatctgt taataatcca  | 60   |
| tccatggctt ggtctagtca ctagtgggtg tatctctctg tgtggaagaa aaagcaagggt | 120  |
| tttttgatca cttggattgt ttttaagatat ggcaactttg aacccttttg atttgttgga | 180  |
| tgatgatgct gaggatccaa gccagctcgc tgtttccatc gagaagattg ataagtccaa  | 240  |
| gaaatctgga ccggtttcga gcttgccctgc taagttagct cctaagcttc cctctaagcc | 300  |
| acttcctcct gctcaagccg tgagagaggg caggagtgtat gctccacgtg gtggtggagg | 360  |
| ccgtggagga tttaatcgtg gtcgtgggtg ttacaaccgt gatgatggta acaatggata  | 420  |
| tttaggggga tacactaagc cctcagatga aggagatgtt tcaaagtctt cttacgagag  | 480  |
| gcgtggcggg ggtgaagggg agcgtcctcg aagggccttt gagcgtcgtg gtggaactgg  | 540  |
| cagagggagt gacttcaagc gtgacggatc tggtcgtggg aattggggaa ctccagggga  | 600  |
| agagatagct gctgagactg aagcagtagc tgggtgttgag actgagaagg atggttgaga | 660  |
| gaagccagct gttgatgatg tagctgctga tgctaacaag gagaatactg ttggttgagg  | 720  |
| gaaagagcct gaggataagg aaatgactct tgatgagtat gagaaaatac ttgaggagaa  | 780  |
| gaaaaaggca cttcaatcat taaccacctc tgagaggaaa gttgatacga aagtgtttga  | 840  |
| atcaatgcaa caactgtcaa acaagaagtc taatgatgaa atcttcatca agctgggttc  | 900  |
| tgataaggac aaacgcaaag atgacaaaga agagaaggct aagaaggctg tgagcatcaa  | 960  |
| tgagtttctg aagccagcag aggggtggga ctactaccga ggaggccgtg gtggccgtgg  | 1020 |
| acgtggtggt cgtggccgtg gaggtgtttc tagtggcgaa tctggtggtt accgtaatga  | 1080 |
| agctgcacca gctattggag atgctgctca gttcccatct cttgggggca agtaagatac  | 1140 |
| atccatgata acgtccatac tcgtgcatcc tcctttagga ttttgtgcga ggatttactg  | 1200 |
| tttactggtc tctcgttgtc agatgtaaata aattaggtgt cgtcgtcagt ttttagattt | 1260 |
| tatgctaaac tttacacttg ttggtgttct ttacttttga aacactacac tcttcttagt  | 1320 |
| tttaccattt tactcgtttt gtgtttgttg ttttcttatt gggatatgaa acatgttttg  | 1380 |

agacggacat atctaattgt atcggggttg agtct

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1498325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Met Ala Thr Leu Asn Pro Phe Asp Leu Leu Asp Asp Asp Ala Glu Asp  
1 5 10 15  
Pro Ser Gln Leu Ala Val Ser Ile Glu Lys Ile Asp Lys Ser Lys Lys  
20 25 30  
Ser Gly Pro Val Ser Ser Leu Pro Ala Lys Ser Ala Pro Lys Leu Pro  
35 40 45  
Ser Lys Pro Leu Pro Pro Ala Gln Ala Val Arg Glu Ala Arg Ser Asp  
50 55 60  
Ala Pro Arg Gly Gly Gly Gly Arg Gly Gly Phe Asn Arg Gly Arg Gly  
65 70 75 80  
Gly Tyr Asn Arg Asp Asp Gly Asn Asn Gly Tyr Leu Gly Gly Tyr Thr  
85 90 95  
Lys Pro Ser Asp Glu Gly Asp Val Ser Lys Ser Ser Tyr Glu Arg Arg  
100 105 110  
Gly Gly Gly Glu Gly Glu Arg Pro Arg Arg Ala Phe Glu Arg Arg Ser  
115 120 125  
Gly Thr Gly Arg Gly Ser Asp Phe Lys Arg Asp Gly Ser Gly Arg Gly  
130 135 140  
Asn Trp Gly Thr Pro Gly Glu Glu Ile Ala Ala Glu Thr Glu Ala Val  
145 150 155 160  
Ala Gly Val Glu Thr Glu Lys Asp Val Gly Glu Lys Pro Ala Val Asp  
165 170 175  
Asp Val Ala Ala Asp Ala Asn Lys Glu Asn Thr Val Val Glu Glu Lys  
180 185 190  
Glu Pro Glu Asp Lys Glu Met Thr Leu Asp Glu Tyr Glu Lys Ile Leu  
195 200 205  
Glu Glu Lys Lys Lys Ala Leu Gln Ser Leu Thr Thr Ser Glu Arg Lys  
210 215 220  
Val Asp Thr Lys Val Phe Glu Ser Met Gln Gln Leu Ser Asn Lys Lys  
225 230 235 240  
Ser Asn Asp Glu Ile Phe Ile Lys Leu Gly Ser Asp Lys Asp Lys Arg  
245 250 255  
Lys Asp Asp Lys Glu Glu Lys Ala Lys Lys Ala Val Ser Ile Asn Glu  
260 265 270  
Phe Leu Lys Pro Ala Glu Gly Gly Asn Tyr Tyr Arg Gly Gly Arg Gly  
275 280 285  
Gly Arg Gly Arg Gly Gly Arg Gly Arg Gly Val Ser Ser Gly Glu  
290 295 300  
Ser Gly Gly Tyr Arg Asn Glu Ala Ala Pro Ala Ile Gly Asp Ala Ala  
305 310 315 320  
Gln Phe Pro Ser Leu Gly Gly Lys  
325

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 525 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..525

(D) OTHER INFORMATION: / Ceres Seq. ID 1498326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

acaaacatta ctcattcaca aaaccatctt aaagcaacta cacaaatctt gaaattttct  
catattttct atttactata taaactttta atcaaataca gattaactat ggctgaggag

60

120

tacaagaaca acgttcccga gcacgagaca ccaacggtcg caacagagga atcaccagcg 180  
acgacaacag aggttacgga tcgtcgattg tttgatttct tggggaagaa ggaagaggaa 240  
gtgaaacctc aagagacaac gacgctcgag tctgagttcg atcataaggc tcagatctct 300  
gaaccggagt tagctgcgga sacgaggaag tgaaggagaa caagattact ctgctagagg 360  
agcttcaaga aaagaccgag gaagatgagg agaacaagcc tagtgatcgc gaaaagcttc 420  
accgatccaa cagctcttct tcctcttcga gcgatgaaga aggtgaggaa aagaaggaga 480  
agaagaagaa gatcggttgaa ggagaggaag ataagaaagg actag

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Thr Asn Ile Thr His Ser Gln Asn His Leu Lys Ala Thr Thr Gln Ile  
1 5 10 15  
Leu Lys Phe Ser His Ile Phe Tyr Leu Leu Tyr Lys Leu Leu Ile Lys  
20 25 30  
Ser Arg Leu Thr Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His  
35 40 45  
Glu Thr Pro Thr Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu  
50 55 60  
Val Thr Asp Arg Arg Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu  
65 70 75 80  
Val Lys Pro Gln Glu Thr Thr Thr Leu Glu Ser Glu Phe Asp His Lys  
85 90 95  
Ala Gln Ile Ser Glu Pro Glu Leu Ala Ala Xaa Thr Arg Lys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His Glu Thr Pro Thr  
1 5 10 15  
Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu Val Thr Asp Arg  
20 25 30  
Arg Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu Val Lys Pro Gln  
35 40 45  
Glu Thr Thr Thr Leu Glu Ser Glu Phe Asp His Lys Ala Gln Ile Ser  
50 55 60  
Glu Pro Glu Leu Ala Ala Xaa Thr Arg Lys  
65 70

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1354

(D) OTHER INFORMATION: / Ceres Seq. ID 1498329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

|            |            |             |            |             |            |      |
|------------|------------|-------------|------------|-------------|------------|------|
| atctctttct | cacaattaga | ttctgtgctt  | cttctgcgat | caactaagat  | cgatccgcg  | 60   |
| agcgtttcag | acttcgatca | gatccgatta  | agagaagcaa | atcgggtcgg  | gtatgactcg | 120  |
| tcgatgttct | cactgcaatc | acaatggcca  | caactctcgg | acttgctcca  | atcgcggcgt | 180  |
| gaagctcttt | ggtgttcggc | tcaccgaagg  | ttcgatccgg | aaaagtgcaa  | gtatgggtaa | 240  |
| tcttagccat | tacacgggtt | ctggatcggg  | tgggcatgga | accgggtcca  | acactccggg | 300  |
| ttctccgggt | gatgtccctg | accatgtcgc  | tggatgatgt | tacgcttctg  | aggatttcgt | 360  |
| tgttggtctt | tcctctagcc | gcgagagaaa  | gaaaggaact | ccatggacag  | aggaagaaca | 420  |
| caggatgttc | ttattagggt | tacagaagct  | gggtaaaggt | gattggagag  | gtatctcaag | 480  |
| aaactatgtg | accactmgha | cacctacaca  | agttgctagc | catgtctcaga | agtatttcat | 540  |
| cagacaatcc | aatgtctctc | gtcgcaaaaag | acgttctagt | ctctttgata  | tggttcctga | 600  |
| tgaggttgga | gatattccca | tggatttgca  | agaaccagag | gaagataata  | ttcctgtgga | 660  |
| aactgaaatg | caaggtgctg | actctattca  | tcagacactt | gctcctagct  | cacttcacgc | 720  |
| accgtcaatc | ttggaatcgc | aagaatgtga  | atcaatggac | tccacaaaat  | ctaccaccgg | 780  |
| ggaaccaacc | gcaactgccc | ctgctgcttc  | ttcttcttcc | agactagaag  | aaaccacaca | 840  |
| actgcaatca | caactgcaac | cgcagccgca  | actacctggc | tcattcccca  | tactatatcc | 900  |
| gacctacttt | tcaccatatt | acccgtttcc  | attcccaata | tggcctgctg  | gttatgttcc | 960  |
| tgaaccaccc | aagaaagagg | aaactcatga  | aattctcaga | ccaactgctg  | tgcactcgaa | 1020 |
| agctcctatc | aatgttgacg | agcttcttgg  | tatgtctaag | ctcagccttg  | cagagtccaa | 1080 |
| caaacatgga | gaatccgata | agtctctttc  | attgaagcta | ggtggcgggt  | catcttcaag | 1140 |
| acaatcagca | tttcacccga | atcctagctc  | tgatagtcca | gacatcaaaa  | gcgtgataca | 1200 |
| cgctttataa | aagacctgag | gaagtgaatg  | tctaaaatgg | gatctgggtt  | ggggtttaca | 1260 |
| ggttagttgt | tggtcacagt | aacttaaatg  | agtttttctt | tgttaggttg  | tttaacttgg | 1320 |
| qtaggatgtt | ttagttcaqc | tttgatcatt  | aqgg       |             |            |      |

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..365

(D) OTHER INFORMATION: / Ceres Seq. ID 1498330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Arg | Arg | Cys | Ser | His | Cys | Asn | His | Asn | Gly | His | Asn | Ser | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Cys | Pro | Asn | Arg | Gly | Val | Lys | Leu | Phe | Gly | Val | Arg | Leu | Thr | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ser | Ile | Arg | Lys | Ser | Ala | Ser | Met | Gly | Asn | Leu | Ser | His | Tyr | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ser | Gly | Ser | Gly | Gly | His | Gly | Thr | Gly | Ser | Asn | Thr | Pro | Gly | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Gly | Asp | Val | Pro | Asp | His | Val | Ala | Gly | Asp | Gly | Tyr | Ala | Ser | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Phe | Val | Ala | Gly | Ser | Ser | Ser | Ser | Arg | Glu | Arg | Lys | Lys | Gly | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Trp | Thr | Glu | Glu | Glu | His | Arg | Met | Phe | Leu | Leu | Gly | Leu | Gln | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Gly | Lys | Gly | Asp | Trp | Arg | Gly | Ile | Ser | Arg | Asn | Tyr | Val | Thr | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Xaa | Thr | Pro | Thr | Gln | Val | Ala | Ser | His | Ala | Gln | Lys | Tyr | Phe | Ile | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Ser | Asn | Val | Ser | Arg | Arg | Lys | Arg | Arg | Ser | Ser | Leu | Phe | Asp | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Asp | Glu | Val | Gly | Asp | Ile | Pro | Met | Asp | Leu | Gln | Glu | Pro | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Asp | Asn | Ile | Pro | Val | Glu | Thr | Glu | Met | Gln | Gly | Ala | Asp | Ser | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Gln | Thr | Leu | Ala | Pro | Ser | Ser | Leu | His | Ala | Pro | Ser | Ile | Leu | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Glu | Glu | Cys | Glu | Ser | Met | Asp | Ser | Thr | Asn | Ser | Thr | Thr | Gly | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Thr | Ala | Thr | Ala | Ala | Ala | Ala | Ser | Ser | Ser | Ser | Arg | Leu | Glu | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Thr | Thr | Gln | Leu | Gln | Ser | Gln | Leu | Gln | Pro | Gln | Pro | Gln | Leu | Pro | Gly |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Ser | Phe | Pro | Ile | Leu | Tyr | Pro | Thr | Tyr | Phe | Ser | Pro | Tyr | Tyr | Pro | Phe |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Pro | Phe | Pro | Ile | Trp | Pro | Ala | Gly | Tyr | Val | Pro | Glu | Pro | Pro | Lys | Lys |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Glu | Thr | His | Glu | Ile | Leu | Arg | Pro | Thr | Ala | Val | His | Ser | Lys | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | Ile | Asn | Val | Asp | Glu | Leu | Leu | Gly | Met | Ser | Lys | Leu | Ser | Leu | Ala |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Ser | Asn | Lys | His | Gly | Glu | Ser | Asp | Gln | Ser | Leu | Ser | Leu | Lys | Leu |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Gly | Gly | Gly | Ser | Ser | Ser | Arg | Gln | Ser | Ala | Phe | His | Pro | Asn | Pro | Ser |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ser | Asp | Ser | Ser | Asp | Ile | Lys | Ser | Val | Ile | His | Ala | Leu |     |     |     |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1498331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asn | Leu | Ser | His | Tyr | Thr | Gly | Ser | Gly | Ser | Gly | Gly | His | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Gly | Ser | Asn | Thr | Pro | Gly | Ser | Pro | Gly | Asp | Val | Pro | Asp | His | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Gly | Asp | Gly | Tyr | Ala | Ser | Glu | Asp | Phe | Val | Ala | Gly | Ser | Ser | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Arg | Glu | Arg | Lys | Lys | Gly | Thr | Pro | Trp | Thr | Glu | Glu | Glu | His | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Phe | Leu | Leu | Gly | Leu | Gln | Lys | Leu | Gly | Lys | Gly | Asp | Trp | Arg | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Ser | Arg | Asn | Tyr | Val | Thr | Thr | Xaa | Thr | Pro | Thr | Gln | Val | Ala | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| His | Ala | Gln | Lys | Tyr | Phe | Ile | Arg | Gln | Ser | Asn | Val | Ser | Arg | Arg | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Ser | Ser | Leu | Phe | Asp | Met | Val | Pro | Asp | Glu | Val | Gly | Asp | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Met | Asp | Leu | Gln | Glu | Pro | Glu | Glu | Asp | Asn | Ile | Pro | Val | Glu | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Met | Gln | Gly | Ala | Asp | Ser | Ile | His | Gln | Thr | Leu | Ala | Pro | Ser | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | His | Ala | Pro | Ser | Ile | Leu | Glu | Ile | Glu | Glu | Cys | Glu | Ser | Met | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Thr | Asn | Ser | Thr | Thr | Gly | Glu | Pro | Thr | Ala | Thr | Ala | Ala | Ala | Ala |

2025 RELEASE UNDER E.O. 14176

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ser | Ser | Ser | Ser | Arg | Leu | Glu | Glu | Thr | Thr | Gln | Leu | Gln | Ser | Gln | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Gln | Pro | Gln | Pro | Gln | Leu | Pro | Gly | Ser | Phe | Pro | Ile | Leu | Tyr | Pro | Thr |  |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |  |
| Tyr | Phe | Ser | Pro | Tyr | Tyr | Pro | Phe | Pro | Phe | Pro | Ile | Trp | Pro | Ala | Gly |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Tyr | Val | Pro | Glu | Pro | Pro | Lys | Lys | Glu | Glu | Thr | His | Glu | Ile | Leu | Arg |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Pro | Thr | Ala | Val | His | Ser | Lys | Ala | Pro | Ile | Asn | Val | Asp | Glu | Leu | Leu |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Gly | Met | Ser | Lys | Leu | Ser | Leu | Ala | Glu | Ser | Asn | Lys | His | Gly | Glu | Ser |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Asp | Gln | Ser | Leu | Ser | Leu | Lys | Leu | Gly | Gly | Gly | Ser | Ser | Ser | Arg | Gln |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Ser | Ala | Phe | His | Pro | Asn | Pro | Ser | Ser | Asp | Ser | Ser | Asp | Ile | Lys | Ser |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Val | Ile | His | Ala | Leu |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1498332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Phe | Leu | Leu | Gly | Leu | Gln | Lys | Leu | Gly | Lys | Gly | Asp | Trp | Arg | Gly |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ile | Ser | Arg | Asn | Tyr | Val | Thr | Thr | Xaa | Thr | Pro | Thr | Gln | Val | Ala | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| His | Ala | Gln | Lys | Tyr | Phe | Ile | Arg | Gln | Ser | Asn | Val | Ser | Arg | Arg | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Arg | Ser | Ser | Leu | Phe | Asp | Met | Val | Pro | Asp | Glu | Val | Gly | Asp | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Pro | Met | Asp | Leu | Gln | Glu | Pro | Glu | Glu | Asp | Asn | Ile | Pro | Val | Glu | Thr |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Glu | Met | Gln | Gly | Ala | Asp | Ser | Ile | His | Gln | Thr | Leu | Ala | Pro | Ser | Ser |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | His | Ala | Pro | Ser | Ile | Leu | Glu | Ile | Glu | Glu | Cys | Glu | Ser | Met | Asp |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Thr | Asn | Ser | Thr | Thr | Gly | Glu | Pro | Thr | Ala | Thr | Ala | Ala | Ala | Ala |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Ser | Ser | Ser | Ser | Arg | Leu | Glu | Thr | Thr | Gln | Leu | Gln | Ser | Gln | Leu |     |  |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |  |
| Gln | Pro | Gln | Pro | Gln | Leu | Pro | Gly | Ser | Phe | Pro | Ile | Leu | Tyr | Pro | Thr |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Tyr | Phe | Ser | Pro | Tyr | Tyr | Pro | Phe | Pro | Phe | Pro | Ile | Trp | Pro | Ala | Gly |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Tyr | Val | Pro | Glu | Pro | Pro | Lys | Lys | Glu | Glu | Thr | His | Glu | Ile | Leu | Arg |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Pro | Thr | Ala | Val | His | Ser | Lys | Ala | Pro | Ile | Asn | Val | Asp | Glu | Leu | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Gly | Met | Ser | Lys | Leu | Ser | Leu | Ala | Glu | Ser | Asn | Lys | His | Gly | Glu | Ser |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Asp | Gln | Ser | Leu | Ser | Leu | Lys | Leu | Gly | Gly | Gly | Ser | Ser | Ser | Arg | Gln |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |

Ser Ala Phe His Pro Asn Pro Ser Ser Asp Ser Ser Asp Ile Lys Ser  
245 250 255  
Val Ile His Ala Leu  
260

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..553
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| acttttagttt | ttttcacagt | tgagaaatct | cgccgccgtt | tgaagaaaga | agaagagatg | 60  |
| ggagttttct  | cattcgtgtg | caaaagcaaa | ggcggagaat | ggaccgcaaa | gcaacacgaa | 120 |
| ggagatcttg  | aagcttcagc | ttcttccacc | tacgatctcc | agcgcaagct | tgttcagact | 180 |
| gctctctccg  | ccgattcatc | tggcggcggt | cagtccttct | tctctcttgt | ctctcctacc | 240 |
| tccgccgtct  | tcgtggtggt | cattggtggt | ggtggtggtg | gaggatttgc | tgccggagga | 300 |
| ggtgcagctg  | ctggaggtgg | tggtggtggt | gaggctgccg | cagccacaaa | ggaggaagag | 360 |
| aagaagaagg  | agaatctga  | agaggaagag | ggagactttg | gatttgatct | ctttggttaa | 420 |
| gagacctaaa  | acaactttgt | tagtgttctg | aggtttttct | atctcaattt | tctctcttta | 480 |
| tgaaatatcg  | tgtttctttt | tcggagaaag | agtaagatac | atgatgaaaa | tctgttttgg | 540 |
| gggcgttttt  | gct        |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Val | Phe | Phe | Thr | Val | Glu | Lys | Ser | Arg | Arg | Arg | Leu | Lys | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Glu | Glu | Met | Gly | Val | Phe | Ser | Phe | Val | Cys | Lys | Ser | Lys | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Trp | Thr | Ala | Lys | Gln | His | Glu | Gly | Asp | Leu | Glu | Ala | Ser | Ala | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Thr | Tyr | Asp | Leu | Gln | Arg | Lys | Leu | Val | Gln | Thr | Ala | Leu | Ser | Ala |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asp | Ser | Ser | Gly | Gly | Val | Gln | Ser | Ser | Phe | Ser | Leu | Val | Ser | Pro | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Ala | Val | Phe | Val | Val | Ile | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Phe |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     | 95  |     |
| Ala | Ala | Gly | Gly | Gly | Ala | Ala | Ala | Gly | Gly | Gly | Gly | Gly | Gly | Glu | Ala |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Ala | Ala | Thr | Lys | Glu | Glu | Glu | Lys | Lys | Lys | Glu | Glu | Ser | Glu | Glu |
|     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Glu | Glu | Gly | Asp | Phe | Gly | Phe | Asp | Leu | Phe | Gly |     |     |     |     |     |
|     |     |     | 130 |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..120  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Val | Phe | Ser | Phe | Val | Cys | Lys | Ser | Lys | Gly | Gly | Glu | Trp | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Lys | Gln | His | Glu | Gly | Asp | Leu | Glu | Ala | Ser | Ala | Ser | Ser | Thr | Tyr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Asp | Leu | Gln | Arg | Lys | Leu | Val | Gln | Thr | Ala | Leu | Ser | Ala | Asp | Ser | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Gly | Val | Gln | Ser | Ser | Phe | Ser | Leu | Val | Ser | Pro | Thr | Ser | Ala | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Val | Val | Val | Ile | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Phe | Ala | Ala | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Gly | Ala | Ala | Ala | Gly | Gly | Gly | Gly | Gly | Gly | Glu | Ala | Ala | Ala | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Lys | Glu | Glu | Lys | Lys | Lys | Glu | Ser | Glu | Glu | Glu | Glu | Glu | Gly |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asp | Phe | Gly | Phe | Asp | Leu | Phe | Gly |     |     |     |     |     |     |     |     |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 623 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..623  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| aatctctctc | aacacaaaaga | agaacaaaaga | agttatgagc | tcaatgatgg | agactctcca | 60  |
| gattcgtaaa | cccacttccc  | tccccgtttc  | tcaacgccct | aatgcagcag | ccamcgccga | 120 |
| cgatgagcct | ggtctcatcc  | gccgtcgtct  | ctcttctcta | tcactcaasc | tctcaaacca | 180 |
| accagyagcg | atmgmagcta  | gattcscgag  | atccaaatct | gtttccgcca | tgggagaaca | 240 |
| agcaggaagc | tctgtgaaaag | aatgggtggga | atgggggttg | tcatggatcc | tttcaagaaa | 300 |
| acctatatcc | atcagagatc  | ttgagcttaa  | caaagacgaa | gctaaatcga | ttggttcaca | 360 |
| aaacagagga | agtataatgc  | acgttttctt  | caaactccgr | tctcagatcc | gtaatttcat | 420 |
| gggaccttct | tcagaagatt  | ctcttctctt  | ttcttgcaaa | tacaagcgtc | aacgataaaa | 480 |
| tgattcatat | aaggttgaga  | ttttgtgatt  | tgtctgttct | ttttttactt | ttgtgcaatg | 540 |
| gagtataatg | aatgtataat  | tcgtcttttt  | tttttaaact | tgatgttgta | ttttgctata | 600 |
| attaatttgc | ctagattatt  | att         |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 158 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..158  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Leu | Asn | Thr | Lys | Lys | Asn | Lys | Glu | Val | Met | Ser | Ser | Met | Met |
| 1   |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| Glu | Thr | Leu | Gln | Ile | Arg | Lys | Pro | Thr | Ser | Leu | Pro | Val | Ser | Gln | Arg |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 20                                                              | 25  | 30  |
| Pro Asn Ala Ala Ala Xaa Ala Asp Asp Glu Pro Gly Leu Ile Arg Arg |     |     |
| 35                                                              | 40  | 45  |
| Arg Leu Ser Ser Leu Ser Leu Xaa Leu Ser Asn Gln Pro Xaa Ala Xaa |     |     |
| 50                                                              | 55  | 60  |
| Xaa Ala Arg Phe Xaa Arg Ser Lys Ser Val Ser Ala Met Gly Glu Gln |     |     |
| 65                                                              | 70  | 75  |
| Ala Gly Ser Ser Val Lys Glu Trp Trp Glu Trp Gly Trp Ser Trp Ile |     |     |
| 85                                                              | 90  | 95  |
| Leu Ser Arg Lys Pro Ile Phe Ile Arg Asp Leu Glu Leu Asn Lys Asp |     |     |
| 100                                                             | 105 | 110 |
| Glu Ala Lys Ser Ile Gly Ser Gln Asn Arg Gly Ser Ile Met His Val |     |     |
| 115                                                             | 120 | 125 |
| Phe Phe Lys Leu Xaa Ser Gln Ile Arg Asn Phe Met Gly Pro Ser Ser |     |     |
| 130                                                             | 135 | 140 |
| Glu Asp Ser Leu Pro Leu Ser Cys Lys Tyr Lys Arg Gln Arg         |     |     |
| 145                                                             | 150 | 155 |

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1498338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Ser Ser Met Met Glu Thr Leu Gln Ile Arg Lys Pro Thr Ser Leu |     |     |
| 1                                                               | 5   | 10  |
| Pro Val Ser Gln Arg Pro Asn Ala Ala Ala Xaa Ala Asp Asp Glu Pro |     |     |
| 20                                                              | 25  | 30  |
| Gly Leu Ile Arg Arg Arg Leu Ser Leu Ser Leu Xaa Leu Ser Asn     |     |     |
| 35                                                              | 40  | 45  |
| Gln Pro Xaa Ala Xaa Xaa Ala Arg Phe Xaa Arg Ser Lys Ser Val Ser |     |     |
| 50                                                              | 55  | 60  |
| Ala Met Gly Glu Gln Ala Gly Ser Ser Val Lys Glu Trp Trp Glu Trp |     |     |
| 65                                                              | 70  | 75  |
| Gly Trp Ser Trp Ile Leu Ser Arg Lys Pro Ile Phe Ile Arg Asp Leu |     |     |
| 85                                                              | 90  | 95  |
| Glu Leu Asn Lys Asp Glu Ala Lys Ser Ile Gly Ser Gln Asn Arg Gly |     |     |
| 100                                                             | 105 | 110 |
| Ser Ile Met His Val Phe Phe Lys Leu Xaa Ser Gln Ile Arg Asn Phe |     |     |
| 115                                                             | 120 | 125 |
| Met Gly Pro Ser Ser Glu Asp Ser Leu Pro Leu Ser Cys Lys Tyr Lys |     |     |
| 130                                                             | 135 | 140 |
| Arg Gln Arg                                                     |     |     |
| 145                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1498339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Glu | Thr | Leu | Gln | Ile | Arg | Lys | Pro | Thr | Ser | Leu | Pro | Val | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Arg | Pro | Asn | Ala | Ala | Ala | Xaa | Ala | Asp | Asp | Glu | Pro | Gly | Leu | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Arg | Leu | Ser | Ser | Leu | Ser | Leu | Xaa | Leu | Ser | Asn | Gln | Pro | Xaa |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Xaa | Xaa | Ala | Arg | Phe | Xaa | Arg | Ser | Lys | Ser | Val | Ser | Ala | Met | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gln | Ala | Gly | Ser | Ser | Val | Lys | Glu | Trp | Trp | Glu | Trp | Gly | Trp | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Trp | Ile | Leu | Ser | Arg | Lys | Pro | Ile | Phe | Ile | Arg | Asp | Leu | Glu | Leu | Asn |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Asp | Glu | Ala | Lys | Ser | Ile | Gly | Ser | Gln | Asn | Arg | Gly | Ser | Ile | Met |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| His | Val | Phe | Phe | Lys | Leu | Xaa | Ser | Gln | Ile | Arg | Asn | Phe | Met | Gly | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Ser | Glu | Asp | Ser | Leu | Pro | Leu | Ser | Cys | Lys | Tyr | Lys | Arg | Gln | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

|             |            |             |            |             |            |      |
|-------------|------------|-------------|------------|-------------|------------|------|
| accactatga  | gaggatccta | gggttactac  | taatctcgaa | atcaatcaaa  | tcaaagcatc | 60   |
| cattttttgat | tcagacttca | gagagacaaa  | gaaggaagaa | gaagaagaag  | aagaagaaaa | 120  |
| aactatggag  | aatgagaggg | aaaagcaggt  | ttacttggct | aagctctccg  | agcaaaccga | 180  |
| aagatacgat  | gaaatggtgg | aggcgatgaa  | gaaagttgct | cagcttgatg  | tggagctaac | 240  |
| tgtggaagag  | aggaatcttg | tatctgtagg  | gtacaagaat | gtgattgggtg | caaggagagc | 300  |
| atcatggaga  | atactatctt | ccattgagca  | gaaggaagag | tccaagggaa  | atgatgaaaa | 360  |
| tgtcaagagg  | cttaagaatt | atcgtaagag  | agttgaagat | gagcttgcta  | aagtttgtaa | 420  |
| tgacatcttg  | tctgtcattg | ataagcatct  | cattccatcg | tctaacgctg  | tggagtcaac | 480  |
| tgtctttttc  | tacaaaaatg | aaggagatta  | ctatcgctat | cttgcgaggt  | tcagttctgg | 540  |
| tgttgaacgc  | aaggaagctg | cagatcagtc  | tcttgaagca | tataaggctg  | ctgttgctgc | 600  |
| tgcagagaat  | ggtttggcac | ccacacatcc  | agttagactt | ggcttggcgt  | tgaacttttc | 660  |
| agtttttctac | tatgagatct | tgaactctcc  | cgaaagcgca | tgccaattgg  | ctaagcaagc | 720  |
| attcgatgat  | gcaattgctg | aacttgacag  | cctcaacgag | gaatcataca  | aagacagcac | 780  |
| tcttatttatg | cagctactta | gagacaatct  | caccttggtg | acttcagacc  | ttaatgagga | 840  |
| aggagatgag  | agaaccaaag | gtgctgatga  | gcctcaagat | gagaactaaa  | tcctctgtga | 900  |
| gaagagaaac  | gactcttgct | gcatacctgaa | tcttgaagtg | aagacagcaa  | gtgtcgttgt | 960  |
| ttgttactcg  | aatgtgtaat | ttttaatcta  | tgtctttctt | gatgatgttt  | tccagattct | 1020 |
| tgaacttttc  | acaacacaac | actgcgttgc  | gtatcttcaa | ccctcttatg  | atgtggttga | 1080 |
| attctgtttt  | acgcttagtt | tgcttctttt  | gttggtgaat | tgagccagca  | ggcatgattt | 1140 |
| gggtttttgt  | tt         |             |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1498349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Met Glu Asn Glu Arg Glu Lys Gln Val Tyr Leu Ala Lys Leu Ser Glu  
1 5 10 15  
Gln Thr Glu Arg Tyr Asp Glu Met Val Glu Ala Met Lys Lys Val Ala  
20 25 30  
Gln Leu Asp Val Glu Leu Thr Val Glu Glu Arg Asn Leu Val Ser Val  
35 40 45  
Gly Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Leu  
50 55 60  
Ser Ser Ile Glu Gln Lys Glu Glu Ser Lys Gly Asn Asp Glu Asn Val  
65 70 75 80  
Lys Arg Leu Lys Asn Tyr Arg Lys Arg Val Glu Asp Glu Leu Ala Lys  
85 90 95  
Val Cys Asn Asp Ile Leu Ser Val Ile Asp Lys His Leu Ile Pro Ser  
100 105 110  
Ser Asn Ala Val Glu Ser Thr Val Phe Phe Tyr Lys Met Lys Gly Asp  
115 120 125  
Tyr Tyr Arg Tyr Leu Ala Glu Phe Ser Ser Gly Ala Glu Arg Lys Glu  
130 135 140  
Ala Ala Asp Gln Ser Leu Glu Ala Tyr Lys Ala Ala Val Ala Ala Ala  
145 150 155 160  
Glu Asn Gly Leu Ala Pro Thr His Pro Val Arg Leu Gly Leu Ala Leu  
165 170 175  
Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Glu Ser Ala  
180 185 190  
Cys Gln Leu Ala Lys Gln Ala Phe Asp Asp Ala Ile Ala Glu Leu Asp  
195 200 205  
Ser Leu Asn Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu  
210 215 220  
Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Leu Asn Glu Glu Gly  
225 230 235 240  
Asp Glu Arg Thr Lys Gly Ala Asp Glu Pro Gln Asp Glu Asn  
245 250

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1498350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Met Val Glu Ala Met Lys Lys Val Ala Gln Leu Asp Val Glu Leu Thr  
1 5 10 15  
Val Glu Glu Arg Asn Leu Val Ser Val Gly Tyr Lys Asn Val Ile Gly  
20 25 30  
Ala Arg Arg Ala Ser Trp Arg Ile Leu Ser Ser Ile Glu Gln Lys Glu  
35 40 45  
Glu Ser Lys Gly Asn Asp Glu Asn Val Lys Arg Leu Lys Asn Tyr Arg  
50 55 60  
Lys Arg Val Glu Asp Glu Leu Ala Lys Val Cys Asn Asp Ile Leu Ser  
65 70 75 80  
Val Ile Asp Lys His Leu Ile Pro Ser Ser Asn Ala Val Glu Ser Thr  
85 90 95  
Val Phe Phe Tyr Lys Met Lys Gly Asp Tyr Tyr Arg Tyr Leu Ala Glu  
100 105 110

Phe Ser Ser Gly Ala Glu Arg Lys Glu Ala Ala Asp Gln Ser Leu Glu  
115 120 125  
Ala Tyr Lys Ala Ala Val Ala Ala Ala Glu Asn Gly Leu Ala Pro Thr  
130 135 140  
His Pro Val Arg Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr  
145 150 155 160  
Glu Ile Leu Asn Ser Pro Glu Ser Ala Cys Gln Leu Ala Lys Gln Ala  
165 170 175  
Phe Asp Asp Ala Ile Ala Glu Leu Asp Ser Leu Asn Glu Glu Ser Tyr  
180 185 190  
Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu  
195 200 205  
Trp Thr Ser Asp Leu Asn Glu Gly Asp Glu Arg Thr Lys Gly Ala  
210 215 220  
Asp Glu Pro Gln Asp Glu Asn  
225 230

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Met Lys Lys Val Ala Gln Leu Asp Val Glu Leu Thr Val Glu Glu Arg  
1 5 10 15  
Asn Leu Val Ser Val Gly Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala  
20 25 30  
Ser Trp Arg Ile Leu Ser Ser Ile Glu Gln Lys Glu Glu Ser Lys Gly  
35 40 45  
Asn Asp Glu Asn Val Lys Arg Leu Lys Asn Tyr Arg Lys Arg Val Glu  
50 55 60  
Asp Glu Leu Ala Lys Val Cys Asn Asp Ile Leu Ser Val Ile Asp Lys  
65 70 75 80  
His Leu Ile Pro Ser Ser Asn Ala Val Glu Ser Thr Val Phe Phe Tyr  
85 90 95  
Lys Met Lys Gly Asp Tyr Tyr Arg Tyr Leu Ala Glu Phe Ser Ser Gly  
100 105 110  
Ala Glu Arg Lys Glu Ala Ala Asp Gln Ser Leu Glu Ala Tyr Lys Ala  
115 120 125  
Ala Val Ala Ala Ala Glu Asn Gly Leu Ala Pro Thr His Pro Val Arg  
130 135 140  
Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn  
145 150 155 160  
Ser Pro Glu Ser Ala Cys Gln Leu Ala Lys Gln Ala Phe Asp Asp Ala  
165 170 175  
Ile Ala Glu Leu Asp Ser Leu Asn Glu Glu Ser Tyr Lys Asp Ser Thr  
180 185 190  
Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp  
195 200 205  
Leu Asn Glu Glu Gly Asp Glu Arg Thr Lys Gly Ala Asp Glu Pro Gln  
210 215 220  
Asp Glu Asn  
225

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs



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 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1396
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498352

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

|             |             |            |             |             |            |      |
|-------------|-------------|------------|-------------|-------------|------------|------|
| aaagatgaaa  | agtaataccc  | ttcctctctt | gccctttttg  | ctgggtctggg | tgaaacatag | 60   |
| aaaagtttct  | cttgotcaag  | ttaatgataa | aagggtgttg  | taggatttgt  | tgctctggct | 120  |
| ctgggtggtag | gtctatgaaa  | tcaaccata  | tcgtgaatgg  | actgcaacat  | ggtatcttcg | 180  |
| tcccagtggtg | attgggagca  | tttgatcatg | tccaatccgt  | caaggactga  | agatgacagc | 240  |
| aaacagctac  | ctactgagtg  | ggaaattgaa | aaagggtgaag | gaattgaatc  | tatagttcca | 300  |
| cattttctcag | gccttgagag  | agtcagtagg | tggctctgcc  | accagcttct  | ggcacactgc | 360  |
| tgtatcgaaa  | agctcacagt  | cgacctctat | caactcatca  | ctctccgaag  | ccaaacgatg | 420  |
| caagcttgca  | tcagaaagtt  | cccttgaga  | ttcttgacgc  | aacatagact  | ttgtccaggt | 480  |
| gaaggctccc  | acagctctcg  | aggatccgt  | tgccctcagct | gaatcagatc  | tttgtttaaa | 540  |
| actaggaaaag | cggacatact  | ctgaagaata | ctggggtaga  | aacaataatg  | aaatttcagc | 600  |
| ggtttctatg  | aagttgttaa  | ctccatctgt | tgctcgtggg  | aaatccaaat  | tgtgtggtca | 660  |
| gagcatgcc   | gtcccgcgtt  | gccaaattga | tggctgtgaa  | ctggatctct  | catctgctaa | 720  |
| gggttatcat  | cgtaagcaca  | aagtctgcga | aaagcattca  | aagtgcccaa  | aagttagcgt | 780  |
| gagtggcctg  | gaacgtcgtg  | tctgccaaca | gtgtagcag   | ttccatgctg  | tctctgaatt | 840  |
| tgatgagaag  | aaacgaagct  | gccgaaaacg | tctttctcat  | cataatgcga  | ggcgtcgtaa | 900  |
| gccacaagga  | gtattttcaa  | tgaattccga | gaggggtgat  | gatcgaagac  | agcatacaaa | 960  |
| tatgttgttg  | aatggggtgt  | cccttaacgc | gagatctgaa  | gaaatgtatg  | aatggggtaa | 1020 |
| taacacttat  | gatacaaagc  | ctagacaaac | ggaaaaaagc  | tttactctga  | gcttccagag | 1080 |
| aggtaatggc  | tctgaggacc  | agctggttgc | tagtagcagc  | cgtatgttcc  | tctacatctc | 1140 |
| aaacctcagg  | tgggttccca  | gcaggaaagt | ccaagtttca  | acttcatggc  | gaagatgtgg | 1200 |
| gagaatactc  | aggagtcttc  | catgaatctc | aagatatcca  | cgtgctctc   | tctcttctgt | 1260 |
| caacctcttc  | ggatccctcg  | gcccaaccac | atgtgcagcc  | attttctcta  | ctctgttcat | 1320 |
| atgatgttgt  | acccaaaatag | atgagtaagt | aatgtgtaat  | ttgtaaacct  | gttactcagt | 1380 |
| agtggtatc   | ttttcc      |            |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1498353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Cys | Asn | Met | Val | Ser | Ser | Ser | Gln | Trp | Asp | Trp | Glu | His | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Met | Ser | Asn | Pro | Ser | Arg | Thr | Glu | Asp | Asp | Ser | Lys | Gln | Leu | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Glu | Trp | Glu | Ile | Glu | Lys | Gly | Glu | Gly | Ile | Glu | Ser | Ile | Val | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Phe | Ser | Gly | Leu | Glu | Arg | Val | Ser | Arg | Trp | Leu | Cys | His | Gln | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | His | Cys | Cys | Ile | Glu | Lys | Leu | Thr | Val | Asp | Leu | Tyr | Gln | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Ile | Ser | Arg | Ser | Gln | Thr | Met | Gln | Ala | Cys | Ile | Arg | Lys | Phe | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | Arg | Phe | Leu | Gln | Gln | His | Arg | Leu | Cys | Pro | Gly | Glu | Gly | Ser | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Arg | Gly | Ile | Arg | Cys | Leu | Ser |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1498354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

```
Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly Lys Ser Lys Leu Cys
 1 5 10 15
Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile Asp Gly Cys Glu Leu
 20 25 30
Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys His Lys Val Cys Glu
 35 40 45
Lys His Ser Lys Cys Pro Lys Val Ser Val Ser Gly Leu Glu Arg Arg
 50 55 60
Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val Ser Glu Phe Asp Glu
 65 70 75 80
Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser His His Asn Ala Arg Arg
 85 90 95
Arg Lys Pro Gln Gly Val Phe Ser Met Asn Pro Glu Arg Val Tyr Asp
 100 105 110
Arg Arg Gln His Thr Asn Met Leu Trp Asn Gly Val Ser Leu Asn Ala
 115 120 125
Arg Ser Glu Glu Met Tyr Glu Trp Gly Asn Asn Thr Tyr Asp Thr Lys
 130 135 140
Pro Arg Gln Thr Glu Lys Ser Phe Thr Leu Ser Phe Gln Arg Gly Asn
 145 150 155 160
Gly Ser Glu Asp Gln Leu Val Ala Ser Ser Arg Met Phe Leu Tyr
 165 170 175
Ile Ser Asn Leu Arg Trp Val Pro Ser Arg Lys Val Gln Val Ser Thr
 180 185 190
Ser Trp Arg Arg Cys Gly Arg Ile Leu Arg Ser Pro Pro
 195 200 205
```

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1498355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```
Met Pro Val Pro Arg Cys Gln Ile Asp Gly Cys Glu Leu Asp Leu Ser
 1 5 10 15
Ser Ala Lys Gly Tyr His Arg Lys His Lys Val Cys Glu Lys His Ser
 20 25 30
Lys Cys Pro Lys Val Ser Val Ser Gly Leu Glu Arg Arg Phe Cys Gln
 35 40 45
Gln Cys Ser Arg Phe His Ala Val Ser Glu Phe Asp Glu Lys Lys Arg
 50 55 60
Ser Cys Arg Lys Arg Leu Ser His His Asn Ala Arg Arg Arg Lys Pro
 65 70 75 80
Gln Gly Val Phe Ser Met Asn Pro Glu Arg Val Tyr Asp Arg Arg Gln
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Lys | Ile | Cys | Phe | Phe | Leu | Leu | Cys | Phe | Phe | Leu | Leu | Ser | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Glu | Arg | Glu | Arg | Glu | Ile | Gln | Arg | Glu | Lys | Phe | Gly | Cys | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Glu | Ala | Ser | Ser | Val | Ser | Leu | Leu | Arg | Leu | Thr | Ile | Val | Asn | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Phe | His | Leu | Gln | Phe | Cys | Phe | Tyr | Phe | Ser | Arg | Ser | Phe | Ser | Ser |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Lys | Tyr | Cys | Phe | Arg | Ser | Ile | Asn | Gln | Ser | Ile | Met | Ala | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Asn | Lys | Asn | Ile | Asn | Ala | Lys | Leu | Val | Leu | Leu | Gly | Asp | Val | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Gly | Lys | Ser | Ser | Leu | Val | Leu | Arg | Phe | Val | Lys | Asp | Gln | Phe | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Phe | Gln | Glu | Ser | Thr | Ile | Gly | Ala | Ala | Phe | Phe | Ser | Gln | Thr | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Val | Asn | Asp | Ala | Thr | Val | Lys | Phe | Glu | Ile | Trp | Asp | Thr | Ala | Gly |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gln | Glu | Arg | Tyr | His | Ser | Leu | Ala | Pro | Met | Tyr | Tyr | Arg | Gly | Ala | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ala | Ile | Ile | Val | Phe | Asp | Ile | Thr | Asn | Gln | Ala | Ser | Phe | Glu | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Xaa | Lys | Trp | Val | Gln | Glu | Leu | Gln | Ala | Gln | Gly | Asn | Pro | Asn | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Met | Ala | Leu | Ala | Gly | Asn | Lys | Ala | Asp | Leu | Leu | Asp | Ala | Arg | Lys |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Ser | Ala | Glu | Glu | Ala | Glu | Ile | Tyr | Ala | Gln | Glu | Asn | Ser | Leu | Phe |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Phe | Met | Glu | Thr | Ser | Ala | Lys | Thr | Ala | Thr | Asn | Val | Lys | Asp | Ile | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Tyr | Glu | Ile | Ala | Lys | Arg | Leu | Pro | Arg | Ile | Gln | Pro | Ala | Glu | Asn | Pro |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Gly | Met | Val | Leu | Pro | Asn | Gly | Pro | Gly | Ala | Thr | Ala | Val | Ser | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Cys | Cys | Ala |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1498358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ser | Gly | Asn | Lys | Asn | Ile | Asn | Ala | Lys | Leu | Val | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Asp | Val | Gly | Ala | Gly | Lys | Ser | Ser | Leu | Val | Leu | Arg | Phe | Val | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Gln | Phe | Val | Glu | Phe | Gln | Glu | Ser | Thr | Ile | Gly | Ala | Ala | Phe | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gln | Thr | Leu | Ala | Val | Asn | Asp | Ala | Thr | Val | Lys | Phe | Glu | Ile | Trp |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Thr | Ala | Gly | Gln | Glu | Arg | Tyr | His | Ser | Leu | Ala | Pro | Met | Tyr | Tyr |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Gly | Ala | Ala | Ala | Ala | Ile | Ile | Val | Phe | Asp | Ile | Thr | Asn | Gln | Ala |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Phe | Glu | Arg | Ala | Xaa | Lys | Trp | Val | Gln | Glu | Leu | Gln | Ala | Gln | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Pro | Asn | Met | Val | Met | Ala | Leu | Ala | Gly | Asn | Lys | Ala | Asp | Leu | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ala | Arg | Lys | Val | Ser | Ala | Glu | Glu | Ala | Glu | Ile | Tyr | Ala | Gln | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asn | Ser | Leu | Phe | Phe | Met | Glu | Thr | Ser | Ala | Lys | Thr | Ala | Thr | Asn | Val |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Ser | Arg | Pro | Phe | Ser | Ser | His | Phe | Leu | Leu | Leu | Thr | Lys |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Pro | Lys | Lys | Lys | Lys | Met | Arg | Glu | Ile | Leu | His | Ile | Gln | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Cys | Gly | Asn | Gln | Ile | Gly | Ala | Lys | Phe | Trp | Glu | Val | Ile | Cys | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | His | Gly | Ile | Asp | His | Thr | Gly | Gln | Tyr | Val | Gly | Asp | Ser | Pro | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Leu | Glu | Arg | Ile | Asp | Val | Tyr | Phe | Asn | Glu | Ala | Ser | Gly | Gly | Lys |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Val | Pro | Arg | Ala | Val | Leu | Met | Asp | Leu | Glu | Pro | Gly | Thr | Met | Asp |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |
| Ser | Leu | Arg | Ser | Gly | Pro | Phe | Gly | Gln | Ile | Phe | Arg | Pro | Asp | Asn | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Phe | Gly | Gln | Ser | Gly | Ala | Gly | Asn | Asn | Trp | Ala | Lys | Gly | His | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Glu | Val | Xaa | Glu | Leu | Ile | Asp | Ser | Val | Leu | Asp | Val | Val | Arg | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ala | Glu | Asn | Ser | Asp | Cys | Leu | Gln | Gly | Phe | Gln | Val | Cys | His | Ser |

(2) INFORMATION FOR SEQ ID NO:375:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:375:

Arg Glu Ile Leu His Ile Gln Gly Gly Gln C

(2) INFORMATION FOR SEQ ID NO:376:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1498365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Met Asp Leu Glu Pro Gly Thr Met Asp Ser Leu Arg Ser Gly Pro Phe  
1 5 10 15

Gly Gln Ile Phe Arg Pro Asp Asn Phe Val Phe Gly Gln Ser Gly Ala  
20 25 30  
Gly Asn Asn Trp Ala Lys Gly His Tyr Thr Glu Val Xaa Glu Leu Ile  
35 40 45  
Asp Ser Val Leu Asp Val Val Arg Lys Glu Ala Glu Asn Ser Asp Cys  
50 55 60  
Leu Gln Gly Phe Gln Val Cys His Ser Leu Gly Gly Gly Thr Gly Ser  
65 70 75 80  
Gly Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro Asp  
85 90 95  
Arg Met Met Met Thr Phe Ser Val Phe Leu Leu Leu Arg Ser Leu Thr  
100 105 110  
Leu Leu Leu Ser Ile Xaa Cys Thr Leu Ser Val His Gln Leu Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..667
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

|             |            |             |             |            |             |     |
|-------------|------------|-------------|-------------|------------|-------------|-----|
| ctgaaagacc  | ctaggctcaa | ctgggctcag  | gctggggctg  | gagagaaacg | attccagact  | 60  |
| gaagggcctg  | accataccat | tttcgtaggt  | gacttggcac  | ctgaggtgac | tgactatatg  | 120 |
| ctctcggaca  | cattcaagaa | tgtgtatggg  | tctgtcaaag  | gggctaaagt | tgtgcttgac  | 180 |
| aggaccactg  | gaaggtccaa | ggggtatggg  | tttgtaggt   | ttgcggatga | aaatgagcag  | 240 |
| atgctgtcca  | tgactgaaat | gaatgggtcaa | tactgctcga  | caaggcctat | gcgtattggt  | 300 |
| ccggctgcca  | ataagaatgc | tcttccgatg  | caaccagcta  | tgtatcaaaa | cactcaagga  | 360 |
| gcaaagtctg  | gagataatga | tcctaataac  | acaacaattt  | ttgttggagg | tctggatgct  | 420 |
| aatgttacag  | acgatgaatt | aaagtcaatt  | tttgggtcaat | ttggtgaact | tcttcattgtg | 480 |
| aaaataccctc | caggaaaacg | ttgtggattc  | gttcaatatg  | ccaacaaggc | gtctgcagag  | 540 |
| catgcacttt  | cggtgctgaa | tggaaacacaa | ttaggtggac  | aaagcatccg | tctttcgtgg  | 600 |
| ggacgtagtc  | caaacaagca | gtctgatcaa  | gcgcaatgga  | acggtggtgg | atactatgga  | 660 |
| taccctc     |            |             |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Leu Lys Asp Pro Arg Leu Asn Trp Ala Gln Ala Gly Ala Gly Glu Lys  
1 5 10 15  
Arg Phe Gln Thr Glu Gly Pro Asp His Thr Ile Phe Val Gly Asp Leu  
20 25 30  
Ala Pro Glu Val Thr Asp Tyr Met Leu Ser Asp Thr Phe Lys Asn Val  
35 40 45  
Tyr Gly Ser Val Lys Gly Ala Lys Val Val Leu Asp Arg Thr Thr Gly  
50 55 60  
Arg Ser Lys Gly Tyr Gly Phe Val Arg Phe Ala Asp Glu Asn Glu Gln  
65 70 75 80  
Met Arg Ala Met Thr Glu Met Asn Gly Gln Tyr Cys Ser Thr Arg Pro

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Met | Arg | Ile | Gly | Pro | Ala | Ala | Asn | Lys | Asn | Ala | Leu | Pro | Met | Gln | Pro |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Ala | Met | Tyr | Gln | Asn | Thr | Gln | Gly | Ala | Asn | Ala | Gly | Asp | Asn | Asp | Pro |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Asn | Asn | Thr | Thr | Ile | Phe | Val | Gly | Gly | Leu | Asp | Ala | Asn | Val | Thr | Asp |  |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Asp | Glu | Leu | Lys | Ser | Ile | Phe | Gly | Gln | Phe | Gly | Glu | Leu | Leu | His | Val |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Lys | Ile | Pro | Pro | Gly | Lys | Arg | Cys | Gly | Phe | Val | Gln | Tyr | Ala | Asn | Lys |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Ala | Ser | Ala | Glu | His | Ala | Leu | Ser | Val | Leu | Asn | Gly | Thr | Gln | Leu | Gly |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Gly | Gln | Ser | Ile | Arg | Leu | Ser | Trp | Gly | Arg | Ser | Pro | Asn | Lys | Gln | Ser |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Asp | Gln | Ala | Gln | Trp | Asn | Gly | Gly | Gly | Tyr | Tyr | Gly | Tyr | Pro |     |     |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1498368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Leu | Ser | Asp | Thr | Phe | Lys | Asn | Val | Tyr | Gly | Ser | Val | Lys | Gly | Ala |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Lys | Val | Val | Leu | Asp | Arg | Thr | Thr | Gly | Arg | Ser | Lys | Gly | Tyr | Gly | Phe |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |  |
| Val | Arg | Phe | Ala | Asp | Glu | Asn | Glu | Gln | Met | Arg | Ala | Met | Thr | Glu | Met |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Asn | Gly | Gln | Tyr | Cys | Ser | Thr | Arg | Pro | Met | Arg | Ile | Gly | Pro | Ala | Ala |  |  |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |
| Asn | Lys | Asn | Ala | Leu | Pro | Met | Gln | Pro | Ala | Met | Tyr | Gln | Asn | Thr | Gln |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Gly | Ala | Asn | Ala | Gly | Asp | Asn | Asp | Pro | Asn | Asn | Thr | Thr | Ile | Phe | Val |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Gly | Gly | Leu | Asp | Ala | Asn | Val | Thr | Asp | Glu | Leu | Lys | Ser | Ile | Phe |     |  |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |  |  |
| Gly | Gln | Phe | Gly | Glu | Leu | Leu | His | Val | Lys | Ile | Pro | Pro | Gly | Lys | Arg |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Cys | Gly | Phe | Val | Gln | Tyr | Ala | Asn | Lys | Ala | Ser | Ala | Glu | His | Ala | Leu |  |  |
|     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |  |  |
| Ser | Val | Leu | Asn | Gly | Thr | Gln | Leu | Gly | Gly | Gln | Ser | Ile | Arg | Leu | Ser |  |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |  |
| Trp | Gly | Arg | Ser | Pro | Asn | Lys | Gln | Ser | Asp | Gln | Ala | Gln | Trp | Asn | Gly |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |  |
| Gly | Gly | Tyr | Tyr | Gly | Tyr | Pro |     |     |     |     |     |     |     |     |     |  |  |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:



- (A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ala | Met | Thr | Glu | Met | Asn | Gly | Gln | Tyr | Cys | Ser | Thr | Arg | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Met | Arg | Ile | Gly | Pro | Ala | Ala | Asn | Lys | Asn | Ala | Leu | Pro | Met | Gln | Pro |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ala | Met | Tyr | Gln | Asn | Thr | Gln | Gly | Ala | Asn | Ala | Gly | Asp | Asn | Asp | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Asn | Thr | Thr | Ile | Phe | Val | Gly | Gly | Leu | Asp | Ala | Asn | Val | Thr | Asp |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Glu | Leu | Lys | Ser | Ile | Phe | Gly | Gln | Phe | Gly | Glu | Leu | Leu | His | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Ile | Pro | Pro | Gly | Lys | Arg | Cys | Gly | Phe | Val | Gln | Tyr | Ala | Asn | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ser | Ala | Glu | His | Ala | Leu | Ser | Val | Leu | Asn | Gly | Thr | Gln | Leu | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gln | Ser | Ile | Arg | Leu | Ser | Trp | Gly | Arg | Ser | Pro | Asn | Lys | Gln | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Gln | Ala | Gln | Trp | Asn | Gly | Gly | Gly | Tyr | Tyr | Gly | Tyr | Pro |     |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1125  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

|             |            |             |             |             |            |      |
|-------------|------------|-------------|-------------|-------------|------------|------|
| agttgaaatt  | ccacaagcaa | ccagtcaccg  | cgctccatct  | cacaagcgac  | ctgaagcagt | 60   |
| tactaagcgg  | tgattcagct | ggacagttac  | tttcatggac  | agtaccagat  | gagacattaa | 120  |
| gagcttcaat  | gaaacaagct | tcattaaaaac | aggcttcatt  | aaaacaggct  | tactgaaac  | 180  |
| aggcttcac   | ggtttagaat | ccaaagcaga  | gaccagtaaa  | tccccctttg  | gtttctctga | 240  |
| ctagaatcga  | aagagctggc | cagggaaactt | aaggacagga  | ccacgtagga  | ggaagcagac | 300  |
| caaagtctga  | acatagtgtt | gtctccgaaa  | gagagtatag  | cgagccactc  | tcaactctgc | 360  |
| tttgttggtg  | agttttcagg | tttgagaagg  | agaaggagaa  | gaggtttggt  | ttgagaattt | 420  |
| gtgtaaatag  | atgaaaagat | tacaagcttt  | ttacagggaa  | gtgtgtgtac  | tgtgtacagt | 480  |
| attgtatttt  | tgcggcctct | ttttttgtat  | tctttacgta  | aaattatttc  | ctacacaaaa | 540  |
| ttcccaactca | ccacacacaa | caaaagaata  | gtgatcgaag  | ctcatggcgt  | ctcttgcaac | 600  |
| cgtcgccgct  | gtgaaaccat | ccgccgccat  | aaaaggactc  | ggcggcagct  | cactcgccgg | 660  |
| agctaagctc  | tccatcaagc | cttcccgcct  | gagctttaaa  | cccaaatacca | tccgggctaa | 720  |
| tggtgtggtg  | gctaagtatg | gagacaaaag  | tgtctacttt  | gacttagaag  | atttgggtaa | 780  |
| cacaacaggt  | caatgggacg | tatacggtc   | tgatgtcctt  | tctccttaca  | atcctcttca | 840  |
| gagcaagttc  | tttgagacat | tcgtgcgcc   | attcacaaaag | agaggattgc  | tcctcaagtt | 900  |
| cttgatcctt  | ggaggaggct | ctttgcttac  | ttatgtcagc  | gctacctcta  | ccggcgaagt | 960  |
| tcttcccatc  | aagagaggtc | ctcaggagcc  | gcctaagctc  | ggtcctcgcg  | gcaagctctg | 1020 |
| atctatatct  | atgttacctt | tctcttcttc  | cttctaaaac  | tcatacaacat | ttctcaatac | 1080 |
| tgcaaacctt  | tttaagtaat | tttatgtata  | ttatgtttat  | ctggtt      |            |      |

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1498371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Met Ala Ser Leu Ala Thr Val Ala Ala Val Lys Pro Ser Ala Ala Ile  
1 5 10 15  
Lys Gly Leu Gly Ser Ser Leu Ala Gly Ala Lys Leu Ser Ile Lys  
20 25 30  
Pro Ser Arg Leu Ser Phe Lys Pro Lys Ser Ile Arg Ala Asn Gly Val  
35 40 45  
Val Ala Lys Tyr Gly Asp Lys Ser Val Tyr Phe Asp Leu Glu Asp Leu  
50 55 60  
Gly Asn Thr Thr Gly Gln Trp Asp Val Tyr Gly Ser Asp Ala Pro Ser  
65 70 75 80  
Pro Tyr Asn Pro Leu Gln Ser Lys Phe Phe Glu Thr Phe Ala Ala Pro  
85 90 95  
Phe Thr Lys Arg Gly Leu Leu Leu Lys Phe Leu Ile Leu Gly Gly Gly  
100 105 110  
Ser Leu Leu Thr Tyr Val Ser Ala Thr Ser Thr Gly Glu Val Leu Pro  
115 120 125  
Ile Lys Arg Gly Pro Gln Glu Pro Pro Lys Leu Gly Pro Arg Gly Lys  
130 135 140  
Leu  
145

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1112 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1112

(D) OTHER INFORMATION: / Ceres Seq. ID 1498379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

aagggtatgac tcaatcttca cttagttggt gaatttagtt ctgattcttta ttagattgta 60  
gtttctggcct ttgtagatat gctatagtta ctggaggaggaa tagagggaatt ggatttgaga 120  
tatgcagaca attagcaaac aaagggatta ggggtatttt gacatctaga gatgagaaac 180  
aagggtctga agctgttgag acattgaaga aagagcttga gatttctgat caaagcattg 240  
tctttcatca gcttgatgtc tctgatccct ctagtgtcac ttctcttgct aagtttgtga 300  
aaacccattt cggaaaactc gatatcttga tcaataatgc tggggttggt ggtgtaatca 360  
ctgatgttga tgctcttaga gctgggacag gaaagaagg tttcaagtgg gaggaacta 420  
tcactgagac ttatgagtta gctgaagaat gcataaagat taactattat ggaccaaaga 480  
gaatgtgtga ggcttttatt catcttctgc agttatctaa ttctccaaga atcgtaaatg 540  
tatcatcctt catgggtcaa gtaaagaatt tactaaacga atgggcaaaa gggatcctga 600  
gtgacgcaga gaatctaacg gaggtaagaa ttgaccaagt gatcaaccaa cttctcaatg 660  
atctgaaaaga agatacggct aagacaaaag attgggctaa agtcatgtcg gcttacgttg 720  
tttcgaaaagc cggtttgaat gcttacacga ggaacttagc gaagaaacat cccgagattc 780  
gcgttaactc ggtttgcctt ggatttgtga agactgatat gaatyttaaa actggaattt 840  
tatctgtgga agaaggagca tcaagtcctg tgagggttagc tttgcttcca catcaagaat 900  
ctccttctgg ttgtttcttt gatcgcaaac aagtttcaga gttctgaaat ctttgtgtgg 960  
agatagataa gccaaagttt tattcatgta atgagaatta ttgtttgaaa gctaaacaga 1020  
aagtatcgac tattcaataa acagaaacat tattaagcct taaaaaaaaa aaaaaaaaaa 1080  
aaaaaaaaaa aaaaaaaaaa attkttcccc cc

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1498380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Met Cys Glu Ala Phe Ile His Leu Leu Gln Leu Ser Asn Ser Pro Arg  
1 5 10 15  
Ile Val Asn Val Ser Ser Phe Met Gly Gln Val Lys Asn Leu Leu Asn  
20 25 30  
Glu Trp Ala Lys Gly Ile Leu Ser Asp Ala Glu Asn Leu Thr Glu Val  
35 40 45  
Arg Ile Asp Gln Val Ile Asn Gln Leu Leu Asn Asp Leu Lys Glu Asp  
50 55 60  
Thr Ala Lys Thr Lys Asp Trp Ala Lys Val Met Ser Ala Tyr Val Val  
65 70 75 80  
Ser Lys Ala Gly Leu Asn Ala Tyr Thr Arg Ile Leu Ala Lys Lys His  
85 90 95  
Pro Glu Ile Arg Val Asn Ser Val Cys Pro Gly Phe Val Lys Thr Asp  
100 105 110  
Met Asn Xaa Lys Thr Gly Ile Leu Ser Val Glu Glu Gly Ala Ser Ser  
115 120 125  
Pro Val Arg Leu Ala Leu Leu Pro His Gln Glu Ser Pro Ser Gly Cys  
130 135 140  
Phe Phe Asp Arg Lys Gln Val Ser Glu Phe  
145 150

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1498381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Met Gly Gln Val Lys Asn Leu Leu Asn Glu Trp Ala Lys Gly Ile Leu  
1 5 10 15  
Ser Asp Ala Glu Asn Leu Thr Glu Val Arg Ile Asp Gln Val Ile Asn  
20 25 30  
Gln Leu Leu Asn Asp Leu Lys Glu Asp Thr Ala Lys Thr Lys Asp Trp  
35 40 45  
Ala Lys Val Met Ser Ala Tyr Val Val Ser Lys Ala Gly Leu Asn Ala  
50 55 60  
Tyr Thr Arg Ile Leu Ala Lys Lys His Pro Glu Ile Arg Val Asn Ser  
65 70 75 80  
Val Cys Pro Gly Phe Val Lys Thr Asp Met Asn Xaa Lys Thr Gly Ile  
85 90 95  
Leu Ser Val Glu Glu Gly Ala Ser Ser Pro Val Arg Leu Ala Leu Leu  
100 105 110  
Pro His Gln Glu Ser Pro Ser Gly Cys Phe Phe Asp Arg Lys Gln Val  
115 120 125  
Ser Glu Phe  
130

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..80  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498382  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Tyr | Val | Ser | Lys | Ala | Gly | Leu | Asn | Ala | Tyr | Thr | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |
| Ile | Leu | Ala | Lys | Lys | His | Pro | Glu | Ile | Arg | Val | Asn | Ser | Val | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     | Pro |
| Gly | Phe | Val | Lys | Thr | Asp | Met | Asn | Xaa | Lys | Thr | Gly | Ile | Leu | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     | Val |
| Glu | Glu | Gly | Ala | Ser | Ser | Pro | Val | Arg | Leu | Ala | Leu | Leu | Pro | His |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     | Gln |
| Glu | Ser | Pro | Ser | Gly | Cys | Phe | Phe | Asp | Arg | Lys | Gln | Val | Ser | Glu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1211 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1211  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498383  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

|             |             |            |            |             |            |      |
|-------------|-------------|------------|------------|-------------|------------|------|
| cttttgccct  | cactcacttg  | tcttcttcaa | tttcgccgac | gacgaatccg  | acgtcagtaa | 60   |
| cttccgaccg  | cagtttccga  | aactcgtgat | cgctttctct | ttcgaaaatg  | ttggcgtcgg | 120  |
| tacgggtgaa  | tcagctgcaa  | agacttcttc | tctctgctcg | tcgattatct  | tcttcaccaa | 180  |
| taataacctcc | gtcgcgttta  | cttcaccagc | ggctattctc | gacctcagac  | actgatgctt | 240  |
| cggctgcatc  | tttttcttct  | tcgcatccga | aaatacaaac | gcttgaaggc  | aaagcttcta | 300  |
| ataaaagccg  | aagcacatcg  | tcaacaacat | ctttgaatga | agatgaactt  | gccaaattct | 360  |
| ctgccattgc  | tcatacctgg  | tggcattctg | aaggaccctt | taaaccgttg  | catcaaatga | 420  |
| atccaactcg  | gttggctttc  | atccgctcga | ccttatgcag | gcacttcagt  | aaggatccga | 480  |
| gttctgctaa  | gccttttygam | ggactgaaat | ttatcgatat | aggttgccgt  | ggcggactac | 540  |
| tttctgagcc  | tctagcacgg  | atgggagcaa | ctgtcacagg | agttgatgct  | gttgataaga | 600  |
| atgtcaaaat  | tgctcgtctt  | cacgctgata | tggatccagt | gacttcaacg  | attgaatact | 660  |
| tatgtactac  | agcagaaaag  | ctagcggatg | aaggcaggaa | gtttgatgct  | gttctttctt | 720  |
| tagagggtcat | cgagcatgta  | gcaaaccctg | cagagtctct | taagtcgttg  | tcagcattga | 780  |
| ctatccccaa  | cggggctaca  | gtactttcta | caatcaatcg | cactatgcga  | gcataatgat | 840  |
| caaccattgt  | tggagcagag  | tacattctac | gttggcttcc | taaaggcaca  | caccagtggg | 900  |
| caagttttgt  | aactcctgaa  | gaaatgagta | tgatattaca | acgtgcttca  | gtcgatgtga | 960  |
| aagagatagc  | tggatttgtg  | tacaacccaa | taacaggaag | atgggttattg | tcagatgata | 1020 |
| ttagtgtcaa  | ctatatgtct  | tatgggacga | aaaggaagga | tcttgagagc  | atataatcaa | 1080 |
| tcgttccaag  | tcgtgtttct  | ctgcatatct | gcttctgagt | tataactcta  | gttcatgctt | 1140 |
| taaaaactag  | gtactctgga  | agttgcttag | gacgaggaca | gtagttgttt  | tgcaataagt | 1200 |
| gagaaacatt  | c           |            |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 322 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1498384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ala | Ser | Val | Arg | Val | Asn | Gln | Leu | Gln | Arg | Leu | Leu | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Arg | Arg | Leu | Ser | Ser | Ser | Pro | Ile | Ile | Pro | Pro | Ser | Arg | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Gln | Arg | Leu | Phe | Ser | Thr | Ser | Asp | Thr | Asp | Ala | Ser | Ala | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ser | Ser | Ser | His | Pro | Lys | Ile | Gln | Thr | Leu | Glu | Gly | Lys | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Lys | Ser | Arg | Ser | Thr | Ser | Ser | Thr | Thr | Ser | Leu | Asn | Glu | Asp | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Ala | Lys | Phe | Ser | Ala | Ile | Ala | His | Thr | Trp | Trp | His | Ser | Glu | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Phe | Lys | Pro | Leu | His | Gln | Met | Asn | Pro | Thr | Arg | Leu | Ala | Phe | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ser | Thr | Leu | Cys | Arg | His | Phe | Ser | Lys | Asp | Pro | Ser | Ser | Ala | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Xaa | Xaa | Gly | Leu | Lys | Phe | Ile | Asp | Ile | Gly | Cys | Gly | Gly | Gly | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ser | Glu | Pro | Leu | Ala | Arg | Met | Gly | Ala | Thr | Val | Thr | Gly | Val | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Val | Asp | Lys | Asn | Val | Lys | Ile | Ala | Arg | Leu | His | Ala | Asp | Met | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Val | Thr | Ser | Thr | Ile | Glu | Tyr | Leu | Cys | Thr | Thr | Ala | Glu | Lys | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Asp | Glu | Gly | Arg | Lys | Phe | Asp | Ala | Val | Leu | Ser | Leu | Glu | Val | Ile |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | His | Val | Ala | Asn | Pro | Ala | Glu | Phe | Cys | Lys | Ser | Leu | Ser | Ala | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Ile | Pro | Asn | Gly | Ala | Thr | Val | Leu | Ser | Thr | Ile | Asn | Arg | Thr | Met |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Ala | Tyr | Ala | Ser | Thr | Ile | Val | Gly | Ala | Glu | Tyr | Ile | Leu | Arg | Trp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Pro | Lys | Gly | Thr | His | Gln | Trp | Ser | Ser | Phe | Val | Thr | Pro | Glu | Glu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Met | Ser | Met | Ile | Leu | Gln | Arg | Ala | Ser | Val | Asp | Val | Lys | Glu | Ile | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Phe | Val | Tyr | Asn | Pro | Ile | Thr | Gly | Arg | Trp | Leu | Leu | Ser | Asp | Asp |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Ser | Val | Asn | Tyr | Ile | Ala | Tyr | Gly | Thr | Lys | Arg | Lys | Asp | Leu | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asp | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1498385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Pro | Thr | Arg | Leu | Ala | Phe | Ile | Arg | Ser | Thr | Leu | Cys | Arg | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ser | Lys | Asp | Pro | Ser | Ser | Ala | Lys | Pro | Xaa | Xaa | Gly | Leu | Lys | Phe |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Ile Asp Ile Gly Cys Gly Gly Gly Leu Leu Ser Glu Pro Leu Ala Arg  
35 40 45  
Met Gly Ala Thr Val Thr Gly Val Asp Ala Val Asp Lys Asn Val Lys  
50 55 60  
Ile Ala Arg Leu His Ala Asp Met Asp Pro Val Thr Ser Thr Ile Glu  
65 70 75 80  
Tyr Leu Cys Thr Thr Ala Glu Lys Leu Ala Asp Glu Gly Arg Lys Phe  
85 90 95  
Asp Ala Val Leu Ser Leu Glu Val Ile Glu His Val Ala Asn Pro Ala  
100 105 110  
Glu Phe Cys Lys Ser Leu Ser Ala Leu Thr Ile Pro Asn Gly Ala Thr  
115 120 125  
Val Leu Ser Thr Ile Asn Arg Thr Met Arg Ala Tyr Ala Ser Thr Ile  
130 135 140  
Val Gly Ala Glu Tyr Ile Leu Arg Trp Leu Pro Lys Gly Thr His Gln  
145 150 155 160  
Trp Ser Ser Phe Val Thr Pro Glu Glu Met Ser Met Ile Leu Gln Arg  
165 170 175  
Ala Ser Val Asp Val Lys Glu Ile Ala Gly Phe Val Tyr Asn Pro Ile  
180 185 190  
Thr Gly Arg Trp Leu Leu Ser Asp Asp Ile Ser Val Asn Tyr Ile Ala  
195 200 205  
Tyr Gly Thr Lys Arg Lys Asp Leu Gly Asp Ile  
210 215

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1498386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met Gly Ala Thr Val Thr Gly Val Asp Ala Val Asp Lys Asn Val Lys  
1 5 10 15  
Ile Ala Arg Leu His Ala Asp Met Asp Pro Val Thr Ser Thr Ile Glu  
20 25 30  
Tyr Leu Cys Thr Thr Ala Glu Lys Leu Ala Asp Glu Gly Arg Lys Phe  
35 40 45  
Asp Ala Val Leu Ser Leu Glu Val Ile Glu His Val Ala Asn Pro Ala  
50 55 60  
Glu Phe Cys Lys Ser Leu Ser Ala Leu Thr Ile Pro Asn Gly Ala Thr  
65 70 75 80  
Val Leu Ser Thr Ile Asn Arg Thr Met Arg Ala Tyr Ala Ser Thr Ile  
85 90 95  
Val Gly Ala Glu Tyr Ile Leu Arg Trp Leu Pro Lys Gly Thr His Gln  
100 105 110  
Trp Ser Ser Phe Val Thr Pro Glu Glu Met Ser Met Ile Leu Gln Arg  
115 120 125  
Ala Ser Val Asp Val Lys Glu Ile Ala Gly Phe Val Tyr Asn Pro Ile  
130 135 140  
Thr Gly Arg Trp Leu Leu Ser Asp Asp Ile Ser Val Asn Tyr Ile Ala  
145 150 155 160  
Tyr Gly Thr Lys Arg Lys Asp Leu Gly Asp Ile  
165 170

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1397 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1397  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

|            |             |             |             |            |             |      |
|------------|-------------|-------------|-------------|------------|-------------|------|
| aaaaaatatt | tatgttgggt  | caggcttaaa  | ccagagagag  | actgtgtgtg | gtcagagccat | 60   |
| ttgaccaaaa | gcaaaaactt  | aaaactggtt  | tcagatctga  | agtaaaaggg | ttttgcttcg  | 120  |
| gattctccgg | cgtcgtttta  | atgatctctg  | acccatcttc  | cttggcctta | taattctggg  | 180  |
| ccctcctttt | atctcttttt  | actgttgatt  | tatctgaata  | tgccacgctc | tttcttccac  | 240  |
| atgtttattc | tctcttcctt  | tcttcaacac  | aagcgtctgg  | actaaggaaa | gccaacaaca  | 300  |
| aaatctgggt | tcaagacggt  | tggcaggagt  | ttgtcaaccg  | tttctccatt | cggattgggt  | 360  |
| tcagatacaa | agttacagtc  | tacattttca  | atztatcctc  | cacactctga | gatcaaccac  | 420  |
| cattctagta | gtgaagctct  | tatgcaaatg  | gattccgcac  | agaatcagtt | caacaaacgt  | 480  |
| gctcgattgt | ttgaagatcc  | tgaactcaaa  | gatgctaagg  | tcatttatcc | atcgaaccct  | 540  |
| gaatctactg | aaccagtgaa  | taaagggtat  | ggcggttcta  | cagccatcca | aagctttttc  | 600  |
| aaagaatcta | aagctgaaga  | aacgcccgaag | gtacttaaga  | agagaggaag | gaagaagaag  | 660  |
| aatcctaata | ccgaggaagt  | aaactcttca  | actcccgggtg | gagatgactc | agagaaccgc  | 720  |
| tcaaagttct | acgagagtgc  | ttctgctaga  | aagagaactg  | taactgcaga | ggaaagagag  | 780  |
| agagccgtca | atgcagccaa  | aacattcgaa  | ccaacaaatc  | ctttacttta | gagttgttct  | 840  |
| gcgaccatca | tatctataca  | gaggttgcat  | catgtacttg  | ccatctgggt | ttgctgagaa  | 900  |
| atacctaagt | gggatattctg | gtttcatcaa  | gctccagctc  | ggtgagaaac | aatggccagt  | 960  |
| gaggtgcctc | tacaaagcag  | ggagagctaa  | gtttagccaa  | ggatggtatg | agttcacact  | 1020 |
| cgagaacaat | ataggcggaag | gagatgtatg  | tgtgtttgag  | ctactcagaa | ctcgggattt  | 1080 |
| cgttctcgaa | gtcaccgcct  | ttcgtgtcaa  | tgagtatgtg  | tgaccaaaaa | agatttccct  | 1140 |
| ttcatcagcg | atcttgcagg  | tagctttcca  | aagttaaaat  | tttatgtagg | ggtctcttaa  | 1200 |
| ccattctctc | tcttgcattg  | gttgtctctg  | ttctagtagt  | gttttgagtg | aaatttcagg  | 1260 |
| ttcctatgtt | tggatgtgga  | taagtatttg  | acgattataa  | taacctctga | gtgaaaactc  | 1320 |
| tttgtttgag | tggtagctag  | gttcaaaagt  | agagttgtat  | atacttttat | cttcatcagg  | 1380 |
| ataattatgt | ttatttg     |             |             |            |             |      |

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..129  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Met | Asp | Ser | Ala | Gln | Asn | Gln | Phe | Asn | Lys | Arg | Ala | Arg | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Glu | Asp | Pro | Glu | Leu | Lys | Asp | Ala | Lys | Val | Ile | Tyr | Pro | Ser | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Glu | Ser | Thr | Glu | Pro | Val | Asn | Lys | Gly | Tyr | Gly | Gly | Ser | Thr | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Gln | Ser | Phe | Phe | Lys | Glu | Ser | Lys | Ala | Glu | Glu | Thr | Pro | Lys | Val |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Lys | Lys | Arg | Gly | Arg | Lys | Lys | Lys | Asn | Pro | Asn | Pro | Glu | Glu | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Asn | Ser | Ser | Thr | Pro | Gly | Gly | Asp | Asp | Ser | Glu | Asn | Arg | Ser | Lys | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Tyr | Glu | Ser | Ala | Ser | Ala | Arg | Lys | Arg | Thr | Val | Thr | Ala | Glu | Glu | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Glu | Arg | Ala | Val | Asn | Ala | Ala | Lys | Thr | Phe | Glu | Pro | Thr | Asn | Pro | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Leu

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ser | Ala | Gln | Asn | Gln | Phe | Asn | Lys | Arg | Ala | Arg | Leu | Phe | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | Pro | Glu | Leu | Lys | Asp | Ala | Lys | Val | Ile | Tyr | Pro | Ser | Asn | Pro | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Thr | Glu | Pro | Val | Asn | Lys | Gly | Tyr | Gly | Gly | Ser | Thr | Ala | Ile | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Phe | Phe | Lys | Glu | Ser | Lys | Ala | Glu | Glu | Thr | Pro | Lys | Val | Leu | Lys |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Arg | Gly | Arg | Lys | Lys | Asn | Pro | Asn | Pro | Glu | Glu | Val | Asn | Ser |     |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Ser | Thr | Pro | Gly | Gly | Asp | Asp | Ser | Glu | Asn | Arg | Ser | Lys | Phe | Tyr | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Ala | Ser | Ala | Arg | Lys | Arg | Thr | Val | Thr | Ala | Glu | Glu | Arg | Glu | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Val | Asn | Ala | Ala | Lys | Thr | Phe | Glu | Pro | Thr | Asn | Pro | Leu | Leu |     |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Pro | Lys | His | Ser | Asn | Gln | Gln | Ile | Leu | Tyr | Phe | Arg | Val | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Arg | Pro | Ser | Tyr | Leu | Tyr | Arg | Gly | Cys | Ile | Met | Tyr | Leu | Pro | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Phe | Ala | Glu | Lys | Tyr | Leu | Ser | Gly | Ile | Ser | Gly | Phe | Ile | Lys | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Leu | Gly | Glu | Lys | Gln | Trp | Pro | Val | Arg | Cys | Leu | Tyr | Lys | Ala | Gly |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Ala | Lys | Phe | Ser | Gln | Gly | Trp | Tyr | Glu | Phe | Thr | Leu | Glu | Asn | Asn |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Ile | Gly | Glu | Gly | Asp | Val | Cys | Val | Phe | Glu | Leu | Leu | Arg | Thr | Arg | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Val | Leu | Glu | Val | Thr | Ala | Phe | Arg | Val | Asn | Glu | Tyr | Val |     |     |
|     |     |     | 100 |     |     | 105 |     |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1267  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| atctatcttt | aaaaacatac | ttgaaaatgc  | aaggaacgat  | ttcttgtgca  | agaaattata  | 60   |
| acatgacgac | aaccgtcggg | gaatctctgc  | ggccgctatc  | gcttaaaacg  | cagggaaacg  | 120  |
| gcgagagagt | tcggatggtg | gtggaggaga  | acgcggtgat  | tgtgattgga  | cggagaggat  | 180  |
| gttgcatgtg | tcatgtggtg | aggaggctgc  | ttcttggact  | tggagtgaat  | ccggcgggtcc | 240  |
| ttgagattga | tgaggagagg | gaagatgaag  | ttttgagtga  | gttgaggaga  | attggaggttc | 300  |
| aaggcggcgg | aggtacggtg | aagttaccgg  | cggtttatgt  | aggagggagg  | aaaaaaaaaa  | 360  |
| actcagagag | acaaatctaa | atggcgatga  | ttacgcgcaa  | caccgccacg  | cgccctccctc | 420  |
| tcctcctcca | atctcaacgc | gccgtcgccg  | ctgcctcggg  | ctctcacctc  | cacacatccc  | 480  |
| ttcccgtctc | ctctccctcc | acatcaccca  | cttccctacac | cagacctggt  | cctccttcga  | 540  |
| cctccctctc | tcctcctggt | ctctctaaag  | cggccgaatt  | tgtgatctcc  | aaggtatgat  | 600  |
| ctcatgaact | gggctcgtac | cggatcgatc  | tggcctatga  | cctttggtct  | cgcttgctgc  | 660  |
| gccgtcgaag | tgatgcatac | cgggtgctgct | cgctacgatc  | tcgatcgatt  | cggtatcatc  | 720  |
| ttcaggccta | gtcctcgcca | gtctgattgt  | atgattgtcg  | ccggtactct  | taccaataag  | 780  |
| atggctccgg | ctcttcgcaa | ggtttatgac  | cagatgcctg  | agccaagggtg | ggtgatttca  | 840  |
| atgggaagtt | gtgccaatgg | atgtggatac  | tatcactact  | cctactcggg  | ggttcgagga  | 900  |
| tgtgacagaa | ttgtcccagc | cgacatatat  | gtcccggggg  | gccaccaaac  | cgctgaggct  | 960  |
| ttgctctatg | gactactcca | gcttcagaag  | aaaatcaaca  | ggcgcaagga  | tttcttgcac  | 1020 |
| tggtggaaca | agtgagcttc | gaaccogtcc  | tccaatcgtg  | aaagggactt  | ttttcagaca  | 1080 |
| gttttaccaa | agttttgggg | ataataaatc  | gtggacgttt  | cattgcatat  | ttctttgtgg  | 1140 |
| tggagatgcc | atgtaaagga | gtgtgtttct  | aagtttggtg  | tggaaactta  | ataaacttaa  | 1200 |
| gatgtttggt | gtctgagttc | ttttatgggc  | tcttttatta  | tatatctctc  | tctaccagtt  | 1260 |
| ttcagcc    |            |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 125 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..125  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ser | Leu | Lys | Thr | Tyr | Leu | Lys | Met | Gln | Gly | Thr | Ile | Ser | Cys | Ala |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Arg | Asn | Tyr | Asn | Met | Thr | Thr | Thr | Val | Gly | Glu | Ser | Leu | Arg | Pro | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Leu | Lys | Thr | Gln | Gly | Asn | Gly | Glu | Arg | Val | Arg | Met | Val | Val | Glu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Asn | Ala | Val | Ile | Val | Ile | Gly | Arg | Arg | Gly | Cys | Cys | Met | Cys | His |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Val | Val | Arg | Arg | Leu | Leu | Gly | Leu | Gly | Val | Asn | Pro | Ala | Val | Leu |     |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Glu | Ile | Asp | Glu | Glu | Arg | Glu | Asp | Glu | Val | Leu | Ser | Glu | Leu | Glu | Asn |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ile | Gly | Val | Gln | Gly | Gly | Gly | Gly | Thr | Val | Lys | Leu | Pro | Ala | Val | Tyr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Val | Gly | Gly | Arg | Lys | Lys | Lys | Asn | Ser | Glu | Arg | Gln | Ile |     |     |     |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 143 amino acids  
    (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..143  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498393  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Met Asn Trp Ala Arg Thr Gly Ser Ile Trp Pro Met Thr Phe Gly Leu  
1 5 10 15  
Ala Cys Cys Ala Val Glu Met Met His Thr Gly Ala Ala Arg Tyr Asp  
20 25 30  
Leu Asp Arg Phe Gly Ile Ile Phe Arg Pro Ser Pro Arg Gln Ser Asp  
35 40 45  
Cys Met Ile Val Ala Gly Thr Leu Thr Asn Lys Met Ala Pro Ala Leu  
50 55 60  
Arg Lys Val Tyr Asp Gln Met Pro Glu Pro Arg Trp Val Ile Ser Met  
65 70 75 80  
Gly Ser Cys Ala Asn Gly Cys Gly Tyr Tyr His Tyr Ser Tyr Ser Val  
85 90 95  
Val Arg Gly Cys Asp Arg Ile Val Pro Val Asp Ile Tyr Val Pro Gly  
100 105 110  
Cys Pro Pro Thr Ala Glu Ala Leu Leu Tyr Gly Leu Leu Gln Leu Gln  
115 120 125  
Lys Lys Ile Asn Arg Arg Lys Asp Phe Leu His Trp Trp Asn Lys  
130 135 140

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..132  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Met Thr Phe Gly Leu Ala Cys Cys Ala Val Glu Met Met His Thr Gly  
1 5 10 15  
Ala Ala Arg Tyr Asp Leu Asp Arg Phe Gly Ile Ile Phe Arg Pro Ser  
20 25 30  
Pro Arg Gln Ser Asp Cys Met Ile Val Ala Gly Thr Leu Thr Asn Lys  
35 40 45  
Met Ala Pro Ala Leu Arg Lys Val Tyr Asp Gln Met Pro Glu Pro Arg  
50 55 60  
Trp Val Ile Ser Met Gly Ser Cys Ala Asn Gly Cys Gly Tyr Tyr His  
65 70 75 80  
Tyr Ser Tyr Ser Val Val Arg Gly Cys Asp Arg Ile Val Pro Val Asp  
85 90 95  
Ile Tyr Val Pro Gly Cys Pro Pro Thr Ala Glu Ala Leu Leu Tyr Gly  
100 105 110  
Leu Leu Gln Leu Gln Lys Lys Ile Asn Arg Arg Lys Asp Phe Leu His  
115 120 125  
Trp Trp Asn Lys  
130

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2084 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..2084  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```
aagcacttct tctccgcctt cgtaagttcc gccgaaaaga accaaatcct tcactactct 60
gtctcagctt tgcacctctc tcttctcatt cctttgcaac ttctcacttc tcgaattcct 120
tctcttcaaa atcagaaatg gctcaagtgg ttgctaccag gtcaattcaa ggctcgaagt 180
tatctcccaa cgggtgatct gtgtctacaa gatccgagaa gctattgaaa ccagcgaagt 240
ttgcagtgaa ggttcttgga aacgaagcaa agagaagtgg aagagtctct ggtaagaagc 300
agaagagggtg gttgatacta ctgtgagatc cgctcgaagt gagactgaag tcattcctgt 360
ttctcctgaa gatgtgccta acagagagga gcagcntgag aggttggttg aaatgcagca 420
gtttggtgat acatcggtag ggatgtggtc gaagccgaca gtgaggagga agacaaagat 480
tggttgaccg gttggtccgt cgaccaacac acgagaaatg atatggaaat tggctgaagc 540
tgggatgaat gttgctagga tgaatatgtc tcatggagat catgcttcac ataagaaggt 600
tattgatatt gttaaagaat acaatgcaca aactaaagac aacactattg ctatcatgct 660
tgacaccaag ggtccggaag ttaggagtgg agatttacct cagccaatta tgtagatcc 720
tggtcaagag ttacctttaa caattgagag aggagtcagc acaccaagtt gtgtcagtgt 780
taactatgat gatttcgtta atgacgtgga agcgggtgac atgcttcttg ttgatggtgg 840
tatgatgtcg tttatggtga agtcaaagac caaagactct gtcaaatgtg aagttggtga 900
tggtggagaa cttaagtcaa ggagacacct gaatgtccga ggaaagagtg caactttacc 960
ttcaatcact gagaaggatt gggaggatat taaatttgga gtggagaaca aagttgactt 1020
ttatgcagtt tcctttgtca aagatgctca agttgtacac gagttgaaga aataccttca 1080
aaatagtggg gctgatatac acgtgatagt gaaaattgag agtgcagact ccatacctaa 1140
cttgcactcc attatcacag catcagatgg ggcaatgggt gcaagagggt atcttggtgc 1200
agagcttcca attgaagaag tccccattct tcaggaggag atcattaacc tgtgccgtag 1260
tatgggaaaa gctgttattg ttgcgactaa catgcttgag agtatgatag ttcatccaac 1320
tccaaccggg gcagagggtc cagacattgc tatcgtgtgt agagaagggt ctgatgcggt 1380
aatgctttca ggagaaactg ctcacggaaa gttcccattg aaagctgctg gagtgatgca 1440
cactgttgca ttgcgaacag aagcaaccat tactagcggg gaaatgccac ctaatcttgg 1500
tcaagccttc aagaaccata tgagtggagt gtttgcatac catgcaacca tgatgtcaaa 1560
cacacttgga acttcaactg ttgtcttcac cagaaccggt ttcatggcca tattgttaag 1620
tcactatcgt ccttcgggca caatctatgc cttcacaaat gagaaaaaaa tacaacaaag 1680
attagctttg tatcaagggt tatgccccat atatatggag ttcacagatg atgcagaaga 1740
aacttttgct aatgcttttg ctacattact gaaacaagga atggtgaaga agggagagga 1800
aatagcaatc gtacagagcg gtacacagcc aatctggcga tctcaatcga cacataacat 1860
ccaagtcgcg aagggtttaa gcttctttta agatgggatg tctttaatat gtagaacctc 1920
gtttttgggt ataattttcg ttgcatgtct ctcttctctt gtactattca cacttggtgt 1980
ttgctgtatc ttcttcttca gtttgctttg ctacgattgt ggtttttgga gacattatag 2040
ctcatthaat gtttgtgaga ccaaattgtg cagaatccgc tatt
```

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 488 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..488  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```
Met Gln Gln Phe Gly Asp Thr Ser Val Gly Met Trp Ser Lys Pro Thr
1 5 10 15
Val Arg Arg Lys Thr Lys Ile Val Cys Thr Val Gly Pro Ser Thr Asn
20 25 30
Thr Arg Glu Met Ile Trp Lys Leu Ala Glu Ala Gly Met Asn Val Ala
35 40 45
Arg Met Asn Met Ser His Gly Asp His Ala Ser His Lys Lys Val Ile
```

(D) TOPOLOGY: linear

[illegible]

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1498397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Ser | Lys | Pro | Thr | Val | Arg | Arg | Lys | Thr | Lys | Ile | Val | Cys | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gly | Pro | Ser | Thr | Asn | Thr | Arg | Glu | Met | Ile | Trp | Lys | Leu | Ala | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Gly | Met | Asn | Val | Ala | Arg | Met | Asn | Met | Ser | His | Gly | Asp | His | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | His | Lys | Lys | Val | Ile | Asp | Leu | Val | Lys | Glu | Tyr | Asn | Ala | Gln | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Asp | Asn | Thr | Ile | Ala | Ile | Met | Leu | Asp | Thr | Lys | Gly | Pro | Glu | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ser | Gly | Asp | Leu | Pro | Gln | Pro | Ile | Met | Leu | Asp | Pro | Gly | Gln | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Thr | Phe | Thr | Ile | Glu | Arg | Gly | Val | Ser | Thr | Pro | Ser | Cys | Val | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Asn | Tyr | Asp | Asp | Phe | Val | Asn | Asp | Val | Glu | Ala | Gly | Asp | Met | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Val | Asp | Gly | Gly | Met | Met | Ser | Phe | Met | Val | Lys | Ser | Lys | Thr | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Ser | Val | Lys | Cys | Glu | Val | Val | Asp | Gly | Gly | Glu | Leu | Lys | Ser | Arg |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Arg | His | Leu | Asn | Val | Arg | Gly | Lys | Ser | Ala | Thr | Leu | Pro | Ser | Ile | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Lys | Asp | Trp | Glu | Asp | Ile | Lys | Phe | Gly | Val | Glu | Asn | Lys | Val | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Tyr | Ala | Val | Ser | Phe | Val | Lys | Asp | Ala | Gln | Val | Val | His | Glu | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Lys | Tyr | Leu | Gln | Asn | Ser | Gly | Ala | Asp | Ile | His | Val | Ile | Val | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Glu | Ser | Ala | Asp | Ser | Ile | Pro | Asn | Leu | His | Ser | Ile | Ile | Thr | Ala |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Asp | Gly | Ala | Met | Val | Ala | Arg | Gly | Asp | Leu | Gly | Ala | Glu | Leu | Pro |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Ile | Glu | Glu | Val | Pro | Ile | Leu | Gln | Glu | Glu | Ile | Ile | Asn | Leu | Cys | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Met | Gly | Lys | Ala | Val | Ile | Val | Ala | Thr | Asn | Met | Leu | Glu | Ser | Met |
|     |     | 275 |     |     |     |     |     | 280 |     |     |     | 285 |     |     |     |
| Ile | Val | His | Pro | Thr | Pro | Thr | Arg | Ala | Glu | Val | Ser | Asp | Ile | Ala | Ile |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Ala | Val | Arg | Glu | Gly | Ala | Asp | Ala | Val | Met | Leu | Ser | Gly | Glu | Thr | Ala |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| His | Gly | Lys | Phe | Pro | Leu | Lys | Ala | Ala | Gly | Val | Met | His | Thr | Val | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Arg | Thr | Glu | Ala | Thr | Ile | Thr | Ser | Gly | Glu | Met | Pro | Pro | Asn | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Gln | Ala | Phe | Lys | Asn | His | Met | Ser | Glu | Met | Phe | Ala | Tyr | His | Ala |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Thr | Met | Met | Ser | Asn | Thr | Leu | Gly | Thr | Ser | Thr | Val | Val | Phe | Thr | Arg |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Thr | Gly | Phe | Met | Ala | Ile | Leu | Leu | Ser | His | Tyr | Arg | Pro | Ser | Gly | Thr |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Ile | Tyr | Ala | Phe | Thr | Asn | Glu | Lys | Lys | Ile | Gln | Gln | Arg | Leu | Ala | Leu |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Tyr | Gln | Gly | Val | Cys | Pro | Ile | Tyr | Met | Glu | Phe | Thr | Asp | Asp | Ala | Glu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     | 430 |     |     |     |
| Glu | Thr | Phe | Ala | Asn | Ala | Leu | Ala | Thr | Leu | Leu | Lys | Gln | Gly | Met | Val |

435 440 445  
Lys Lys Gly Glu Glu Ile Ala Ile Val Gln Ser Gly Thr Gln Pro Ile  
450 455 460  
Trp Arg Ser Gln Ser Thr His Asn Ile Gln Val Arg Lys Val  
465 470 475

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1498398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met Ile Trp Lys Leu Ala Glu Ala Gly Met Asn Val Ala Arg Met Asn  
1 5 10 15  
Met Ser His Gly Asp His Ala Ser His Lys Lys Val Ile Asp Leu Val  
20 25 30  
Lys Glu Tyr Asn Ala Gln Thr Lys Asp Asn Thr Ile Ala Ile Met Leu  
35 40 45  
Asp Thr Lys Gly Pro Glu Val Arg Ser Gly Asp Leu Pro Gln Pro Ile  
50 55 60  
Met Leu Asp Pro Gly Gln Glu Phe Thr Phe Thr Ile Glu Arg Gly Val  
65 70 75 80  
Ser Thr Pro Ser Cys Val Ser Val Asn Tyr Asp Asp Phe Val Asn Asp  
85 90 95  
Val Glu Ala Gly Asp Met Leu Leu Val Asp Gly Gly Met Met Ser Phe  
100 105 110  
Met Val Lys Ser Lys Thr Lys Asp Ser Val Lys Cys Glu Val Val Asp  
115 120 125  
Gly Gly Glu Leu Lys Ser Arg Arg His Leu Asn Val Arg Gly Lys Ser  
130 135 140  
Ala Thr Leu Pro Ser Ile Thr Glu Lys Asp Trp Glu Asp Ile Lys Phe  
145 150 155 160  
Gly Val Glu Asn Lys Val Asp Phe Tyr Ala Val Ser Phe Val Lys Asp  
165 170 175  
Ala Gln Val Val His Glu Leu Lys Lys Tyr Leu Gln Asn Ser Gly Ala  
180 185 190  
Asp Ile His Val Ile Val Lys Ile Glu Ser Ala Asp Ser Ile Pro Asn  
195 200 205  
Leu His Ser Ile Ile Thr Ala Ser Asp Gly Ala Met Val Ala Arg Gly  
210 215 220  
Asp Leu Gly Ala Glu Leu Pro Ile Glu Glu Val Pro Ile Leu Gln Glu  
225 230 235 240  
Glu Ile Ile Asn Leu Cys Arg Ser Met Gly Lys Ala Val Ile Val Ala  
245 250 255  
Thr Asn Met Leu Glu Ser Met Ile Val His Pro Thr Pro Thr Arg Ala  
260 265 270  
Glu Val Ser Asp Ile Ala Ile Ala Val Arg Glu Gly Ala Asp Ala Val  
275 280 285  
Met Leu Ser Gly Glu Thr Ala His Gly Lys Phe Pro Leu Lys Ala Ala  
290 295 300  
Gly Val Met His Thr Val Ala Leu Arg Thr Glu Ala Thr Ile Thr Ser  
305 310 315 320  
Gly Glu Met Pro Pro Asn Leu Gly Gln Ala Phe Lys Asn His Met Ser  
325 330 335  
Glu Met Phe Ala Tyr His Ala Thr Met Met Ser Asn Thr Leu Gly Thr  
340 345 350

Ser Thr Val Val Phe Thr Arg Thr Gly Phe Met Ala Ile Leu Leu Ser  
355 360 365  
His Tyr Arg Pro Ser Gly Thr Ile Tyr Ala Phe Thr Asn Glu Lys Lys  
370 375 380  
Ile Gln Gln Arg Leu Ala Leu Tyr Gln Gly Val Cys Pro Ile Tyr Met  
385 390 395 400  
Glu Phe Thr Asp Asp Ala Glu Glu Thr Phe Ala Asn Ala Leu Ala Thr  
405 410 415  
Leu Leu Lys Gln Gly Met Val Lys Lys Gly Glu Glu Ile Ala Ile Val  
420 425 430  
Gln Ser Gly Thr Gln Pro Ile Trp Arg Ser Gln Ser Thr His Asn Ile  
435 440 445  
Gln Val Arg Lys Val  
450

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..692
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

|             |            |             |            |             |             |     |
|-------------|------------|-------------|------------|-------------|-------------|-----|
| atcacttact  | taacatacta | agagagttat  | tagatcttga | aaaacatggc  | ttccaaggct  | 60  |
| ttgattctgt  | tgggtctctt | cgcaattctt  | ctggtggtct | ccgaagtttc  | tgccgcaagg  | 120 |
| atncgggcat  | ggtgaagcca | gagagtgagg  | aaactgtgca | acctgaaggt  | tatcacggag  | 180 |
| gacatggttg  | tcacggaggg | ggaggccact  | acggaggagg | aggccacggg  | catggaggac  | 240 |
| acaacggagg  | agggggccac | ggacttgacg  | gatacggagg | aggacatgga  | ggacactacg  | 300 |
| gaggaggagg  | ccacggactt | gacggatacg  | gaggagggtg | aggacactat  | ggaggagggtg | 360 |
| gaggacacta  | cggaggaggt | ggaggacact  | acggaggagg | tggaggacac  | tacggaggag  | 420 |
| gtggtggagg  | acacggaggt | ggaggacact  | acggagggtg | tggaggagga  | tacggagggtg | 480 |
| gaggaggaca  | ccacggagga | ggaggccacg  | ggctaaacga | acctgttcag  | actaagccgg  | 540 |
| gtgttttaaaa | ctatataata | tcttctactac | catgcatgat | tgcataatata | tatatacgct  | 600 |
| tatgtattat  | ctatatgcct | ataaataaac  | catggtgagt | ttgtaacgca  | gtgccttcag  | 660 |
| aaatgttcgg  | aataaatttc | cataatatta  | gt         |             |             |     |

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Leu | Leu | Asn | Ile | Leu | Arg | Glu | Leu | Asp | Leu | Glu | Lys | His | Gly |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Phe | Gln | Gly | Phe | Asp | Ser | Val | Gly | Ser | Leu | Arg | Asn | Ser | Ser | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Leu | Arg | Ser | Phe | Cys | Arg | Lys | Asp | Xaa | Gly | Met | Val | Lys | Pro | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Glu | Glu | Thr | Val | Gln | Pro | Glu | Gly | Tyr | His | Gly | Gly | His | Gly | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Gly | Gly | Gly | Gly | His | Tyr | Gly | Gly | Gly | Gly | His | Gly | His | Gly | Gly |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Asn | Gly | Gly | Gly | Gly | His | Gly | Leu | Asp | Gly | Tyr | Gly | Gly | Gly | His |

85 90 95  
Gly His Tyr Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly Gly  
100 105 110  
Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly  
115 120 125  
His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Gly His  
130 135 140  
Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Tyr Gly Gly Gly  
145 150 155 160  
Gly Gly His His Gly Gly Gly Gly His Gly Leu Asn Glu Pro Val Gln  
165 170 175  
Thr Lys Pro Gly Val  
180

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His  
1 5 10 15  
Gly Gly His Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly  
20 25 30  
His Gly His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly  
35 40 45  
Tyr Gly Gly Gly His Gly Gly His Tyr Gly Gly Gly Gly His Gly Leu  
50 55 60  
Asp Gly Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His  
65 70 75 80  
Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly His Tyr Gly  
85 90 95  
Gly Gly Gly Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly  
100 105 110  
Gly Gly Tyr Gly Gly Gly Gly Gly His His Gly Gly Gly Gly His Gly  
115 120 125  
Leu Asn Glu Pro Val Gln Thr Lys Pro Gly Val  
130 135

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Val Val Thr Glu Gly Glu Ala Thr Thr Glu Glu Glu Ala Thr Gly  
1 5 10 15  
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu  
20 25 30  
Glu Asp Met Glu Asp Thr Thr Glu Glu Glu Ala Thr Asp Leu Thr Asp  
35 40 45



Thr Glu Glu Val Glu Asp Thr Met Glu Glu Val Glu Asp Thr Thr Glu  
50 55 60  
Glu Val Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu Glu Val  
65 70 75 80  
Val Glu Asp Thr Glu Val Glu Asp Thr Thr Glu Val Val Glu Glu Asp  
85 90 95  
Thr Glu Val Glu Glu Asp Thr Thr Glu Glu Glu Ala Thr Gly  
100 105 110

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

|            |            |             |            |             |             |      |
|------------|------------|-------------|------------|-------------|-------------|------|
| accagaagaa | gagccacaca | ctcacaaatt  | aaaaagagag | agagagagag  | agagacagag  | 60   |
| agagagagag | attctgcgga | ggagcttctt  | cttcgtaggg | tgttcacgt   | tattaacgtt  | 120  |
| atcgccccta | cgtcagctcc | atctccagaa  | acatgggtgc | aggtggaaga  | atgccggttc  | 180  |
| ctacttcttc | caagaaatcg | gaaaccgaca  | ccacaaagcg | tgtgccgtgc  | gagaaaccgc  | 240  |
| ctttctcggt | gggagatctg | aagaaagcaa  | tcccgcgcga | ttgtttcaaa  | cgctcaatcc  | 300  |
| ctcgctcttt | ctcctacctt | atcagtgaca  | tcattatagc | ctcatgcttc  | tactacgtcg  | 360  |
| ccaccaatta | cttctctctc | ctccctcagc  | ctctctctta | cttggttgg   | ccactctatt  | 420  |
| gggcctgtca | aggctgtgtc | ctaactggta  | tctgggtcat | agcccacgaa  | tgcggtcacc  | 480  |
| acgcattcag | cgaactacaa | tggctggatg  | acacagttgg | tcttatcttc  | cattccttcc  | 540  |
| tcctcgctcc | ttactttctc | tgggaagtata | gtcatcgccg | tcaccattcc  | aacactggat  | 600  |
| ccctcgaaag | agatgaagta | tttgtcccaa  | agcagaaatc | agcaatcaag  | tggtagcgga  | 660  |
| aatacctcaa | caaccctctt | ggacgcacat  | tgatgttaac | cgtccagttt  | gtcctcgggt  | 720  |
| ggcccttgta | cttagccttt | aacgtctctg  | gcagaccgta | tgacgggttc  | gcttgccatt  | 780  |
| tcttccccaa | cgctcccata | tacaatgacc  | gagaacgcct | ccagatatata | ctctctgatg  | 840  |
| cgggtattct | agcctgtgtg | tttggctctt  | accgttacgc | tgtcgcacaa  | gggatggcct  | 900  |
| cgatgatctg | cctctacgga | gtaccgcttc  | tgatagtga  | tgcgttcctc  | gtcttgatca  | 960  |
| cttacttgca | gcacactcat | ccctcgttgc  | ctcactacga | ttcatcagag  | tgggactggc  | 1020 |
| tcaggggagc | tttggctacc | gtagacagag  | actacnga   | attgaacaag  | gtgttccaca  | 1080 |
| acattacaga | cacacacgtg | gctcatcacc  | tgttctcgac | aatgccgcat  | tataacgcaa  | 1140 |
| tggaagctac | aaaggcgata | aagccaattc  | tgggagacta | ttaccagttc  | gatggaacac  | 1200 |
| cgtggtatgt | ggcgatgtat | agggaggcaa  | aggagtgtat | ctatgtagaa  | ccggacaggg  | 1260 |
| aaggtgacaa | gaaaggtgtg | tactggtaca  | acaataagtt | atgaggatga  | tggatgaagaa | 1320 |
| attgtcgact | tttctctgtg | ctgtttgtct  | tttgttaaag | aagctatgct  | tcgtttta    | 1380 |
| aatcttattg | tccattttgt | tgtgttatga  | cattttgggt | gctcattatg  | ttatgtggga  | 1440 |
| agttagtgtc | c          |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser |  |
| 1 5 10 15                                                       |  |
| Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser |  |
| 20 25 30                                                        |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Asp | Leu | Lys | Lys | Ala | Ile | Pro | Pro | His | Cys | Phe | Lys | Arg | Ser |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Pro | Arg | Ser | Phe | Ser | Tyr | Leu | Ile | Ser | Asp | Ile | Ile | Ile | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Phe | Tyr | Tyr | Val | Ala | Thr | Asn | Tyr | Phe | Ser | Leu | Leu | Pro | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Leu | Ser | Tyr | Leu | Ala | Trp | Pro | Leu | Tyr | Trp | Ala | Cys | Gln | Gly | Cys | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Thr | Gly | Ile | Trp | Val | Ile | Ala | His | Glu | Cys | Gly | His | His | Ala | Phe |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Asp | Tyr | Gln | Trp | Leu | Asp | Asp | Thr | Val | Gly | Leu | Ile | Phe | His | Ser |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Phe | Leu | Leu | Val | Pro | Tyr | Phe | Ser | Trp | Lys | Tyr | Ser | His | Arg | Arg | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Ser | Asn | Thr | Gly | Ser | Leu | Glu | Arg | Asp | Glu | Val | Phe | Val | Pro | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Lys | Ser | Ala | Ile | Lys | Trp | Tyr | Gly | Lys | Tyr | Leu | Asn | Asn | Pro | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Arg | Ile | Met | Met | Leu | Thr | Val | Gln | Phe | Val | Leu | Gly | Trp | Pro | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Leu | Ala | Phe | Asn | Val | Ser | Gly | Arg | Pro | Tyr | Asp | Gly | Phe | Ala | Cys |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Phe | Phe | Pro | Asn | Ala | Pro | Ile | Tyr | Asn | Asp | Arg | Glu | Arg | Leu | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Tyr | Leu | Ser | Asp | Ala | Gly | Ile | Leu | Ala | Val | Cys | Phe | Gly | Leu | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Tyr | Ala | Ala | Ala | Gln | Gly | Met | Ala | Ser | Met | Ile | Cys | Leu | Tyr | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Pro | Leu | Leu | Ile | Val | Asn | Ala | Phe | Leu | Val | Leu | Ile | Thr | Tyr | Leu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | His | Thr | His | Pro | Ser | Leu | Pro | His | Tyr | Asp | Ser | Ser | Glu | Trp | Asp |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Trp | Leu | Arg | Gly | Ala | Leu | Ala | Thr | Val | Asp | Arg | Asp | Tyr | Xaa | Ile | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Lys | Val | Phe | His | Asn | Ile | Thr | Asp | Thr | His | Val | Ala | His | His | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Ser | Thr | Met | Pro | His | Tyr | Asn | Ala | Met | Glu | Ala | Thr | Lys | Ala | Ile |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Pro | Ile | Leu | Gly | Asp | Tyr | Tyr | Gln | Phe | Asp | Gly | Thr | Pro | Trp | Tyr |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val | Ala | Met | Tyr | Arg | Glu | Ala | Lys | Glu | Cys | Ile | Tyr | Val | Glu | Pro | Asp |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Arg | Glu | Gly | Asp | Lys | Lys | Gly | Val | Tyr | Trp | Tyr | Asn | Asn | Lys | Leu |     |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..377

(D) OTHER INFORMATION: / Ceres Seq. ID 1498409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Val | Pro | Thr | Ser | Ser | Lys | Lys | Ser | Glu | Thr | Asp | Thr | Thr | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Val | Pro | Cys | Glu | Lys | Pro | Pro | Phe | Ser | Val | Gly | Asp | Leu | Lys | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Pro | Pro | His | Cys | Phe | Lys | Arg | Ser | Ile | Pro | Arg | Ser | Phe | Ser |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 35  |     | 40  |     | 45  |     |     |     |     |     |     |     |     |     |     |
| Tyr | Leu | Ile | Ser | Asp | Ile | Ile | Ile | Ala | Ser | Cys | Phe | Tyr | Tyr | Val | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Asn | Tyr | Phe | Ser | Leu | Leu | Pro | Gln | Pro | Leu | Ser | Tyr | Leu | Ala | Trp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Leu | Tyr | Trp | Ala | Cys | Gln | Gly | Cys | Val | Leu | Thr | Gly | Ile | Trp | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ala | His | Glu | Cys | Gly | His | His | Ala | Phe | Ser | Asp | Tyr | Gln | Trp | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Asp | Thr | Val | Gly | Leu | Ile | Phe | His | Ser | Phe | Leu | Leu | Val | Pro | Tyr |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Phe | Ser | Trp | Lys | Tyr | Ser | His | Arg | Arg | His | His | Ser | Asn | Thr | Gly | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Glu | Arg | Asp | Glu | Val | Phe | Val | Pro | Lys | Gln | Lys | Ser | Ala | Ile | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Trp | Tyr | Gly | Lys | Tyr | Leu | Asn | Asn | Pro | Leu | Gly | Arg | Ile | Met | Met | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Val | Gln | Phe | Val | Leu | Gly | Trp | Pro | Leu | Tyr | Leu | Ala | Phe | Asn | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Gly | Arg | Pro | Tyr | Asp | Gly | Phe | Ala | Cys | His | Phe | Phe | Pro | Asn | Ala |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Ile | Tyr | Asn | Asp | Arg | Glu | Arg | Leu | Gln | Ile | Tyr | Leu | Ser | Asp | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Ile | Leu | Ala | Val | Cys | Phe | Gly | Leu | Tyr | Arg | Tyr | Ala | Ala | Ala | Gln |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Met | Ala | Ser | Met | Ile | Cys | Leu | Tyr | Gly | Val | Pro | Leu | Leu | Ile | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Ala | Phe | Leu | Val | Leu | Ile | Thr | Tyr | Leu | Gln | His | Thr | His | Pro | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Pro | His | Tyr | Asp | Ser | Ser | Glu | Trp | Asp | Trp | Leu | Arg | Gly | Ala | Leu |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Thr | Val | Asp | Arg | Asp | Tyr | Xaa | Ile | Leu | Asn | Lys | Val | Phe | His | Asn |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Thr | Asp | Thr | His | Val | Ala | His | His | Leu | Phe | Ser | Thr | Met | Pro | His |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Tyr | Asn | Ala | Met | Glu | Ala | Thr | Lys | Ala | Ile | Lys | Pro | Ile | Leu | Gly | Asp |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Tyr | Tyr | Gln | Phe | Asp | Gly | Thr | Pro | Trp | Tyr | Val | Ala | Met | Tyr | Arg | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     | 350 |     |     |     |
| Ala | Lys | Glu | Cys | Ile | Tyr | Val | Glu | Pro | Asp | Arg | Glu | Gly | Asp | Lys | Lys |
|     | 355 |     |     |     |     |     | 360 |     |     |     | 365 |     |     |     |     |
| Gly | Val | Tyr | Trp | Tyr | Asn | Asn | Lys | Leu |     |     |     |     |     |     |     |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1498410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Leu | Thr | Val | Gln | Phe | Val | Leu | Gly | Trp | Pro | Leu | Tyr | Leu | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Asn | Val | Ser | Gly | Arg | Pro | Tyr | Asp | Gly | Phe | Ala | Cys | His | Phe | Phe |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Pro | Asn | Ala | Pro | Ile | Tyr | Asn | Asp | Arg | Glu | Arg | Leu | Gln | Ile | Tyr | Leu |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala  
50 55 60  
Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu  
65 70 75 80  
Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr  
85 90 95  
His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg  
100 105 110  
Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Xaa Ile Leu Asn Lys Val  
115 120 125  
Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr  
130 135 140  
Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile  
145 150 155 160  
Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met  
165 170 175  
Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly  
180 185 190  
Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu  
195 200

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| aaaccaa    | amcaattaag  | ctaaaaaaaa  | aaccaaagga  | tgtctcagaa  | actcatgttc  | 60   |
| ttgttcaccc | ttgcctgcct  | ctcctcggtta | ccatctcctt  | ttatctccgc  | ccaaataccg  | 120  |
| gccattggaa | atgccacttc  | accgtcaa    | atatgtagat  | tcgcgcgga   | tccatcttat  | 180  |
| tgtagatcgg | ttcttccaaa  | ccagcccga   | gatatatatt  | cctacggacg  | tttgtctcta  | 240  |
| cgaagatccc | tctccagccc  | gccggttcat  | ttcgatgac   | gacgctgaac  | ttgaccggaa  | 300  |
| aggcaaagt  | gctgctaaat  | ccacagtagg  | ggctctcgaa  | gactgcaa    | tcctagccag  | 360  |
| cctgactatg | gactacctcc  | ttagtagctc  | acagacggct  | gattccacca  | aaacactgtc  | 420  |
| gttatctagg | gccgaggatg  | ttcatacatt  | tctgagtgt   | gccatcacca  | atgagcagac  | 480  |
| ttgtcttgaa | ggacttaaat  | caacggcgct  | cgaaaatggt  | ctttccggtg  | atcttttcaa  | 540  |
| cgatacaaaa | ctctatgggg  | tgctctctgc  | ccctttctcc  | aaagggtggg  | tgccaagaa   | 600  |
| gcaaagatcg | agaccgattt  | ggcaaccaca  | agccagggtc  | aaaaagtgtt  | ttgggtttccg | 660  |
| taacggtaaa | ttaccgttaa  | agatgacgga  | aagggcacgt  | gccgtttaca  | acaccgtgac  | 720  |
| tagaagaaa  | cttctccaat  | cggatgcaga  | cgccgttcag  | gtgagcgaca  | ttgtgacggt  | 780  |
| gatccagaac | gggacgggaa  | acttcacgac  | cataaacgcc  | gccattgcag  | ctgcaccaaa  | 840  |
| taaaactgac | ggtagtaacg  | gttacttctt  | gatctacgta  | acggcgggat  | tgtacgagga  | 900  |
| atacgtggaa | gttcccaaga  | acaagagata  | tgtgatgatg  | atcgggtgacg | gcatcaacca  | 960  |
| gaccgttatc | accggaaca   | ggagtgtcgt  | tgatggatgg  | acaactttca  | attcagccac  | 1020 |
| atctattcta | tcagggtcca  | actttattgg  | tgtaaacata  | acaatccgca  | atacggcagg  | 1080 |
| accaacaaa  | ggccaagctg  | tggcattgag  | gagtgggtggg | gacttgtctg  | ttttctacag  | 1140 |
| ttgtagtgtt | gaagcctatc  | aagacacgtt  | atacacacat  | tctctcagac  | agttttatcg  | 1200 |
| tgaatgtgat | gtctatggta  | ctggtgattt  | tatatttggt  | aacgctgcag  | tggtattaca  | 1260 |
| aaactgtaat | ttgtatccac  | gtcaacctcg  | caaagggtcaa | tcgaacgagg  | ttacgggtca  | 1320 |
| aggtcgtact | gatccgaacc  | aaaacactgg  | gacggcaatt  | catggttgta  | ctataagacc  | 1380 |
| ggcagatgat | ttgggtacga  | gcaactatac  | agtgaagact  | tatcttggtc  | gaccatggaa  | 1440 |
| ggaatattct | agaaccgttg  | tcattgcaaac | ttacatagac  | gggtttctag  | aaccgagttg  | 1500 |
| ttggaatgca | tgggtctggtg | attttgcatt  | gagcacactt  | tactacgcgg  | aatataataa  | 1560 |
| taccggacct | ggttctgaca  | cgacaaaccg  | agtcacttgg  | cctgggttatc | acgtcatcaa  | 1620 |
| cgcaactgat | gcttccaatt  | tcacggtcac  | caatttcctt  | gttggtgaag  | gttggtattg  | 1680 |
| acaaaccgga | gtgcctttcg  | tgggtggact  | gatcgcataa  | tcaaccaacc  | ttatactata  | 1740 |

tatgatatgt taattagtta aattatttaa tcattcatgt gttgtttttt taatcaaata 1800  
attatttagt ggtgcctgat tcaatagat ttgtaataac tttaacttac tattgtacaa 1860  
ccgaatgggtt ttcttcg

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Leu | His | Arg | Gln | Ile | Tyr | Val | Asp | Ser | Arg | Arg | Ile | His | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Val | Asp | Arg | Phe | Phe | Gln | Thr | Ser | Pro | Glu | Ile | Tyr | Ile | Pro | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Val | Cys | Leu | Tyr | Glu | Asp | Pro | Ser | Pro | Ala | Arg | Arg | Phe | Ile | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Ile | Asp | Ala | Glu | Leu | Asp | Arg | Lys | Gly | Lys | Val | Ala | Ala | Lys | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Val | Gly | Ala | Leu | Glu | Asp | Cys | Lys | Phe | Leu | Ala | Ser | Leu | Thr | Met |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Tyr | Leu | Leu | Ser | Ser | Gln | Thr | Ala | Asp | Ser | Thr | Lys | Thr | Leu |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Leu | Ser | Arg | Ala | Glu | Asp | Val | His | Thr | Phe | Leu | Ser | Ala | Ala | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Asn | Glu | Gln | Thr | Cys | Leu | Glu | Gly | Leu | Lys | Ser | Thr | Ala | Ser | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Gly | Leu | Ser | Gly | Asp | Leu | Phe | Asn | Asp | Thr | Lys | Leu | Tyr | Gly | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Leu | Ala | Leu | Phe | Ser | Lys | Gly | Trp | Val | Pro | Arg | Arg | Gln | Arg | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Pro | Ile | Trp | Gln | Pro | Gln | Ala | Arg | Phe | Lys | Lys | Phe | Phe | Gly | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Arg | Asn | Gly | Lys | Leu | Pro | Leu | Lys | Met | Thr | Glu | Arg | Ala | Arg | Ala | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Tyr | Asn | Thr | Val | Thr | Arg | Arg | Lys | Leu | Leu | Gln | Ser | Asp | Ala | Asp | Ala |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Gln | Val | Ser | Asp | Ile | Val | Thr | Val | Ile | Gln | Asn | Gly | Thr | Gly | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Thr | Thr | Ile | Asn | Ala | Ala | Ile | Ala | Ala | Ala | Pro | Asn | Lys | Thr | Asp |
| 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |     |
| Gly | Ser | Asn | Gly | Tyr | Phe | Leu | Ile | Tyr | Val | Thr | Ala | Gly | Leu | Tyr | Glu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Glu | Tyr | Val | Glu | Val | Pro | Lys | Asn | Lys | Arg | Tyr | Val | Met | Met | Ile | Gly |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Gly | Ile | Asn | Gln | Thr | Val | Ile | Thr | Gly | Asn | Arg | Ser | Val | Val | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Trp | Thr | Thr | Phe | Asn | Ser | Ala | Thr | Phe | Ile | Leu | Ser | Gly | Pro | Asn |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | Ile | Gly | Val | Asn | Ile | Thr | Ile | Arg | Asn | Thr | Ala | Gly | Pro | Thr | Lys |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Gly | Gln | Ala | Val | Ala | Leu | Arg | Ser | Gly | Gly | Asp | Leu | Ser | Val | Phe | Tyr |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Cys | Ser | Phe | Glu | Ala | Tyr | Gln | Asp | Thr | Leu | Tyr | Thr | His | Ser | Leu |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Arg | Gln | Phe | Tyr | Arg | Glu | Cys | Asp | Val | Tyr | Gly | Thr | Val | Asp | Phe | Ile |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |

Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro Arg  
370 375 380  
Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg Thr  
385 390 395 400  
Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile Arg  
405 410 415  
Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr Leu  
420 425 430  
Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr Tyr  
435 440 445  
Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly Asp  
450 455 460  
Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly Pro  
465 470 475 480  
Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val Ile  
485 490 495  
Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val Gly  
500 505 510  
Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu Ile  
515 520 525  
Ala

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1498413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Met Ile Asp Ala Glu Leu Asp Arg Lys Gly Lys Val Ala Ala Lys Ser  
1 5 10 15  
Thr Val Gly Ala Leu Glu Asp Cys Lys Phe Leu Ala Ser Leu Thr Met  
20 25 30  
Asp Tyr Leu Leu Ser Ser Ser Gln Thr Ala Asp Ser Thr Lys Thr Leu  
35 40 45  
Ser Leu Ser Arg Ala Glu Asp Val His Thr Phe Leu Ser Ala Ala Ile  
50 55 60  
Thr Asn Glu Gln Thr Cys Leu Glu Gly Leu Lys Ser Thr Ala Ser Glu  
65 70 75 80  
Asn Gly Leu Ser Gly Asp Leu Phe Asn Asp Thr Lys Leu Tyr Gly Val  
85 90 95  
Ser Leu Ala Leu Phe Ser Lys Gly Trp Val Pro Arg Arg Gln Arg Ser  
100 105 110  
Arg Pro Ile Trp Gln Pro Gln Ala Arg Phe Lys Lys Phe Phe Gly Phe  
115 120 125  
Arg Asn Gly Lys Leu Pro Leu Lys Met Thr Glu Arg Ala Arg Ala Val  
130 135 140  
Tyr Asn Thr Val Thr Arg Arg Lys Leu Leu Gln Ser Asp Ala Asp Ala  
145 150 155 160  
Val Gln Val Ser Asp Ile Val Thr Val Ile Gln Asn Gly Thr Gly Asn  
165 170 175  
Phe Thr Thr Ile Asn Ala Ala Ile Ala Ala Pro Asn Lys Thr Asp  
180 185 190  
Gly Ser Asn Gly Tyr Phe Leu Ile Tyr Val Thr Ala Gly Leu Tyr Glu  
195 200 205  
Glu Tyr Val Glu Val Pro Lys Asn Lys Arg Tyr Val Met Met Ile Gly

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 210                                                             | 215 | 220 |
| Asp Gly Ile Asn Gln Thr Val Ile Thr Gly Asn Arg Ser Val Val Asp |     |     |
| 225                                                             | 230 | 235 |
| Gly Trp Thr Thr Phe Asn Ser Ala Thr Phe Ile Leu Ser Gly Pro Asn |     | 240 |
|                                                                 | 245 | 250 |
| Phe Ile Gly Val Asn Ile Thr Ile Arg Asn Thr Ala Gly Pro Thr Lys |     | 255 |
|                                                                 | 260 | 265 |
| Gly Gln Ala Val Ala Leu Arg Ser Gly Gly Asp Leu Ser Val Phe Tyr |     | 270 |
|                                                                 | 275 | 280 |
| Ser Cys Ser Phe Glu Ala Tyr Gln Asp Thr Leu Tyr Thr His Ser Leu |     | 285 |
|                                                                 | 290 | 295 |
| Arg Gln Phe Tyr Arg Glu Cys Asp Val Tyr Gly Thr Val Asp Phe Ile |     | 300 |
| 305                                                             | 310 | 315 |
| Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro Arg |     | 320 |
|                                                                 | 325 | 330 |
| Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg Thr |     | 335 |
|                                                                 | 340 | 345 |
| Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile Arg |     | 350 |
|                                                                 | 355 | 360 |
| Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr Leu |     | 365 |
|                                                                 | 370 | 375 |
| Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr Tyr |     | 380 |
| 385                                                             | 390 | 395 |
| Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly Asp |     | 400 |
|                                                                 | 405 | 410 |
| Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly Pro |     | 415 |
|                                                                 | 420 | 425 |
| Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val Ile |     | 430 |
|                                                                 | 435 | 440 |
| Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val Gly |     | 445 |
|                                                                 | 450 | 455 |
| Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu Ile |     | 460 |
| 465                                                             | 470 | 475 |
| Ala                                                             |     | 480 |

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 450 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..450

(D) OTHER INFORMATION: / Ceres Seq. ID 1498414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Asp Tyr Leu Ser Ser Ser Gln Thr Ala Asp Ser Thr Lys Thr     |     |
| 1                                                               | 5   |
| Leu Ser Leu Ser Arg Ala Glu Asp Val His Thr Phe Leu Ser Ala Ala |     |
|                                                                 | 20  |
| Ile Thr Asn Glu Gln Thr Cys Leu Glu Gly Leu Lys Ser Thr Ala Ser |     |
|                                                                 | 35  |
| Glu Asn Gly Leu Ser Gly Asp Leu Phe Asn Asp Thr Lys Leu Tyr Gly |     |
|                                                                 | 50  |
| Val Ser Leu Ala Leu Phe Ser Lys Gly Trp Val Pro Arg Arg Gln Arg |     |
| 65                                                              | 70  |
| Ser Arg Pro Ile Trp Gln Pro Gln Ala Arg Phe Lys Lys Phe Phe Gly |     |
|                                                                 | 85  |
| Phe Arg Asn Gly Lys Leu Pro Leu Lys Met Thr Glu Arg Ala Arg Ala |     |
|                                                                 | 100 |

Val Tyr Asn Thr Val Thr Arg Arg Lys Leu Leu Gln Ser Asp Ala Asp  
115 120 125  
Ala Val Gln Val Ser Asp Ile Val Thr Val Ile Gln Asn Gly Thr Gly  
130 135 140  
Asn Phe Thr Thr Ile Asn Ala Ala Ile Ala Ala Pro Asn Lys Thr  
145 150 155 160  
Asp Gly Ser Asn Gly Tyr Phe Leu Ile Tyr Val Thr Ala Gly Leu Tyr  
165 170 175  
Glu Glu Tyr Val Glu Val Pro Lys Asn Lys Arg Tyr Val Met Met Ile  
180 185 190  
Gly Asp Gly Ile Asn Gln Thr Val Ile Thr Gly Asn Arg Ser Val Val  
195 200 205  
Asp Gly Trp Thr Thr Phe Asn Ser Ala Thr Phe Ile Leu Ser Gly Pro  
210 215 220  
Asn Phe Ile Gly Val Asn Ile Thr Ile Arg Asn Thr Ala Gly Pro Thr  
225 230 235 240  
Lys Gly Gln Ala Val Ala Leu Arg Ser Gly Gly Asp Leu Ser Val Phe  
245 250 255  
Tyr Ser Cys Ser Phe Glu Ala Tyr Gln Asp Thr Leu Tyr Thr His Ser  
260 265 270  
Leu Arg Gln Phe Tyr Arg Glu Cys Asp Val Tyr Gly Thr Val Asp Phe  
275 280 285  
Ile Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro  
290 295 300  
Arg Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg  
305 310 315 320  
Thr Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile  
325 330 335  
Arg Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr  
340 345 350  
Leu Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr  
355 360 365  
Tyr Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly  
370 375 380  
Asp Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly  
385 390 395 400  
Pro Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val  
405 410 415  
Ile Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val  
420 425 430  
Gly Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu  
435 440 445  
Ile Ala  
450

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| attttttgcc cctcgaaaga aagtcaaatt actcaacagc gtcgtttctt cttgtttatc  | 60  |
| gccaatcgcc attattatcg cgggtgcctct tctcacctct cgccgtctct ttgaaccgga | 120 |
| ggtttcctcc accccttgaa aattccatca tcgattgacc tatagctccg agatctgctc  | 180 |
| ttcaatttga tgctcttcca ttagttagaa aagttgcttt tgatcggagc aactatgggg  | 240 |
| tcgtcttttg agaccatcga tatcggtagc agtgctcgga gaattggcgt agataatcgt  | 300 |



|            |            |             |            |             |            |      |
|------------|------------|-------------|------------|-------------|------------|------|
| atttctctca | aattttactt | caggatcgct  | gataatatcc | tcaaacaggc  | caacatattt | 360  |
| cgggcagaga | agaatgttat | tgatttatat  | gtcatgtctc | tgcggttttc  | aagcttggct | 420  |
| ctcgagacta | taccgtccca | tcgagattac  | agaacatctc | taaaaagcaa  | taaagagtat | 480  |
| ttgagaatga | gactactaga | tgtcttgacg  | gagctggaga | agttgaaacc  | agttgtacag | 540  |
| caaaggattg | atgaactgta | tcccaagctc  | aaacctcgat | ataacgttca  | agctcatcca | 600  |
| gcaaattggt | ccctaggctg | gtcttctgcc  | gtgaaaccgt | catttaatat  | ctatgatcat | 660  |
| gcaaaggtaa | gaaatcctcc | tggacataat  | tctggctaca | tgggttccag  | gggtcagcaa | 720  |
| tttttgaacg | ctgcaccact | tgaagagcgt  | ttccgaaaga | tgctcggtgaa | cttccgacca | 780  |
| aatgaagaaa | ccctttccaa | gcattctatc  | ttgggtccag | gtggactctc  | tgcacagtgg | 840  |
| cagccaccaa | agtatgatac | aaagggttcaa | tatccaagca | atatagattt  | ttcgcctggt | 900  |
| gtaatcccaa | gcttccaaca | acttgtggac  | agcaaaccaa | tgataacgaa  | tggcagtaac | 960  |
| gatgaacctg | aaaagccaat | tgtggaacct  | agtgttgcat | ctaataaaaa  | aatccagaaa | 1020 |
| aattacactg | aagagctttc | ttccatgatt  | tctttcgaag | agccagaaa   | cgtaaatgag | 1080 |
| aacaatctca | ttaggcaacc | ttcaccacct  | ccagtgttag | cagaagttca  | agacttggtt | 1140 |
| cctgctttat | gtcctgaagt | tagagaaccg  | gaatgtatga | tagaaaactc  | tctgccggat | 1200 |
| gagtctctac | ggtcggagtc | tctcttgaa   | cttcatattg | cgacttcaat  | gatggatacc | 1260 |
| tttatgaggc | ttgccaagtc | aaacactaaa  | aagaatttag | agacgtgtgg  | tattcttgcc | 1320 |
| ggttcactaa | aaaacagaaa | attttacatt  | acagctctca | tcataccaaa  | gcaggaatcg | 1380 |
| acatctgact | cgtgtcaggc | cacgaacgaa  | gaagagatat | ttgaagtaca  | ggacaagcaa | 1440 |
| tcccttttcc | cactcggatg | gattcatacg  | catccgacac | agtcttggtt  | catgtcatcc | 1500 |
| attgatgttc | acacacacta | ttcataccag  | attatgttac | cagaagctgt  | ggcaatcggt | 1560 |
| atggcgccac | aagactcttc | aaggaatcac  | ggaatatctc | ggctgacgac  | gccgggagga | 1620 |
| atgacggtga | taaggaattg | tgaccggcgt  | gggtttcatg | cgcacagttc  | accggaggac | 1680 |
| ggaggaccaa | tttacaatac | ctgtaaggaa  | gtttacatga | acccaaatct  | caagtttgat | 1740 |
| gtcattgatc | tcagatagca | tcacttgccg  | gtttgaaagt | gaaactatgt  | tctcaaggcc | 1800 |
| atcttttctc | tacgattgta | acaattatgt  | atctgtttat | atcccgattt  | taatatgatc | 1860 |
| tacgtaagtt | ttcgtgc    |             |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..507

(D) OTHER INFORMATION: / Ceres Seq. ID 1498424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Ser | Phe | Glu | Thr | Ile | Asp | Ile | Gly | Thr | Ser | Ala | Arg | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Gly | Val | Asp | Asn | Arg | Ile | Ser | Leu | Lys | Phe | Tyr | Phe | Arg | Ile | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asp | Asn | Ile | Leu | Lys | Gln | Ala | Asn | Ile | Phe | Arg | Ala | Glu | Lys | Asn | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ile | Asp | Leu | Tyr | Val | Met | Leu | Arg | Phe | Ser | Ser | Leu | Ala | Leu | Glu |     |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Thr | Ile | Pro | Ser | His | Arg | Asp | Tyr | Arg | Thr | Ser | Leu | Lys | Ser | Asn | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Tyr | Leu | Arg | Met | Arg | Leu | Leu | Asp | Val | Leu | Thr | Glu | Leu | Glu | Lys |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Leu | Lys | Pro | Val | Val | Gln | Gln | Arg | Ile | Asp | Glu | Leu | Tyr | Pro | Lys | Leu |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Lys | Pro | Arg | Tyr | Asn | Val | Gln | Ala | His | Pro | Ala | Asn | Gly | Ser | Leu | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Trp | Ser | Ser | Ala | Val | Lys | Pro | Ser | Phe | Asn | Ser | Tyr | Asp | His | Ala | Lys |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Val | Arg | Asn | Pro | Pro | Gly | His | Asn | Ser | Gly | Tyr | Met | Gly | Ser | Arg | Gly |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Gln | Gln | Phe | Leu | Asn | Ala | Ala | Pro | Leu | Glu | Arg | Phe | Arg | Lys | Met |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |

Ser Val Asn Phe Arg Pro Asn Glu Glu Thr Leu Ser Lys His Ser Ile  
180 185 190  
Leu Gly Pro Gly Gly Leu Ser Ala Gln Trp Gln Pro Pro Lys Tyr Asp  
195 200 205  
Thr Lys Val Gln Tyr Pro Ser Asn Ile Asp Phe Ser Pro Val Val Ile  
210 215 220  
Pro Ser Phe Gln Gln Leu Val Asp Ser Lys Pro Met Ile Thr Asn Gly  
225 230 235 240  
Ser Asn Asp Glu Pro Glu Lys Pro Ile Val Glu Pro Ser Val Ala Ser  
245 250 255  
Asn Glu Lys Ile Gln Lys Asn Tyr Thr Glu Glu Leu Ser Ser Met Ile  
260 265 270  
Ser Phe Glu Glu Pro Glu Ser Val Asn Glu Asn Asn Leu Ile Arg Gln  
275 280 285  
Pro Ser Pro Pro Pro Val Leu Ala Glu Val Gln Asp Leu Val Pro Ala  
290 295 300  
Leu Cys Pro Glu Val Arg Glu Pro Glu Cys Met Ile Glu Asn Ser Leu  
305 310 315 320  
Pro Asp Glu Ser Leu Arg Ser Glu Ser Pro Leu Glu Leu His Ile Ala  
325 330 335  
Thr Ser Met Met Asp Thr Phe Met Arg Leu Ala Lys Ser Asn Thr Lys  
340 345 350  
Lys Asn Leu Glu Thr Cys Gly Ile Leu Ala Gly Ser Leu Lys Asn Arg  
355 360 365  
Lys Phe Tyr Ile Thr Ala Leu Ile Ile Pro Lys Gln Glu Ser Thr Ser  
370 375 380  
Asp Ser Cys Gln Ala Thr Asn Glu Glu Glu Ile Phe Glu Val Gln Asp  
385 390 395 400  
Lys Gln Ser Leu Phe Pro Leu Gly Trp Ile His Thr His Pro Thr Gln  
405 410 415  
Ser Cys Phe Met Ser Ser Ile Asp Val His Thr His Tyr Ser Tyr Gln  
420 425 430  
Ile Met Leu Pro Glu Ala Val Ala Ile Val Met Ala Pro Gln Asp Ser  
435 440 445  
Ser Arg Asn His Gly Ile Phe Arg Leu Thr Thr Pro Gly Gly Met Thr  
450 455 460  
Val Ile Arg Asn Cys Asp Arg Arg Gly Phe His Ala His Ser Ser Pro  
465 470 475 480  
Glu Asp Gly Gly Pro Ile Tyr Asn Thr Cys Lys Glu Val Tyr Met Asn  
485 490 495  
Pro Asn Leu Lys Phe Asp Val Ile Asp Leu Arg  
500 505

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..454
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Met Leu Leu Arg Phe Ser Ser Leu Ala Leu Glu Thr Ile Pro Ser His  
1 5 10 15  
Arg Asp Tyr Arg Thr Ser Leu Lys Ser Asn Lys Glu Tyr Leu Arg Met  
20 25 30  
Arg Leu Leu Asp Val Leu Thr Glu Leu Glu Lys Leu Lys Pro Val Val  
35 40 45  
Gln Gln Arg Ile Asp Glu Leu Tyr Pro Lys Leu Lys Pro Arg Tyr Asn

|                     |                     |                         |             |  |  |
|---------------------|---------------------|-------------------------|-------------|--|--|
| 50                  | 55                  | 60                      |             |  |  |
| Val Gln Ala His Pro | Ala Asn Gly Ser Leu | Gly Trp Ser Ser Ala Val |             |  |  |
| 65                  | 70                  | 75                      | 80          |  |  |
| Lys Pro Ser Phe Asn | Ser Tyr Asp His Ala | Lys Val Arg Asn Pro     | Pro         |  |  |
|                     | 85                  | 90                      | 95          |  |  |
| Gly His Asn Ser Gly | Tyr Met Gly Ser     | Arg Gly Gln Gln Phe     | Leu Asn     |  |  |
|                     | 100                 | 105                     | 110         |  |  |
| Ala Ala Pro Leu Glu | Glu Arg Phe Arg     | Lys Met Ser Val         | Asn Phe Arg |  |  |
|                     | 115                 | 120                     | 125         |  |  |
| Pro Asn Glu Glu Thr | Leu Ser Lys His     | Ser Ile Leu Gly         | Pro Gly Gly |  |  |
|                     | 130                 | 135                     | 140         |  |  |
| Leu Ser Ala Gln Trp | Gln Pro Pro Lys     | Tyr Asp Thr Lys         | Val Gln Tyr |  |  |
| 145                 | 150                 | 155                     | 160         |  |  |
| Pro Ser Asn Ile Asp | Phe Ser Pro Val     | Val Ile Pro Ser         | Phe Gln Gln |  |  |
|                     | 165                 | 170                     | 175         |  |  |
| Leu Val Asp Ser Lys | Pro Met Ile Thr     | Asn Gly Ser Asn         | Asp Glu Pro |  |  |
|                     | 180                 | 185                     | 190         |  |  |
| Glu Lys Pro Ile Val | Glu Pro Ser Val     | Ala Ser Asn Glu         | Lys Ile Gln |  |  |
|                     | 195                 | 200                     | 205         |  |  |
| Lys Asn Tyr Thr Glu | Glu Leu Ser Ser     | Met Ile Ser Phe         | Glu Glu Pro |  |  |
|                     | 210                 | 215                     | 220         |  |  |
| Glu Ser Val Asn Glu | Asn Asn Leu Ile     | Arg Gln Pro Ser         | Pro Pro Pro |  |  |
| 225                 | 230                 | 235                     | 240         |  |  |
| Val Leu Ala Glu Val | Gln Asp Leu Val     | Pro Ala Leu Cys         | Pro Glu Val |  |  |
|                     | 245                 | 250                     | 255         |  |  |
| Arg Glu Pro Glu Cys | Met Ile Glu Asn     | Ser Leu Pro Asp         | Glu Ser Leu |  |  |
|                     | 260                 | 265                     | 270         |  |  |
| Arg Ser Glu Ser Pro | Leu Glu Leu His     | Ile Ala Thr Ser         | Met Met Asp |  |  |
|                     | 275                 | 280                     | 285         |  |  |
| Thr Phe Met Arg Leu | Ala Lys Ser Asn     | Thr Lys Lys Asn         | Leu Glu Thr |  |  |
|                     | 290                 | 295                     | 300         |  |  |
| Cys Gly Ile Leu Ala | Gly Ser Leu Lys     | Asn Arg Lys Phe         | Tyr Ile Thr |  |  |
| 305                 | 310                 | 315                     | 320         |  |  |
| Ala Leu Ile Ile Pro | Lys Gln Glu Ser     | Thr Ser Asp Ser         | Cys Gln Ala |  |  |
|                     | 325                 | 330                     | 335         |  |  |
| Thr Asn Glu Glu Glu | Ile Phe Glu Val     | Gln Asp Lys Gln         | Ser Leu Phe |  |  |
|                     | 340                 | 345                     | 350         |  |  |
| Pro Leu Gly Trp Ile | His Thr His Pro     | Thr Gln Ser Cys         | Phe Met Ser |  |  |
|                     | 355                 | 360                     | 365         |  |  |
| Ser Ile Asp Val His | Thr His Tyr Ser     | Tyr Gln Ile Met         | Leu Pro Glu |  |  |
|                     | 370                 | 375                     | 380         |  |  |
| Ala Val Ala Ile Val | Met Ala Pro Gln     | Asp Ser Ser Arg         | Asn His Gly |  |  |
| 385                 | 390                 | 395                     | 400         |  |  |
| Ile Phe Arg Leu Thr | Pro Gly Gly Met     | Thr Val Ile Arg         | Asn Cys     |  |  |
|                     | 405                 | 410                     | 415         |  |  |
| Asp Arg Arg Gly Phe | His Ala His Ser     | Ser Pro Glu Asp         | Gly Gly Pro |  |  |
|                     | 420                 | 425                     | 430         |  |  |
| Ile Tyr Asn Thr Cys | Lys Glu Val Tyr     | Met Asn Pro Asn         | Leu Lys Phe |  |  |
|                     | 435                 | 440                     | 445         |  |  |
| Asp Val Ile Asp Leu | Arg                 |                         |             |  |  |
| 450                 |                     |                         |             |  |  |

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..423

(D) OTHER INFORMATION: / Ceres Seq. ID 1498426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Leu | Leu | Asp | Val | Leu | Thr | Glu | Leu | Glu | Lys | Leu | Lys | Pro | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Gln | Gln | Arg | Ile | Asp | Glu | Leu | Tyr | Pro | Lys | Leu | Lys | Pro | Arg | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Val | Gln | Ala | His | Pro | Ala | Asn | Gly | Ser | Leu | Gly | Trp | Ser | Ser | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Lys | Pro | Ser | Phe | Asn | Ser | Tyr | Asp | His | Ala | Lys | Val | Arg | Asn | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Pro | Gly | His | Asn | Ser | Gly | Tyr | Met | Gly | Ser | Arg | Gly | Gln | Gln | Phe | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Ala | Ala | Pro | Leu | Glu | Glu | Arg | Phe | Arg | Lys | Met | Ser | Val | Asn | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Pro | Asn | Glu | Glu | Thr | Leu | Ser | Lys | His | Ser | Ile | Leu | Gly | Pro | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Leu | Ser | Ala | Gln | Trp | Gln | Pro | Pro | Lys | Tyr | Asp | Thr | Lys | Val | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Tyr | Pro | Ser | Asn | Ile | Asp | Phe | Ser | Pro | Val | Val | Ile | Pro | Ser | Phe | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Gln | Leu | Val | Asp | Ser | Lys | Pro | Met | Ile | Thr | Asn | Gly | Ser | Asn | Asp | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |
| Pro | Glu | Lys | Pro | Ile | Val | Glu | Pro | Ser | Val | Ala | Ser | Asn | Glu | Lys | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Lys | Asn | Tyr | Thr | Glu | Glu | Leu | Ser | Ser | Met | Ile | Ser | Phe | Glu | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Glu | Ser | Val | Asn | Glu | Asn | Asn | Leu | Ile | Arg | Gln | Pro | Ser | Pro | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Val | Leu | Ala | Glu | Val | Gln | Asp | Leu | Val | Pro | Ala | Leu | Cys | Pro | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Arg | Glu | Pro | Glu | Cys | Met | Ile | Glu | Asn | Ser | Leu | Pro | Asp | Glu | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Leu | Arg | Ser | Glu | Ser | Pro | Leu | Glu | Leu | His | Ile | Ala | Thr | Ser | Met | Met |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Thr | Phe | Met | Arg | Leu | Ala | Lys | Ser | Asn | Thr | Lys | Lys | Asn | Leu | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Cys | Gly | Ile | Leu | Ala | Gly | Ser | Leu | Lys | Asn | Arg | Lys | Phe | Tyr | Ile |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Thr | Ala | Leu | Ile | Ile | Pro | Lys | Gln | Glu | Ser | Thr | Ser | Asp | Ser | Cys | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Thr | Asn | Glu | Glu | Glu | Ile | Phe | Glu | Val | Gln | Asp | Lys | Gln | Ser | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Pro | Leu | Gly | Trp | Ile | His | Thr | His | Pro | Thr | Gln | Ser | Cys | Phe | Met |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Ser | Ile | Asp | Val | His | Thr | His | Tyr | Ser | Tyr | Gln | Ile | Met | Leu | Pro |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Ala | Val | Ala | Ile | Val | Met | Ala | Pro | Gln | Asp | Ser | Ser | Arg | Asn | His |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Gly | Ile | Phe | Arg | Leu | Thr | Thr | Pro | Gly | Gly | Met | Thr | Val | Ile | Arg | Asn |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Cys | Asp | Arg | Arg | Gly | Phe | His | Ala | His | Ser | Ser | Pro | Glu | Asp | Gly | Gly |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Pro | Ile | Tyr | Asn | Thr | Cys | Lys | Glu | Val | Tyr | Met | Asn | Pro | Asn | Leu | Lys |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Phe | Asp | Val | Ile | Asp | Leu | Arg |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 420 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1321  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

|            |            |             |            |             |            |      |
|------------|------------|-------------|------------|-------------|------------|------|
| ttttcatcat | catctcagtc | tctctcgaag  | tttcaagttc | gcgactatgg  | cagcagcgat | 60   |
| gtcttcttct | tgttgcgctt | cctcgcttcg  | tttaatccca | ttcaaacgga  | ccttggtttc | 120  |
| ttcaatccat | tatccggcca | aaacccttct  | tctacgacca | ctaaaaccgt  | cggaagttcc | 180  |
| ttcctttcgc | cggacgatca | tcactttcca  | gaaaatttca | accgggattg  | ttcctccacc | 240  |
| atcggttca  | tcatctccgt | cgagctatgg  | agaccttcaa | ccaatcgaag  | agcttccacc | 300  |
| gaagctacaa | gagatcgta  | agcttttcca  | atcggtacaa | gagccaaagg  | ctaaatacga | 360  |
| gcagcttatg | ttctacggga | agaatctgac  | acctctcgat | tctcaattca  | agacgaggga | 420  |
| gaataaagta | gaaggatgtg | tttctcaggt  | ttgggttagg | gctttctttg  | atgaggaacg | 480  |
| taatgttgtg | tatgaagctg | attctgattc  | ggttctcact | aaagggttag  | ctgctctatt | 540  |
| agtcaagggt | ttatctggaa | gacctgtccc  | tgagattttg | aggataacac  | ctgatttcgc | 600  |
| tgttcttctc | gggttgacgc | agagtctgtc  | tccttctaga | aacaatggat  | tacttaatat | 660  |
| gcttaagctg | atgcagaaaa | aggctcttca  | tttggaagtc | aaagggtgagg | aagattcaag | 720  |
| ttctggagag | agttcagaat | ccagctttgt  | gtctattcct | gagactaagg  | acgaagctaa | 780  |
| tgttccggag | gtggattttg | agtctaaacc  | tgatctagtt | gaggattttg  | gaacagaaaa | 840  |
| gattgatgat | tctgagagtg | ggtaaatgtg  | tggtgcttta | gggagtagag  | ggatgaggat | 900  |
| aagagagaaa | ttggagaagg | agctagatcc  | tgttgagtta | gaagttgaag  | atgtttctta | 960  |
| ccagcacgca | ggacatgccg | ctgttagagg  | tagtgctggg | gatgatgggg  | aaacacattt | 1020 |
| caacttgcca | atcgtttcgg | atgctttcca  | aggtaaaagc | ttgggtcaaga | gacataggct | 1080 |
| gatatatgac | ttgttgcaag | atgagttgaa  | gagcgggtta | catgctctct  | ctattgtggc | 1140 |
| aaagactcct | gctgagggtt | gaggggtgaa  | cattggaaga | agtcagggtc  | tgattctttt | 1200 |
| acttcttttg | gtccatttgc | tttggaatatt | gttctctgga | ccttctaata  | atgtaaagag | 1260 |
| ctcgatcagg | attgtgttaa | atgagagata  | gatattgaag | gatataaata  | atgttttcgt | 1320 |

c

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 386 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..386  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | His | His | His | Ser | Leu | Ser | Arg | Ser | Phe | Lys | Phe | Ala | Thr | Met |     |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Ala | Ala | Ala | Met | Ser | Ser | Ser | Cys | Cys | Ala | Ser | Ser | Leu | Arg | Leu | Ile |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Pro | Phe | Lys | Arg | Thr | Leu | Phe | Ser | Ile | His | Tyr | Pro | Ala | Lys | Thr |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Leu | Leu | Arg | Pro | Leu | Lys | Pro | Ser | Glu | Val | Pro | Ser | Phe | Arg | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Ile | Ile | Thr | Phe | Gln | Lys | Ile | Ser | Thr | Gly | Ile | Val | Pro | Pro | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Ala | Ser | Ser | Ser | Pro | Ser | Ser | Tyr | Gly | Asp | Leu | Gln | Pro | Ile | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Leu | Pro | Pro | Lys | Leu | Gln | Glu | Ile | Val | Lys | Leu | Phe | Gln | Ser | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Gln | Glu | Pro | Lys | Ala | Lys | Tyr | Glu | Gln | Leu | Met | Phe | Tyr | Gly | Lys | Asn |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Leu | Thr | Pro | Leu | Asp | Ser | Gln | Phe | Lys | Thr | Arg | Glu | Asn | Lys | Val | Glu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Cys | Val | Ser | Gln | Val | Trp | Val | Arg | Ala | Phe | Phe | Asp | Glu | Glu | Arg |

```
(2) INFORMATION FOR SEQ ID NO:421:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..371
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498429
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:
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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Met | Ser | Ser | Ser | Cys | Cys | Ala | Ser | Ser | Leu | Arg | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Pro | Phe | Lys | Arg | Thr | Leu | Phe | Ser | Ser | Ile | His | Tyr | Pro | Ala | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Leu | Leu | Leu | Arg | Pro | Leu | Lys | Pro | Ser | Glu | Val | Pro | Ser | Phe | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Thr | Ile | Ile | Thr | Phe | Gln | Lys | Ile | Ser | Thr | Gly | Ile | Val | Pro | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Ala | Ser | Ser | Ser | Pro | Ser | Ser | Tyr | Gly | Asp | Leu | Gln | Pro | Ile |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Glu | Leu | Pro | Pro | Lys | Leu | Gln | Glu | Ile | Val | Lys | Leu | Phe | Gln | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Gln | Glu | Pro | Lys | Ala | Lys | Tyr | Glu | Gln | Leu | Met | Phe | Tyr | Gly | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Leu | Thr | Pro | Leu | Asp | Ser | Gln | Phe | Lys | Thr | Arg | Glu | Asn | Lys | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Gly | Cys | Val | Ser | Gln | Val | Trp | Val | Arg | Ala | Phe | Phe | Asp | Glu | Glu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

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Arg Asn Val Val Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly
145 150 155 160
Leu Ala Ala Leu Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu
 165 170 175
Ile Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln
 180 185 190
Ser Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu
 195 200 205
Met Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser
210 215 220
Ser Ser Gly Glu Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr
225 230 235 240
Lys Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp
 245 250 255
Leu Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly
260 265 270
Ser Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys
275 280 285
Leu Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser
290 295 300
Tyr Gln His Ala Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp
305 310 315 320
Gly Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly
 325 330 335
Lys Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp
340 345 350
Glu Leu Lys Ser Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro
355 360 365
Ala Glu Val
370

```

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1498430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

```

Met Ser Ser Ser Cys Cys Ala Ser Ser Leu Arg Leu Ile Pro Phe Lys
1 5 10 15
Arg Thr Leu Phe Ser Ser Ile His Tyr Pro Ala Lys Thr Leu Leu Leu
20 25 30
Arg Pro Leu Lys Pro Ser Glu Val Pro Ser Phe Arg Arg Thr Ile Ile
35 40 45
Thr Phe Gln Lys Ile Ser Thr Gly Ile Val Pro Pro Pro Ser Ala Ser
50 55 60
Ser Ser Pro Ser Ser Tyr Gly Asp Leu Gln Pro Ile Glu Glu Leu Pro
65 70 75 80
Pro Lys Leu Gln Glu Ile Val Lys Leu Phe Gln Ser Val Gln Glu Pro
85 90 95
Lys Ala Lys Tyr Glu Gln Leu Met Phe Tyr Gly Lys Asn Leu Thr Pro
100 105 110
Leu Asp Ser Gln Phe Lys Thr Arg Glu Asn Lys Val Glu Gly Cys Val
115 120 125
Ser Gln Val Trp Val Arg Ala Phe Phe Asp Glu Glu Arg Asn Val Val
130 135 140
Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly Leu Ala Ala Leu

```

145 150 155 160  
Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu Ile Leu Arg Ile  
165 170 175  
Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln Ser Leu Ser Pro  
180 185 190  
Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu Met Gln Lys Lys  
195 200 205  
Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser Ser Ser Gly Glu  
210 215 220  
Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr Lys Asp Glu Ala  
225 230 235 240  
Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp Leu Val Glu Asp  
245 250 255  
Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly Ser Asn Val Val  
260 265 270  
Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys Leu Glu Lys Glu  
275 280 285  
Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser Tyr Gln His Ala  
290 295 300  
Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp Gly Glu Thr His  
305 310 315 320  
Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly Lys Ser Leu Val  
325 330 335  
Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp Glu Leu Lys Ser  
340 345 350  
Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro Ala Glu Val  
355 360 365

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1725  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

|            |            |            |            |             |             |      |
|------------|------------|------------|------------|-------------|-------------|------|
| attttcttaa | cattgttcca | ccaactcctc | ccacattctc | tccgcctctc  | tcgtttacaa  | 60   |
| atcccacctc | aaaggtcgac | tctttatctc | tctttctacc | aacccaactt  | ctccaattgc  | 120  |
| ttctcagagt | tcagtcgccc | tcatttcctc | cgcgcgcgcc | agagggtgaat | cattcccaga  | 180  |
| ttcaaagaaa | ccaatcggtt | cagttcggtt | ccaacaaccc | ctcgcgtctc  | ccttctcgta  | 240  |
| ctgtaagtca | gggaatatgt | catctagaat | ctgcgctatg | gccaaaccaa  | atgatgctga  | 300  |
| gactctttca | tcatcagtag | atatgtcact | tagcccgcca | gttcagtctc  | taaaaccttc  | 360  |
| caagactatg | gttataaccg | atcttgcagc | cactcttggt | caatccggtg  | ttccggttat  | 420  |
| tagactagct | gcgggagaac | ccgatttcga | cactcccaaa | gtcgtagctg  | aggctgggat  | 480  |
| caacgcgatt | cgagaaggtt | ttactaggta | tacgttaaat | gcagggtatta | cagaactcag  | 540  |
| agaagcaata | tgtcgaaagc | taaaagagga | gaatggattg | tcttatgcgc  | ctgatcagat  | 600  |
| cttggttagt | aatggagcta | aacaaagtct | cttacaagca | gtgcttgccg  | tttgttctcc  | 660  |
| tggagatgaa | gttataattc | ctgcaccgta | ttgggtgagt | tacacagaa   | aggcgagatt  | 720  |
| ggctgatgca | acgcccgtgg | ttattcctac | caagatttct | aacaattttt  | tgttgatccc  | 780  |
| aaaggatctt | gagtctaaat | tgactgaaaa | atctagactt | cttattctct  | gctctccttc  | 840  |
| caaccctact | ggatctgttt | acccaagag  | tttgctcgaa | gagattgcac  | ggatcattgc  | 900  |
| taagcatcca | agacttctgg | tgcttttcga | tgaaatatat | gaacacatta  | tttatgcacc  | 960  |
| tgcaacacac | acaagctttg | cttcttttgc | tgacatgtat | gaaagaactt  | tgacagtaaa  | 1020 |
| cggtttctca | aaggctttcg | caatgacggg | ttggaggctt | ggatatcttg  | ctgggtcctaa | 1080 |
| acatattgtg | gcagcttgca | gtaaattaca | aggccagggt | agttcaggag  | ctagtagcat  | 1140 |
| tgctcagaaa | gcaggtgttg | ctgcgcttgg | gttaggcaaa | gctggaggag  | aaacggttgc  | 1200 |
| agagatggtt | aaagcttata | gagaaagacg | agatttcttg | gttaaaagct  | taggtgatat  | 1260 |
| caaaggtgtt | aagatctctg | aacctcaggg | agctttttat | ctcttttattg | acttcagtgc  | 1320 |



ttactatgga tcagaagctg aagggttttg tttgatcaat gattcgctcg ctcttgcaact 1380  
atacttttctt gacaagtttc aggttgcaat gggttcctgg gatgcttttg gagatcatag 1440  
ttgtatccga atatcttatg ccacatctct cgacgttctt caagcagctg ttgagaagat 1500  
caggaaagcc cttgagccac tccgtgccac tgtctccgtt taacagttcg gacacagaaa 1560  
tgtgtttaag attgtttatg atatgttgta acttatttat cagctttgtc tccaatccaa 1620  
taaaaagtct ttttctatgc tttgttcgtt ccttcaaatt catatataac cataaacaat 1680  
tatcttaatt gtaaatacatt tattagtatt taaggttgct tgtgc

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..475

(D) OTHER INFORMATION: / Ceres Seq. ID 1498432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Met Ala Ser Gln Ser Ser Val Ala Val Ile Ser Ser Ala Ala Ala Arg  
1 5 10 15  
Gly Glu Ser Phe Pro Asp Ser Lys Lys Pro Ile Gly Ser Val Arg Phe  
20 25 30  
Gln Gln Pro Leu Arg Leu Ser Phe Ser Tyr Cys Lys Ser Gly Asn Met  
35 40 45  
Ser Ser Arg Ile Cys Ala Met Ala Lys Pro Asn Asp Ala Glu Thr Leu  
50 55 60  
Ser Ser Ser Val Asp Met Ser Leu Ser Pro Arg Val Gln Ser Leu Lys  
65 70 75 80  
Pro Ser Lys Thr Met Val Ile Thr Asp Leu Ala Ala Thr Leu Val Gln  
85 90 95  
Ser Gly Val Pro Val Ile Arg Leu Ala Ala Gly Glu Pro Asp Phe Asp  
100 105 110  
Thr Pro Lys Val Val Ala Glu Ala Gly Ile Asn Ala Ile Arg Glu Gly  
115 120 125  
Phe Thr Arg Tyr Thr Leu Asn Ala Gly Ile Thr Glu Leu Arg Glu Ala  
130 135 140  
Ile Cys Arg Lys Leu Lys Glu Glu Asn Gly Leu Ser Tyr Ala Pro Asp  
145 150 155 160  
Gln Ile Leu Val Ser Asn Gly Ala Lys Gln Ser Leu Leu Gln Ala Val  
165 170 175  
Leu Ala Val Cys Ser Pro Gly Asp Glu Val Ile Ile Pro Ala Pro Tyr  
180 185 190  
Trp Val Ser Tyr Thr Glu Gln Ala Arg Leu Ala Asp Ala Thr Pro Val  
195 200 205  
Val Ile Pro Thr Lys Ile Ser Asn Asn Phe Leu Leu Asp Pro Lys Asp  
210 215 220  
Leu Glu Ser Lys Leu Thr Glu Lys Ser Arg Leu Leu Ile Leu Cys Ser  
225 230 235 240  
Pro Ser Asn Pro Thr Gly Ser Val Tyr Pro Lys Ser Leu Leu Glu Glu  
245 250 255  
Ile Ala Arg Ile Ile Ala Lys His Pro Arg Leu Leu Val Leu Ser Asp  
260 265 270  
Glu Ile Tyr Glu His Ile Ile Tyr Ala Pro Ala Thr His Thr Ser Phe  
275 280 285  
Ala Ser Leu Pro Asp Met Tyr Glu Arg Thr Leu Thr Val Asn Gly Phe  
290 295 300  
Ser Lys Ala Phe Ala Met Thr Gly Trp Arg Leu Gly Tyr Leu Ala Gly  
305 310 315 320  
Pro Lys His Ile Val Ala Ala Cys Ser Lys Leu Gln Gly Gln Val Ser  
325 330 335

Ser Gly Ala Ser Ser Ile Ala Gln Lys Ala Gly Val Ala Ala Leu Gly  
340 345 350  
Leu Gly Lys Ala Gly Gly Glu Thr Val Ala Glu Met Val Lys Ala Tyr  
355 360 365  
Arg Glu Arg Arg Asp Phe Leu Val Lys Ser Leu Gly Asp Ile Lys Gly  
370 375 380  
Val Lys Ile Ser Glu Pro Gln Gly Ala Phe Tyr Leu Phe Ile Asp Phe  
385 390 395 400  
Ser Ala Tyr Tyr Gly Ser Glu Ala Glu Gly Phe Gly Leu Ile Asn Asp  
405 410 415  
Ser Ser Ser Leu Ala Leu Tyr Phe Leu Asp Lys Phe Gln Val Ala Met  
420 425 430  
Val Pro Gly Asp Ala Phe Gly Asp His Ser Cys Ile Arg Ile Ser Tyr  
435 440 445  
Ala Thr Ser Leu Asp Val Leu Gln Ala Ala Val Glu Lys Ile Arg Lys  
450 455 460  
Ala Leu Glu Pro Leu Arg Ala Thr Val Ser Val  
465 470 475

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met Ser Ser Arg Ile Cys Ala Met Ala Lys Pro Asn Asp Ala Glu Thr  
1 5 10 15  
Leu Ser Ser Ser Val Asp Met Ser Leu Ser Pro Arg Val Gln Ser Leu  
20 25 30  
Lys Pro Ser Lys Thr Met Val Ile Thr Asp Leu Ala Ala Thr Leu Val  
35 40 45  
Gln Ser Gly Val Pro Val Ile Arg Leu Ala Ala Gly Glu Pro Asp Phe  
50 55 60  
Asp Thr Pro Lys Val Val Ala Glu Ala Gly Ile Asn Ala Ile Arg Glu  
65 70 75 80  
Gly Phe Thr Arg Tyr Thr Leu Asn Ala Gly Ile Thr Glu Leu Arg Glu  
85 90 95  
Ala Ile Cys Arg Lys Leu Lys Glu Glu Asn Gly Leu Ser Tyr Ala Pro  
100 105 110  
Asp Gln Ile Leu Val Ser Asn Gly Ala Lys Gln Ser Leu Leu Gln Ala  
115 120 125  
Val Leu Ala Val Cys Ser Pro Gly Asp Glu Val Ile Ile Pro Ala Pro  
130 135 140  
Tyr Trp Val Ser Tyr Thr Glu Gln Ala Arg Leu Ala Asp Ala Thr Pro  
145 150 155 160  
Val Val Ile Pro Thr Lys Ile Ser Asn Asn Phe Leu Leu Asp Pro Lys  
165 170 175  
Asp Leu Glu Ser Lys Leu Thr Glu Lys Ser Arg Leu Leu Ile Leu Cys  
180 185 190  
Ser Pro Ser Asn Pro Thr Gly Ser Val Tyr Pro Lys Ser Leu Leu Glu  
195 200 205  
Glu Ile Ala Arg Ile Ile Ala Lys His Pro Arg Leu Leu Val Leu Ser  
210 215 220  
Asp Glu Ile Tyr Glu His Ile Ile Tyr Ala Pro Ala Thr His Thr Ser  
225 230 235 240  
Phe Ala Ser Leu Pro Asp Met Tyr Glu Arg Thr Leu Thr Val Asn Gly

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Ser | Lys | Ala | Phe | Ala | Met | Thr | Gly | Trp | Arg | Leu | Gly | Tyr | Leu | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Pro | Lys | His | Ile | Val | Ala | Ala | Cys | Ser | Lys | Leu | Gln | Gly | Gln | Val |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ser | Ser | Gly | Ala | Ser | Ser | Ile | Ala | Gln | Lys | Ala | Gly | Val | Ala | Ala | Leu |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Leu | Gly | Lys | Ala | Gly | Gly | Glu | Thr | Val | Ala | Glu | Met | Val | Lys | Ala |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Tyr | Arg | Glu | Arg | Arg | Asp | Phe | Leu | Val | Lys | Ser | Leu | Gly | Asp | Ile | Lys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Val | Lys | Ile | Ser | Glu | Pro | Gln | Gly | Ala | Phe | Tyr | Leu | Phe | Ile | Asp |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Phe | Ser | Ala | Tyr | Tyr | Gly | Ser | Glu | Ala | Glu | Gly | Phe | Gly | Leu | Ile | Asn |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Asp | Ser | Ser | Ser | Leu | Ala | Leu | Tyr | Phe | Leu | Asp | Lys | Phe | Gln | Val | Ala |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Met | Val | Pro | Gly | Asp | Ala | Phe | Gly | Asp | His | Ser | Cys | Ile | Arg | Ile | Ser |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Tyr | Ala | Thr | Ser | Leu | Asp | Val | Leu | Gln | Ala | Ala | Val | Glu | Lys | Ile | Arg |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Ala | Leu | Glu | Pro | Leu | Arg | Ala | Thr | Val | Ser | Val |     |     |     |     |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..421  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Pro | Asn | Asp | Ala | Glu | Thr | Leu | Ser | Ser | Ser | Val | Asp | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Ser | Pro | Arg | Val | Gln | Ser | Leu | Lys | Pro | Ser | Lys | Thr | Met | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Thr | Asp | Leu | Ala | Ala | Thr | Leu | Val | Gln | Ser | Gly | Val | Pro | Val | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Leu | Ala | Ala | Gly | Glu | Pro | Asp | Phe | Asp | Thr | Pro | Lys | Val | Val | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Ala | Gly | Ile | Asn | Ala | Ile | Arg | Glu | Gly | Phe | Thr | Arg | Tyr | Thr | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Ala | Gly | Ile | Thr | Glu | Leu | Arg | Glu | Ala | Ile | Cys | Arg | Lys | Leu | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Glu | Asn | Gly | Leu | Ser | Tyr | Ala | Pro | Asp | Gln | Ile | Leu | Val | Ser | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ala | Lys | Gln | Ser | Leu | Leu | Gln | Ala | Val | Leu | Ala | Val | Cys | Ser | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Asp | Glu | Val | Ile | Ile | Pro | Ala | Pro | Tyr | Trp | Val | Ser | Tyr | Thr | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Ala | Arg | Leu | Ala | Asp | Ala | Thr | Pro | Val | Val | Ile | Pro | Thr | Lys | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Asn | Asn | Phe | Leu | Leu | Asp | Pro | Lys | Asp | Leu | Glu | Ser | Lys | Leu | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Lys | Ser | Arg | Leu | Leu | Ile | Leu | Cys | Ser | Pro | Ser | Asn | Pro | Thr | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Val | Tyr | Pro | Lys | Ser | Leu | Leu | Glu | Glu | Ile | Ala | Arg | Ile | Ile | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

Lys His Pro Arg Leu Leu Val Leu Ser Asp Glu Ile Tyr Glu His Ile  
210 215 220  
Ile Tyr Ala Pro Ala Thr His Thr Ser Phe Ala Ser Leu Pro Asp Met  
225 230 235 240  
Tyr Glu Arg Thr Leu Thr Val Asn Gly Phe Ser Lys Ala Phe Ala Met  
245 250 255  
Thr Gly Trp Arg Leu Gly Tyr Leu Ala Gly Pro Lys His Ile Val Ala  
260 265 270  
Ala Cys Ser Lys Leu Gln Gly Gln Val Ser Ser Gly Ala Ser Ser Ile  
275 280 285  
Ala Gln Lys Ala Gly Val Ala Ala Leu Gly Leu Gly Lys Ala Gly Gly  
290 295 300  
Glu Thr Val Ala Glu Met Val Lys Ala Tyr Arg Glu Arg Arg Asp Phe  
305 310 315 320  
Leu Val Lys Ser Leu Gly Asp Ile Lys Gly Val Lys Ile Ser Glu Pro  
325 330 335  
Gln Gly Ala Phe Tyr Leu Phe Ile Asp Phe Ser Ala Tyr Tyr Gly Ser  
340 345 350  
Glu Ala Glu Gly Phe Gly Leu Ile Asn Asp Ser Ser Ser Leu Ala Leu  
355 360 365  
Tyr Phe Leu Asp Lys Phe Gln Val Ala Met Val Pro Gly Asp Ala Phe  
370 375 380  
Gly Asp His Ser Cys Ile Arg Ile Ser Tyr Ala Thr Ser Leu Asp Val  
385 390 395 400  
Leu Gln Ala Ala Val Glu Lys Ile Arg Lys Ala Leu Glu Pro Leu Arg  
405 410 415  
Ala Thr Val Ser Val  
420

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1052
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| cctagtccaa | aaattttctca | tactataaaa | agattttttt | ttttgcttcg | ctccctcttt | 60   |
| ttcacttcgt | taacggcccc  | gcctccactc | tatcctaccg | ccgacgtccg | tgatcgccga | 120  |
| aatgactgaa | gcagagtcca  | agactgttgt | tcctgagtca | gtgttgaaga | agagaaagag | 180  |
| ggaggaagaa | tgggcacttg  | ccaagaaaca | ggagcttgag | gctgccaaaa | agcagaatgc | 240  |
| tgagaagagg | aaactcatat  | ttaaccgggc | taaacagtac | tccaaggagt | accaggagaa | 300  |
| agaaagggaa | ttaatccagc  | tgaagcgtga | ggcaaaattg | aaaggaggct | tttatgttga | 360  |
| cccagaagct | aaactgcttt  | tcattatccg | tatccgtggg | atcaatgcca | ttgacccaaa | 420  |
| gacaaagaag | attttgcaac  | ttttgcgttt | aagacagatt | tkcaatggtg | tgktcttgaa | 480  |
| ggtcaacaag | gcaaccatta  | acatgcttcg | ccgtgttgaa | ccctatgtaa | cctatggata | 540  |
| cccgaactta | aaaagtgtga  | aggaattgat | ttacaaacga | ggttttggaa | agcttaacca | 600  |
| ccagaggatt | gccttaacag  | acaattctat | tgtagatcag | gggctaggaa | agcatggcat | 660  |
| catctgcgtt | gaggatctga  | tccatgagat | catgacgggt | gggccacatt | tcaaggaagc | 720  |
| caataacttt | ttgtggccat  | tccagttgaa | ggctccattg | ggagggatga | agaagaagag | 780  |
| gaaccattac | gtggaaggag  | gagatgctgg | aaaccgcgag | aacttcatca | acgagctcgt | 840  |
| taggagaatg | aactgaagcg  | taagcgttat | tgctctgaaa | ctccctagga | aacgttttgc | 900  |
| tataggtgga | aaacttctgt  | tcgcttgctt | gtgttgccat | tgaggcgaag | taaacattta | 960  |
| cggtgaaaga | ctttgatatt  | ttataagttg | gcaattgtaa | gaacacatca | tttatttcct | 1020 |
| tccacattac | atcgtcactt  | gcattgcatt | tt         |            |            |      |

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..244  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498436  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Glu | Ala | Glu | Ser | Lys | Thr | Val | Val | Pro | Glu | Ser | Val | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Arg | Lys | Arg | Glu | Glu | Glu | Trp | Ala | Leu | Ala | Lys | Lys | Gln | Glu | Leu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Glu | Ala | Ala | Lys | Lys | Gln | Asn | Ala | Glu | Lys | Arg | Lys | Leu | Ile | Phe | Asn |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Ala | Lys | Gln | Tyr | Ser | Lys | Glu | Tyr | Gln | Glu | Lys | Glu | Arg | Glu | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Gln | Leu | Lys | Arg | Glu | Ala | Lys | Leu | Lys | Gly | Gly | Phe | Tyr | Val | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Glu | Ala | Lys | Leu | Phe | Ile | Ile | Arg | Ile | Arg | Gly | Ile | Asn | Ala |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Asp | Pro | Lys | Thr | Lys | Lys | Ile | Leu | Gln | Leu | Leu | Arg | Leu | Arg | Gln |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Xaa | Asn | Gly | Val | Xaa | Leu | Lys | Val | Asn | Lys | Ala | Thr | Ile | Asn | Met |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | Arg | Arg | Val | Glu | Pro | Tyr | Val | Thr | Tyr | Gly | Tyr | Pro | Asn | Leu | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Val | Lys | Glu | Leu | Ile | Tyr | Lys | Arg | Gly | Phe | Gly | Lys | Leu | Asn | His |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Gln | Arg | Ile | Ala | Leu | Thr | Asp | Asn | Ser | Ile | Val | Asp | Gln | Gly | Leu | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | His | Gly | Ile | Ile | Cys | Val | Glu | Asp | Leu | Ile | His | Glu | Ile | Met | Thr |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Gly | Pro | His | Phe | Lys | Glu | Ala | Asn | Asn | Phe | Leu | Trp | Pro | Phe | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Leu | Lys | Ala | Pro | Leu | Gly | Gly | Met | Lys | Lys | Lys | Arg | Asn | His | Tyr | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Gly | Gly | Asp | Ala | Gly | Asn | Arg | Glu | Asn | Phe | Ile | Asn | Glu | Leu | Val |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Arg | Arg | Met | Asn |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1252  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| attgttttgg | gatacttgaa | ctccttggtg | ggtgttgagc | acgatcagct | taatgctgct  | 60  |
| tccaaagctg | aagacgatgt | gaacttttat | caaacagtga | atcctgatgt | tgcaaagatg  | 120 |
| tttcaccttg | atccggagtc | taaaaggcct | gctcttgctc | tagttaagaa | ggaagaggag  | 180 |
| aaaattagcc | attttgatgg | agaatttggt | aagtctgctc | tagttagttt | tgtgtctgcc  | 240 |
| aacaagcttg | ctttggtctc | tgttttcacc | agagagactg | ctccggaaat | ttttgagagt  | 300 |
| gcaatcaaga | aacagttggt | gttgtttgta | acaaaaaatg | aatctgaaaa | ggttccttacg | 360 |
| gaatttcaag | aagcagcgaa | atcattcaaa | ggaaagctca | tctttgtatc | tgtggatctg  | 420 |
| gataatgagg | attatgggaa | gccagtcgct | gaatactttg | gtgtgtctgg | aaatggtcct  | 480 |

```
aaacttattg gctacacagg gaatgaagac cctaaaaaat actttttcga tggcgagatc 540
cagtcagata aaattaagat atttggggag gatttcctga acgacaagtt aaagcctttc 600
tataagtcag accccattcc tgaaaagaac gatgaagatg tgaaaatagt gggtggagat 660
aactttgatg aaattgttct ggacgattct aaagatgtgc ttctcgaggt ctacgcacca 720
tgggtgtggc attgccaagc ccttgagcca atgtataaca aacttgccaa gcatttacga 780
agtattgatt ctctcgtcat aaccgagatg gatggaacaa ccaatgaaca tcccaaggca 840
aaggctgagg ggttccctac cattctcttc ttccctgcgg gcaacaagac ttcagagccg 900
attactgtag atacagaccg cactgtgggt gcattttaca agttcttaag gaaacacgca 960
acgatcccat tcaaaactgga gaaacctgca tcaaccgaaw cacctaaaac tgcagagtcc 1020
acacaaaaag tagaaactac cgagacaaaa gaatcacccg atagcacgac aaagagtagc 1080
caaagtgact cgaaggacga attgtgatca gaaaagggtg taatatatat tacatgtctc 1140
cttaagttgt tatatgtatg atcagaattg tcacatcatg agtttggtgact agataaagat 1200
gggaattaaa gtaattttag ttttgagaaa gacaatttct tttgatttgg tc
```

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..368
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

```
Ile Val Leu Gly Tyr Leu Asn Ser Leu Val Gly Val Glu His Asp Gln
1 5 10 15
Leu Asn Ala Ala Ser Lys Ala Glu Asp Asp Val Asn Phe Tyr Gln Thr
20 25 30
Val Asn Pro Asp Val Ala Lys Met Phe His Leu Asp Pro Glu Ser Lys
35 40 45
Arg Pro Ala Leu Val Leu Val Lys Lys Glu Glu Glu Lys Ile Ser His
50 55 60
Phe Asp Gly Glu Phe Val Lys Ser Ala Leu Val Ser Phe Val Ser Ala
65 70 75 80
Asn Lys Leu Ala Leu Val Ser Val Phe Thr Arg Glu Thr Ala Pro Glu
85 90 95
Ile Phe Glu Ser Ala Ile Lys Lys Gln Leu Leu Leu Phe Val Thr Lys
100 105 110
Asn Glu Ser Glu Lys Val Leu Thr Glu Phe Gln Glu Ala Ala Lys Ser
115 120 125
Phe Lys Gly Lys Leu Ile Phe Val Ser Val Asp Leu Asp Asn Glu Asp
130 135 140
Tyr Gly Lys Pro Val Ala Glu Tyr Phe Gly Val Ser Gly Asn Gly Pro
145 150 155 160
Lys Leu Ile Gly Tyr Thr Gly Asn Glu Asp Pro Lys Lys Tyr Phe Phe
165 170 175
Asp Gly Glu Ile Gln Ser Asp Lys Ile Lys Ile Phe Gly Glu Asp Phe
180 185 190
Leu Asn Asp Lys Leu Lys Pro Phe Tyr Lys Ser Asp Pro Ile Pro Glu
195 200 205
Lys Asn Asp Glu Asp Val Lys Ile Val Val Gly Asp Asn Phe Asp Glu
210 215 220
Ile Val Leu Asp Asp Ser Lys Asp Val Leu Leu Glu Val Tyr Ala Pro
225 230 235 240
Trp Cys Gly His Cys Gln Ala Leu Glu Pro Met Tyr Asn Lys Leu Ala
245 250 255
Lys His Leu Arg Ser Ile Asp Ser Leu Val Ile Thr Glu Met Asp Gly
260 265 270
Thr Thr Asn Glu His Pro Lys Ala Lys Ala Glu Gly Phe Pro Thr Ile
275 280 285
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Phe | Pro | Ala | Gly | Asn | Lys | Thr | Ser | Glu | Pro | Ile | Thr | Val | Asp |
| 290 |     |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Thr | Asp | Arg | Thr | Val | Val | Ala | Phe | Tyr | Lys | Phe | Leu | Arg | Lys | His | Ala |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Ile | Pro | Phe | Lys | Leu | Glu | Lys | Pro | Ala | Ser | Thr | Glu | Xaa | Pro | Lys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Thr | Ala | Glu | Ser | Thr | Pro | Lys | Val | Glu | Thr | Thr | Glu | Thr | Lys | Glu | Ser |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Pro | Asp | Ser | Thr | Thr | Lys | Ser | Ser | Gln | Ser | Asp | Ser | Lys | Asp | Glu | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..329

(D) OTHER INFORMATION: / Ceres Seq. ID 1498439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | His | Leu | Asp | Pro | Glu | Ser | Lys | Arg | Pro | Ala | Leu | Val | Leu | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Lys | Glu | Glu | Lys | Ile | Ser | His | Phe | Asp | Gly | Glu | Phe | Val | Lys |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Ala | Leu | Val | Ser | Phe | Val | Ser | Ala | Asn | Lys | Leu | Ala | Leu | Val | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Phe | Thr | Arg | Glu | Thr | Ala | Pro | Glu | Ile | Phe | Glu | Ser | Ala | Ile | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Gln | Leu | Leu | Leu | Phe | Val | Thr | Lys | Asn | Glu | Ser | Glu | Lys | Val | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Glu | Phe | Gln | Glu | Ala | Ala | Lys | Ser | Phe | Lys | Gly | Lys | Leu | Ile | Phe |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Ser | Val | Asp | Leu | Asp | Asn | Glu | Asp | Tyr | Gly | Lys | Pro | Val | Ala | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Phe | Gly | Val | Ser | Gly | Asn | Gly | Pro | Lys | Leu | Ile | Gly | Tyr | Thr | Gly |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Glu | Asp | Pro | Lys | Lys | Tyr | Phe | Phe | Asp | Gly | Glu | Ile | Gln | Ser | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ile | Lys | Ile | Phe | Gly | Glu | Asp | Phe | Leu | Asn | Asp | Lys | Leu | Lys | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Tyr | Lys | Ser | Asp | Pro | Ile | Pro | Glu | Lys | Asn | Asp | Glu | Asp | Val | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ile | Val | Val | Gly | Asp | Asn | Phe | Asp | Glu | Ile | Val | Leu | Asp | Asp | Ser | Lys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Val | Leu | Glu | Val | Tyr | Ala | Pro | Trp | Cys | Gly | His | Cys | Gln | Ala |     |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Leu | Glu | Pro | Met | Tyr | Asn | Lys | Leu | Ala | Lys | His | Leu | Arg | Ser | Ile | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Leu | Val | Ile | Thr | Glu | Met | Asp | Gly | Thr | Thr | Asn | Glu | His | Pro | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Lys | Ala | Glu | Gly | Phe | Pro | Thr | Ile | Leu | Phe | Phe | Pro | Ala | Gly | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Thr | Ser | Glu | Pro | Ile | Thr | Val | Asp | Thr | Asp | Arg | Thr | Val | Val | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Tyr | Lys | Phe | Leu | Arg | Lys | His | Ala | Thr | Ile | Pro | Phe | Lys | Leu | Glu |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Pro | Ala | Ser | Thr | Glu | Xaa | Pro | Lys | Thr | Ala | Glu | Ser | Thr | Pro | Lys |

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290 295 300  
Val Glu Thr Thr Glu Thr Lys Glu Ser Pro Asp Ser Thr Thr Lys Ser  
305 310 315 320  
Ser Gln Ser Asp Ser Lys Asp Glu Leu  
325

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1755  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

aaacaagggt tcttgctccg acacgacaac aaatccagat tctgagctta gggaaacttg 60  
agaaggagaa aaaaatgtcg aacatagaca tagaagggat cttgaaggat ctacctaatg 120  
atgggaggat cccaaagacg aagatagttt gcacattagg accagcttct cgcactgttt 180  
ccatgatcga aaagcttttg aaagccggta tgaatgtggc tcgcttcaac ttctcacatg 240  
gaagccatga ataccatcaa gagacactcg acaaccctcg ctctgctatg cataataccg 300  
gcattctcgc tgctgtcatg cttgatacta aggggacctga gattcgtact ggtttcttga 360  
aagatgggaa ccctatacaa ctgaaggaag gtcaagagat tactataacc actgattatg 420  
acattcaagg agacgaatca acgatatcca tgagctataa aaagctgcct ttggatgtga 480  
agcccggaaa caccatactc tgtgcagatg gaagcataag tctagctgtc ttgtcatgtg 540  
atcctgagtc tggaactggt aggtgccggg gtgaaaactc ggcatgctt ggtgaaagaa 600  
agaatgtgaa tcttcctggc gttgttggtt atcttcccac tttagacagat aaggatattg 660  
aagatattct cggttggggg gttccgaaca gcattgatat gattgctctt tcgtttgccc 720  
gtaaaggttc ggatcttggt aatgtccgca aggttcttggt atctcatgct aaaagcataa 780  
tgctcatgtc aaagggttgag aaccaggaag gtgtgattaa ctttgatgag atcttgctgtg 840  
aaacagatgc gttcatgggt gcccggtgtg atctcgggat ggagattccg atagagaaga 900  
tcttcttggt tcaaaagttg atgatctaca agtgtaacct tgcgggtaaa ccggtggtca 960  
cagccactca gatgctggag tcaatgatca aatcacctcg gccaacccga gctgaagcca 1020  
cagatgttgc aaatgctggt cttgatggta ctgactgtgt gatgcttagc ggtgagagtg 1080  
cagcaggaga ttatccgga atagctgtga aagtcattgc taagatctgc attgaagccg 1140  
aatcctcgct tgattacaac acaatcttta aagagatgat ccgagcaact ccacttccaa 1200  
tgagccactc cgagagtctt gcatcatccg ctgtacggac tgctaacaaa gcgagggcaa 1260  
aactcatcat tgtgttgaca cgtggagggt caactgctaa tctcgtggct aaatacagac 1320  
cggctgttcc gattctgtca gtggttggtc cggttatgac cactgattcc tttgactggt 1380  
cttgtagtga cgagtcacct gcaaggcata gtctgatata cagagggtcta atccctatgt 1440  
tggtgaagg atctgcaaag gcaacagata gtgaagccac cgaagtatc attgaagctg 1500  
ctctgaagtc ggctactcag agaggactgt gcaaccgtgg tgatgcaatc gtggcgctgc 1560  
accgtattgg agctgcctca gttattaaga tctgtgtggt taagtgaatg tacagacttc 1620  
tttcaatacc tcaaatcttg gattgttggt aatcgtaact gagattttgc tttgtagcat 1680  
gaaataaaga aaacagggtc caatagttcc tgaaactctg ttacttttaa gatattcttc 1740  
tctctttttt ttttc

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..534  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Thr Arg Val Leu Ala Pro Thr Arg Gln Ile Gln Ile Leu Ser Leu  
1 5 10 15



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | Leu | Glu | Lys | Glu | Lys | Lys | Met | Ser | Asn | Ile | Asp | Ile | Glu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Leu | Lys | Asp | Leu | Pro | Asn | Asp | Gly | Arg | Ile | Pro | Lys | Thr | Lys | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Cys | Thr | Leu | Gly | Pro | Ala | Ser | Arg | Thr | Val | Ser | Met | Ile | Glu | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Leu | Lys | Ala | Gly | Met | Asn | Val | Ala | Arg | Phe | Asn | Phe | Ser | His | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | His | Glu | Tyr | His | Gln | Glu | Thr | Leu | Asp | Asn | Leu | Arg | Ser | Ala | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| His | Asn | Thr | Gly | Ile | Leu | Ala | Ala | Val | Met | Leu | Asp | Thr | Lys | Gly | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ile | Arg | Thr | Gly | Phe | Leu | Lys | Asp | Gly | Asn | Pro | Ile | Gln | Leu | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Gly | Gln | Glu | Ile | Thr | Ile | Thr | Thr | Asp | Tyr | Asp | Ile | Gln | Gly | Asp |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Glu | Ser | Thr | Ile | Ser | Met | Ser | Tyr | Lys | Lys | Leu | Pro | Leu | Asp | Val | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Gly | Asn | Thr | Ile | Leu | Cys | Ala | Asp | Gly | Ser | Ile | Ser | Leu | Ala | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ser | Cys | Asp | Pro | Glu | Ser | Gly | Thr | Val | Arg | Cys | Arg | Cys | Glu | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ala | Met | Leu | Gly | Glu | Arg | Lys | Asn | Val | Asn | Leu | Pro | Gly | Val | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Asp | Leu | Pro | Thr | Leu | Thr | Asp | Lys | Asp | Ile | Glu | Asp | Ile | Leu | Gly |
|     |     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Trp | Gly | Val | Pro | Asn | Ser | Ile | Asp | Met | Ile | Ala | Leu | Ser | Phe | Val | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Gly | Ser | Asp | Leu | Val | Asn | Val | Arg | Lys | Val | Leu | Gly | Ser | His | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Ser | Ile | Met | Leu | Met | Ser | Lys | Val | Glu | Asn | Gln | Glu | Gly | Val | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Phe | Asp | Glu | Ile | Leu | Arg | Glu | Thr | Asp | Ala | Phe | Met | Val | Ala | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Asp | Leu | Gly | Met | Glu | Ile | Pro | Ile | Glu | Lys | Ile | Phe | Leu | Ala | Gln |
|     |     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Lys | Leu | Met | Ile | Tyr | Lys | Cys | Asn | Leu | Ala | Gly | Lys | Pro | Val | Val | Thr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ala | Thr | Gln | Met | Leu | Glu | Ser | Met | Ile | Lys | Ser | Pro | Arg | Pro | Thr | Arg |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ala | Glu | Ala | Thr | Asp | Val | Ala | Asn | Ala | Val | Leu | Asp | Gly | Thr | Asp | Cys |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val | Met | Leu | Ser | Gly | Glu | Ser | Ala | Ala | Gly | Ala | Tyr | Pro | Glu | Ile | Ala |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Val | Lys | Val | Met | Ala | Lys | Ile | Cys | Ile | Glu | Ala | Glu | Ser | Ser | Leu | Asp |
|     |     | 370 |     |     |     |     | 375 |     |     |     | 380 |     |     |     |     |
| Tyr | Asn | Thr | Ile | Phe | Lys | Glu | Met | Ile | Arg | Ala | Thr | Pro | Leu | Pro | Met |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ser | Pro | Leu | Glu | Ser | Leu | Ala | Ser | Ser | Ala | Val | Arg | Thr | Ala | Asn | Lys |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ala | Arg | Ala | Lys | Leu | Ile | Ile | Val | Leu | Thr | Arg | Gly | Gly | Ser | Thr | Ala |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Asn | Leu | Val | Ala | Lys | Tyr | Arg | Pro | Ala | Val | Pro | Ile | Leu | Ser | Val | Val |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Val | Pro | Val | Met | Thr | Thr | Asp | Ser | Phe | Asp | Trp | Ser | Cys | Ser | Asp | Glu |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Ser | Pro | Ala | Arg | His | Ser | Leu | Ile | Tyr | Arg | Gly | Leu | Ile | Pro | Met | Leu |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ala | Glu | Gly | Ser | Ala | Lys | Ala | Thr | Asp | Ser | Glu | Ala | Thr | Glu | Val | Ile |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Ile | Glu | Ala | Ala | Leu | Lys | Ser | Ala | Thr | Gln | Arg | Gly | Leu | Cys | Asn | Arg |

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500 505 510  
Gly Asp Ala Ile Val Ala Leu His Arg Ile Gly Ala Ala Ser Val Ile  
515 520 525  
Lys Ile Cys Val Val Lys  
530

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..510

(D) OTHER INFORMATION: / Ceres Seq. ID 1498442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met Ser Asn Ile Asp Ile Glu Gly Ile Leu Lys Asp Leu Pro Asn Asp  
1 5 10 15  
Gly Arg Ile Pro Lys Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Ser  
20 25 30  
Arg Thr Val Ser Met Ile Glu Lys Leu Leu Lys Ala Gly Met Asn Val  
35 40 45  
Ala Arg Phe Asn Phe Ser His Gly Ser His Glu Tyr His Gln Glu Thr  
50 55 60  
Leu Asp Asn Leu Arg Ser Ala Met His Asn Thr Gly Ile Leu Ala Ala  
65 70 75 80  
Val Met Leu Asp Thr Lys Gly Pro Glu Ile Arg Thr Gly Phe Leu Lys  
85 90 95  
Asp Gly Asn Pro Ile Gln Leu Lys Glu Gly Gln Glu Ile Thr Ile Thr  
100 105 110  
Thr Asp Tyr Asp Ile Gln Gly Asp Glu Ser Thr Ile Ser Met Ser Tyr  
115 120 125  
Lys Lys Leu Pro Leu Asp Val Lys Pro Gly Asn Thr Ile Leu Cys Ala  
130 135 140  
Asp Gly Ser Ile Ser Leu Ala Val Leu Ser Cys Asp Pro Glu Ser Gly  
145 150 155 160  
Thr Val Arg Cys Arg Cys Glu Asn Ser Ala Met Leu Gly Glu Arg Lys  
165 170 175  
Asn Val Asn Leu Pro Gly Val Val Val Asp Leu Pro Thr Leu Thr Asp  
180 185 190  
Lys Asp Ile Glu Asp Ile Leu Gly Trp Gly Val Pro Asn Ser Ile Asp  
195 200 205  
Met Ile Ala Leu Ser Phe Val Arg Lys Gly Ser Asp Leu Val Asn Val  
210 215 220  
Arg Lys Val Leu Gly Ser His Ala Lys Ser Ile Met Leu Met Ser Lys  
225 230 235 240  
Val Glu Asn Gln Glu Gly Val Ile Asn Phe Asp Glu Ile Leu Arg Glu  
245 250 255  
Thr Asp Ala Phe Met Val Ala Arg Gly Asp Leu Gly Met Glu Ile Pro  
260 265 270  
Ile Glu Lys Ile Phe Leu Ala Gln Lys Leu Met Ile Tyr Lys Cys Asn  
275 280 285  
Leu Ala Gly Lys Pro Val Val Thr Ala Thr Gln Met Leu Glu Ser Met  
290 295 300  
Ile Lys Ser Pro Arg Pro Thr Arg Ala Glu Ala Thr Asp Val Ala Asn  
305 310 315 320  
Ala Val Leu Asp Gly Thr Asp Cys Val Met Leu Ser Gly Glu Ser Ala  
325 330 335  
Ala Gly Ala Tyr Pro Glu Ile Ala Val Lys Val Met Ala Lys Ile Cys  
340 345 350

Ile Glu Ala Glu Ser Ser Leu Asp Tyr Asn Thr Ile Phe Lys Glu Met  
355 360 365  
Ile Arg Ala Thr Pro Leu Pro Met Ser Pro Leu Glu Ser Leu Ala Ser  
370 375 380  
Ser Ala Val Arg Thr Ala Asn Lys Ala Arg Ala Lys Leu Ile Ile Val  
385 390 395 400  
Leu Thr Arg Gly Gly Ser Thr Ala Asn Leu Val Ala Lys Tyr Arg Pro  
405 410 415  
Ala Val Pro Ile Leu Ser Val Val Val Pro Val Met Thr Thr Asp Ser  
420 425 430  
Phe Asp Trp Ser Cys Ser Asp Glu Ser Pro Ala Arg His Ser Leu Ile  
435 440 445  
Tyr Arg Gly Leu Ile Pro Met Leu Ala Glu Gly Ser Ala Lys Ala Thr  
450 455 460  
Asp Ser Glu Ala Thr Glu Val Ile Ile Glu Ala Ala Leu Lys Ser Ala  
465 470 475 480  
Thr Gln Arg Gly Leu Cys Asn Arg Gly Asp Ala Ile Val Ala Leu His  
485 490 495  
Arg Ile Gly Ala Ala Ser Val Ile Lys Ile Cys Val Val Lys  
500 505 510

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..474

(D) OTHER INFORMATION: / Ceres Seq. ID 1498443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Met Ile Glu Lys Leu Leu Lys Ala Gly Met Asn Val Ala Arg Phe Asn  
1 5 10 15  
Phe Ser His Gly Ser His Glu Tyr His Gln Glu Thr Leu Asp Asn Leu  
20 25 30  
Arg Ser Ala Met His Asn Thr Gly Ile Leu Ala Ala Val Met Leu Asp  
35 40 45  
Thr Lys Gly Pro Glu Ile Arg Thr Gly Phe Leu Lys Asp Gly Asn Pro  
50 55 60  
Ile Gln Leu Lys Glu Gly Gln Glu Ile Thr Ile Thr Thr Asp Tyr Asp  
65 70 75 80  
Ile Gln Gly Asp Glu Ser Thr Ile Ser Met Ser Tyr Lys Lys Leu Pro  
85 90 95  
Leu Asp Val Lys Pro Gly Asn Thr Ile Leu Cys Ala Asp Gly Ser Ile  
100 105 110  
Ser Leu Ala Val Leu Ser Cys Asp Pro Glu Ser Gly Thr Val Arg Cys  
115 120 125  
Arg Cys Glu Asn Ser Ala Met Leu Gly Glu Arg Lys Asn Val Asn Leu  
130 135 140  
Pro Gly Val Val Val Asp Leu Pro Thr Leu Thr Asp Lys Asp Ile Glu  
145 150 155 160  
Asp Ile Leu Gly Trp Gly Val Pro Asn Ser Ile Asp Met Ile Ala Leu  
165 170 175  
Ser Phe Val Arg Lys Gly Ser Asp Leu Val Asn Val Arg Lys Val Leu  
180 185 190  
Gly Ser His Ala Lys Ser Ile Met Leu Met Ser Lys Val Glu Asn Gln  
195 200 205  
Glu Gly Val Ile Asn Phe Asp Glu Ile Leu Arg Glu Thr Asp Ala Phe  
210 215 220  
Met Val Ala Arg Gly Asp Leu Gly Met Glu Ile Pro Ile Glu Lys Ile

2750-1097P-80143.003

225 230 235 240  
Phe Leu Ala Gln Lys Leu Met Ile Tyr Lys Cys Asn Leu Ala Gly Lys  
245 250 255  
Pro Val Val Thr Ala Thr Gln Met Leu Glu Ser Met Ile Lys Ser Pro  
260 265 270  
Arg Pro Thr Arg Ala Glu Ala Thr Asp Val Ala Asn Ala Val Leu Asp  
275 280 285  
Gly Thr Asp Cys Val Met Leu Ser Gly Glu Ser Ala Ala Gly Ala Tyr  
290 295 300  
Pro Glu Ile Ala Val Lys Val Met Ala Lys Ile Cys Ile Glu Ala Glu  
305 310 315 320  
Ser Ser Leu Asp Tyr Asn Thr Ile Phe Lys Glu Met Ile Arg Ala Thr  
325 330 335  
Pro Leu Pro Met Ser Pro Leu Glu Ser Leu Ala Ser Ser Ala Val Arg  
340 345 350  
Thr Ala Asn Lys Ala Arg Ala Lys Leu Ile Ile Val Leu Thr Arg Gly  
355 360 365  
Gly Ser Thr Ala Asn Leu Val Ala Lys Tyr Arg Pro Ala Val Pro Ile  
370 375 380  
Leu Ser Val Val Val Pro Val Met Thr Thr Asp Ser Phe Asp Trp Ser  
385 390 395 400  
Cys Ser Asp Glu Ser Pro Ala Arg His Ser Leu Ile Tyr Arg Gly Leu  
405 410 415  
Ile Pro Met Leu Ala Glu Gly Ser Ala Lys Ala Thr Asp Ser Glu Ala  
420 425 430  
Thr Glu Val Ile Ile Glu Ala Ala Leu Lys Ser Ala Thr Gln Arg Gly  
435 440 445  
Leu Cys Asn Arg Gly Asp Ala Ile Val Ala Leu His Arg Ile Gly Ala  
450 455 460  
Ala Ser Val Ile Lys Ile Cys Val Val Lys  
465 470

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1397
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

|            |            |             |            |            |             |      |
|------------|------------|-------------|------------|------------|-------------|------|
| caagctgttc | gagattcttc | cagtccttacg | atatctcadc | tatactccaa | cgtaccatag  | 60   |
| tctgcatcat | caagaaatgg | ggaccaactt  | ttgtctattt | atgcctctct | ttgatgtttt  | 120  |
| gggcgataca | caaaacccaa | actcatggga  | actccaaaag | aagattcggt | tgagtgcagg  | 180  |
| ggaacggaag | agagtgccgg | agtttggtgt  | cttagctcac | ggagttgatg | taatgtcggc  | 240  |
| gatgcatgca | ccgttcgtgt | tcagatcttt  | tgcttcaatg | ccatatacca | caaggatatt  | 300  |
| cttgctaccg | atgtggccat | tcacgttctg  | tgttatgttg | ggcatgtggg | cttgggtcaaa | 360  |
| gacttttctt | ttcagcttct | ataccctcag  | gaacaatctt | tgtcagactt | ggggcggttc  | 420  |
| tagattcgga | ttccaatact | tcttaccggt  | tgctacaaaa | ggaattaatg | atcaaattga  | 480  |
| ggctgcgatt | cttagagctg | ataagattgg  | tgtaaagttt | ataagcttgg | ctgctctcaa  | 540  |
| caagaacgaa | gctctaaatg | gtggtggaac  | actgtttgtc | aacaagcatc | ctgaccttag  | 600  |
| agttcgtgtg | gttcatggga | acactttaac  | tgcagcagtg | attctctatg | aaattccaaa  | 660  |
| agatgtgaat | gaggttttct | tgactggagc  | cacttctaag | ctgggaagag | ctattgctct  | 720  |
| ttacctttgt | cgccgtggag | tgagagttct  | catgttgaca | ttgtctatgg | aaaggttcca  | 780  |
| aaagattcag | aaagaggctc | ctgttgagtt  | ccagaacaac | cttgtaacag | tgaccaataa  | 840  |
| caatgctgct | caacactgca | agacttggtg  | cgttggaaaa | tggttaacac | caagagagca  | 900  |
| gagctgggct | cctgcaggga | cgcatttcca  | tcagtttggt | gtgccaccaa | tccttaagtt  | 960  |
| tagaaggaac | tgcaattacg | gtgatctagc  | agctatgaag | ctccctaaag | atgttggaagg | 1020 |
| actcggaact | tgcgagtaca | cgatggagag  | aggggtggta | catgcgtgcc | atgcaggagg  | 1080 |

agtgggttcat atgcttgagg gttggaagca tcatgaggtt ggagccattg atgttgaccg 1140  
tatcgatttg gtgtgggaag cagccatgaa gtatggtctt agtgctgttt cttcactcac 1200  
aaattgagtg aagagagaga cacgtttcat tgttgctctt tgactctccc aagattgggc 1260  
attctttgta caggtgaaag gagatgcaag caggaaaaaa aagtagaatt tcaccttatg 1320  
tattgtttta tcttttatta atgatgtatt actttctttt tagatttcct taatattaat 1380  
atatgcacct aatttcc

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1498449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Leu | Phe | Glu | Ile | Leu | Pro | Val | Leu | Arg | Tyr | Leu | Ile | Tyr | Thr | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Tyr | His | Ser | Leu | His | His | Gln | Glu | Met | Gly | Thr | Asn | Phe | Cys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Met | Pro | Leu | Phe | Asp | Val | Leu | Gly | Asp | Thr | Gln | Asn | Pro | Asn | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Glu | Leu | Gln | Lys | Lys | Ile | Arg | Leu | Ser | Ala | Gly | Glu | Arg | Lys | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Pro | Glu | Phe | Val | Phe | Leu | Ala | His | Gly | Val | Asp | Val | Met | Ser | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | His | Ala | Pro | Phe | Val | Phe | Arg | Ser | Phe | Ala | Ser | Met | Pro | Tyr | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Arg | Ile | Phe | Leu | Leu | Pro | Met | Trp | Pro | Phe | Thr | Phe | Cys | Val | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Gly | Met | Trp | Ala | Trp | Ser | Lys | Thr | Phe | Leu | Phe | Ser | Phe | Tyr | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Arg | Asn | Asn | Leu | Cys | Gln | Thr | Trp | Gly | Val | Pro | Arg | Phe | Gly | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Tyr | Phe | Leu | Pro | Phe | Ala | Thr | Lys | Gly | Ile | Asn | Asp | Gln | Ile | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ala | Ile | Leu | Arg | Ala | Asp | Lys | Ile | Gly | Val | Lys | Val | Ile | Ser | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Ala | Leu | Asn | Lys | Asn | Glu | Ala | Leu | Asn | Gly | Gly | Gly | Thr | Leu | Phe |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Asn | Lys | His | Pro | Asp | Leu | Arg | Val | Arg | Val | Val | His | Gly | Asn | Thr |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Leu | Thr | Ala | Ala | Val | Ile | Leu | Tyr | Glu | Ile | Pro | Lys | Asp | Val | Asn | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Phe | Leu | Thr | Gly | Ala | Thr | Ser | Lys | Leu | Gly | Arg | Ala | Ile | Ala | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Tyr | Leu | Cys | Arg | Arg | Gly | Val | Arg | Val | Leu | Met | Leu | Thr | Leu | Ser | Met |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Arg | Phe | Gln | Lys | Ile | Gln | Lys | Glu | Ala | Pro | Val | Glu | Phe | Gln | Asn |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Leu | Val | Gln | Val | Thr | Lys | Tyr | Asn | Ala | Ala | Gln | His | Cys | Lys | Thr |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Trp | Ile | Val | Gly | Lys | Trp | Leu | Thr | Pro | Arg | Glu | Gln | Ser | Trp | Ala | Pro |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Gly | Thr | His | Phe | His | Gln | Phe | Val | Val | Pro | Pro | Ile | Leu | Lys | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Arg | Asn | Cys | Thr | Tyr | Gly | Asp | Leu | Ala | Ala | Met | Lys | Leu | Pro | Lys |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Asp | Val | Glu | Gly | Leu | Gly | Thr | Cys | Glu | Tyr | Thr | Met | Glu | Arg | Gly | Val |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |
| Val | His | Ala | Cys | His | Ala | Gly | Gly | Val | Val | His | Met | Leu | Glu | Gly | Trp |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |
| Lys | His | His | Glu | Val | Gly | Ala | Ile | Asp | Val | Asp | Arg | Ile | Asp | Leu | Val |  |  |
|     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |     |  |  |
| Trp | Glu | Ala | Ala | Met | Lys | Tyr | Gly | Leu | Ser | Ala | Val | Ser | Ser | Leu | Thr |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |
| Asn |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1498450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Gly | Thr | Asn | Phe | Cys | Leu | Phe | Met | Pro | Leu | Phe | Asp | Val | Leu | Gly |  |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Asp | Thr | Gln | Asn | Pro | Asn | Ser | Trp | Glu | Leu | Gln | Lys | Lys | Ile | Arg | Leu |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |  |
| Ser | Ala | Gly | Glu | Arg | Lys | Arg | Val | Pro | Glu | Phe | Val | Phe | Leu | Ala | His |  |  |
|     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |  |  |
| Gly | Val | Asp | Val | Met | Ser | Ala | Met | His | Ala | Pro | Phe | Val | Phe | Arg | Ser |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Phe | Ala | Ser | Met | Pro | Tyr | Thr | Thr | Arg | Ile | Phe | Leu | Leu | Pro | Met | Trp |  |  |
| 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |     |  |  |
| Pro | Phe | Thr | Phe | Cys | Val | Met | Leu | Gly | Met | Trp | Ala | Trp | Ser | Lys | Thr |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |
| Phe | Leu | Phe | Ser | Phe | Tyr | Thr | Leu | Arg | Asn | Asn | Leu | Cys | Gln | Thr | Trp |  |  |
|     | 100 |     |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Gly | Val | Pro | Arg | Phe | Gly | Phe | Gln | Tyr | Phe | Leu | Pro | Phe | Ala | Thr | Lys |  |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |  |
| Gly | Ile | Asn | Asp | Gln | Ile | Glu | Ala | Ala | Ile | Leu | Arg | Ala | Asp | Lys | Ile |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Gly | Val | Lys | Val | Ile | Ser | Leu | Ala | Ala | Leu | Asn | Lys | Asn | Glu | Ala | Leu |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Asn | Gly | Gly | Gly | Thr | Leu | Phe | Val | Asn | Lys | His | Pro | Asp | Leu | Arg | Val |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |
| Arg | Val | Val | His | Gly | Asn | Thr | Leu | Thr | Ala | Ala | Val | Ile | Leu | Tyr | Glu |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Ile | Pro | Lys | Asp | Val | Asn | Glu | Val | Phe | Leu | Thr | Gly | Ala | Thr | Ser | Lys |  |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |  |  |
| Leu | Gly | Arg | Ala | Ile | Ala | Leu | Tyr | Leu | Cys | Arg | Arg | Gly | Val | Arg | Val |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |  |  |
| Leu | Met | Leu | Thr | Leu | Ser | Met | Glu | Arg | Phe | Gln | Lys | Ile | Gln | Lys | Glu |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Ala | Pro | Val | Glu | Phe | Gln | Asn | Asn | Leu | Val | Gln | Val | Thr | Lys | Tyr | Asn |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     |     | 255 |  |  |
| Ala | Ala | Gln | His | Cys | Lys | Thr | Trp | Ile | Val | Gly | Lys | Trp | Leu | Thr | Pro |  |  |
|     | 260 |     |     |     |     |     |     | 265 |     |     |     |     |     | 270 |     |  |  |
| Arg | Glu | Gln | Ser | Trp | Ala | Pro | Ala | Gly | Thr | His | Phe | His | Gln | Phe | Val |  |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |  |  |
| Val | Pro | Pro | Ile | Leu | Lys | Phe | Arg | Arg | Asn | Cys | Thr | Tyr | Gly | Asp | Leu |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Ala | Ala | Met | Lys | Leu | Pro | Lys | Asp | Val | Glu | Gly | Leu | Gly | Thr | Cys | Glu |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |

Tyr Thr Met Glu Arg Gly Val Val His Ala Cys His Ala Gly Gly Val  
325 330 335  
Val His Met Leu Glu Gly Trp Lys His His Glu Val Gly Ala Ile Asp  
340 345 350  
Val Asp Arg Ile Asp Leu Val Trp Glu Ala Ala Met Lys Tyr Gly Leu  
355 360 365  
Ser Ala Val Ser Ser Leu Thr Asn  
370 375

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..368

(D) OTHER INFORMATION: / Ceres Seq. ID 1498451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Met Pro Leu Phe Asp Val Leu Gly Asp Thr Gln Asn Pro Asn Ser Trp  
1 5 10 15  
Glu Leu Gln Lys Lys Ile Arg Leu Ser Ala Gly Glu Arg Lys Arg Val  
20 25 30  
Pro Glu Phe Val Phe Leu Ala His Gly Val Asp Val Met Ser Ala Met  
35 40 45  
His Ala Pro Phe Val Phe Arg Ser Phe Ala Ser Met Pro Tyr Thr Thr  
50 55 60  
Arg Ile Phe Leu Leu Pro Met Trp Pro Phe Thr Phe Cys Val Met Leu  
65 70 75 80  
Gly Met Trp Ala Trp Ser Lys Thr Phe Leu Phe Ser Phe Tyr Thr Leu  
85 90 95  
Arg Asn Asn Leu Cys Gln Thr Trp Gly Val Pro Arg Phe Gly Phe Gln  
100 105 110  
Tyr Phe Leu Pro Phe Ala Thr Lys Gly Ile Asn Asp Gln Ile Glu Ala  
115 120 125  
Ala Ile Leu Arg Ala Asp Lys Ile Gly Val Lys Val Ile Ser Leu Ala  
130 135 140  
Ala Leu Asn Lys Asn Glu Ala Leu Asn Gly Gly Gly Thr Leu Phe Val  
145 150 155 160  
Asn Lys His Pro Asp Leu Arg Val Arg Val Val His Gly Asn Thr Leu  
165 170 175  
Thr Ala Ala Val Ile Leu Tyr Glu Ile Pro Lys Asp Val Asn Glu Val  
180 185 190  
Phe Leu Thr Gly Ala Thr Ser Lys Leu Gly Arg Ala Ile Ala Leu Tyr  
195 200 205  
Leu Cys Arg Arg Gly Val Arg Val Leu Met Leu Thr Leu Ser Met Glu  
210 215 220  
Arg Phe Gln Lys Ile Gln Lys Glu Ala Pro Val Glu Phe Gln Asn Asn  
225 230 235 240  
Leu Val Gln Val Thr Lys Tyr Asn Ala Ala Gln His Cys Lys Thr Trp  
245 250 255  
Ile Val Gly Lys Trp Leu Thr Pro Arg Glu Gln Ser Trp Ala Pro Ala  
260 265 270  
Gly Thr His Phe His Gln Phe Val Val Pro Pro Ile Leu Lys Phe Arg  
275 280 285  
Arg Asn Cys Thr Tyr Gly Asp Leu Ala Ala Met Lys Leu Pro Lys Asp  
290 295 300  
Val Glu Gly Leu Gly Thr Cys Glu Tyr Thr Met Glu Arg Gly Val Val  
305 310 315 320  
His Ala Cys His Ala Gly Gly Val Val His Met Leu Glu Gly Trp Lys

```

 325 330 335
His His Glu Val Gly Ala Ile Asp Val Asp Arg Ile Asp Leu Val Trp
 340 345 350
Glu Ala Ala Met Lys Tyr Gly Leu Ser Ala Val Ser Ser Leu Thr Asn
 355 360 365
```

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1424
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

gtattgtggt gttggagact gaaccatcaa cgctttttcg acacttcttc ttcttcctcc 60
tttctctctt catgcaaaat cacagttaca agaaataaac aaaagattat aaatcaaaac 120
ataaagagac aaaaatgagt gatggtcgag ttaacgcaga tcctcaacaa gaagagaaca 180
tggttaaacc accggttaag agatctctca ctctcctcat cgtgacttac ttttttctct 240
tcttcggctc tategcttcg agccttctcg cgaagtacta tttcgtctac ggtggctcga 300
gccggtgggt ctccacgtgg gttcaatctg ctggcttttc cctctcctcc tcacccaat 360
ctacttcccc tcaactacgt ctcaaaacca ccactcgccg tcctttcacg cgcttcacgc 420
tccgccatct catcttctcc gtgttgatcg ggcttggtct cggtttcaac aacttctctt 480
tctcatgggg aacctcgta cttccgggtg ccacgtcacc gcttctcctc tcgacacaac 540
tcgtcttcac tctcattttg tctaggatca ttgtgaaaca gaagatcact ttctcaaacc 600
tcaactgcgt tgccttggtg acgttaagct ctgttttggt ggctcttgat tcgagtaaag 660
ataaaccgtc cggtttaacc aaaaccaagt atttcatcgg gtatgtatcc acgatcggag 720
ccggtttact cttcgtctct tacctccccg tgacggagaa gctataccgt accgtttatt 780
gttacgcgat ggatcatggg gtgcaactgg tgatggaatt cgcagcgacg gttttcgcga 840
caatcgggat ggcttgcgaa ggcgggttta aggaaatggt taaggaagcg aaccatgttt 900
tcaccaaagg accaacatct tattggacgt ttgcgatact agcaaattgt gtgacgtggc 960
agctctcttt cgcagccacg tcagggatgg tttacttgac gtcaggtatc accggaggta 1020
tctgcatgac ggcgttgctc gcgatgaatg tgataggagg tgtgggtggc tacggtgacg 1080
tgtttggtgg agtgaagatt gtgtcgacgg tgctatgtat ttggggattc tcactttaca 1140
catacgggat gtatatgaag atgaagaagg aggagaagga gaagggagaa tattccggcg 1200
taaagacgac ggaagacagc ggagagatgg aggtggaaat gggaaatgtt aaagatgacg 1260
tggcggcggc ggatgatagg gcttgaagat atctgtgtga ttgagacggc cgttatgatt 1320
attattagga aggaagccaa caaaaaaaaa aaaagtagta gtatcttttt gtgttctttt 1380
tttttctcac cttatgtttt tttagtaatg catttgcttt tgct
```

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

```

Met Val Met Glu Val Gln Leu Val Met Glu Phe Ala Ala Thr Val Phe
1 5 10 15
Ala Thr Ile Gly Met Ala Cys Glu Gly Gly Phe Lys Glu Met Val Lys
 20 25 30
Glu Ala Asn His Val Phe Thr Lys Gly Pro Thr Phe Tyr Trp Thr Phe
 35 40 45
```



Ala Ile Leu Ala Asn Val Val Thr Trp Gln Leu Ser Phe Ala Ala Thr  
50 55 60  
Ser Gly Met Val Tyr Leu Thr Ser Gly Ile Thr Gly Gly Ile Cys Met  
65 70 75 80  
Thr Ala Leu Leu Ala Met Asn Val Ile Gly Gly Val Val Ala Tyr Gly  
85 90 95  
Asp Val Phe Gly Gly Val Lys Ile Val Ser Thr Val Leu Cys Ile Trp  
100 105 110  
Gly Phe Ser Ser Tyr Thr Tyr Gly Met Tyr Met Lys Met Lys Lys Glu  
115 120 125  
Glu Lys Glu Lys Gly Glu Tyr Ser Gly Val Lys Thr Thr Glu Asp Ser  
130 135 140  
Gly Glu Met Glu Val Glu Met Gly Asn Val Lys Asp Asp Val Ala Ala  
145 150 155 160  
Ala Asp Asp Arg Ala  
165

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

Met Glu Val Gln Leu Val Met Glu Phe Ala Thr Val Phe Ala Thr  
1 5 10 15  
Ile Gly Met Ala Cys Glu Gly Gly Phe Lys Glu Met Val Lys Glu Ala  
20 25 30  
Asn His Val Phe Thr Lys Gly Pro Thr Phe Tyr Trp Thr Phe Ala Ile  
35 40 45  
Leu Ala Asn Val Val Thr Trp Gln Leu Ser Phe Ala Thr Ser Gly  
50 55 60  
Met Val Tyr Leu Thr Ser Gly Ile Thr Gly Gly Ile Cys Met Thr Ala  
65 70 75 80  
Leu Leu Ala Met Asn Val Ile Gly Gly Val Val Ala Tyr Gly Asp Val  
85 90 95  
Phe Gly Gly Val Lys Ile Val Ser Thr Val Leu Cys Ile Trp Gly Phe  
100 105 110  
Ser Ser Tyr Thr Tyr Gly Met Tyr Met Lys Met Lys Lys Glu Glu Lys  
115 120 125  
Glu Lys Gly Glu Tyr Ser Gly Val Lys Thr Thr Glu Asp Ser Gly Glu  
130 135 140  
Met Glu Val Glu Met Gly Asn Val Lys Asp Asp Val Ala Ala Ala Asp  
145 150 155 160  
Asp Arg Ala

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Met Glu Phe Ala Ala Thr Val Phe Ala Thr Ile Gly Met Ala Cys Glu  
1 5 10 15  
Gly Gly Phe Lys Glu Met Val Lys Glu Ala Asn His Val Phe Thr Lys  
20 25 30  
Gly Pro Thr Phe Tyr Trp Thr Phe Ala Ile Leu Ala Asn Val Val Thr  
35 40 45  
Trp Gln Leu Ser Phe Ala Ala Thr Ser Gly Met Val Tyr Leu Thr Ser  
50 55 60  
Gly Ile Thr Gly Gly Ile Cys Met Thr Ala Leu Leu Ala Met Asn Val  
65 70 75 80  
Ile Gly Gly Val Val Ala Tyr Gly Asp Val Phe Gly Gly Val Lys Ile  
85 90 95  
Val Ser Thr Val Leu Cys Ile Trp Gly Phe Ser Ser Tyr Thr Tyr Gly  
100 105 110  
Met Tyr Met Lys Met Lys Lys Glu Glu Lys Glu Lys Gly Glu Tyr Ser  
115 120 125  
Gly Val Lys Thr Thr Glu Asp Ser Gly Glu Met Glu Val Glu Met Gly  
130 135 140  
Asn Val Lys Asp Asp Val Ala Ala Ala Asp Asp Arg Ala  
145 150 155

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1005
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

agggtttttt tcagcggaga ttagcttcag tatccattgg cggattagcc tcagagtgc 60  
ctgatcaagg ttttgagggt tgcatttgag tgaggagatg ttttcggctc agcataagat 120  
tcataaggag aagggtgtgg aactttctga attggatgag caagttgctc aggtcttctt 180  
tgatttgagg aacaccaatc aagaattgaa aagtgagctg aaggatttat acgtcaactc 240  
ggctgttcaa gttgatatac ctggaggacg caaggcaatt gttgtcaatg ttccttacag 300  
actgagaaaa gcttgaacag ccgagttgrc gtataaatcc ttcagstcac tktcaattc 360  
tytcatagtc ktatggctac taaattcatc accctcabtc aaatccaccg ccctaaaacc 420  
ttactatcca ccacaaaatc tcgtcgacgc aataataaca aacccaaacc atccaaaacc 480  
ataagcgaaa acatgttgaa caacgtcttt tctggcaaaa cgtaacaga aatctaccat 540  
aataagataa attcacaccc acttactaat cctactactgt ttcttgaaga tcagttcgta 600  
aaagaagagg agacgaatca acaagaacac gggaaggctc cgaacaaaga tggtaagtcc 660  
ataaccgcga ccaaatacgg agatttgagg cgtgatgttg ctcgattaag cttgttgagg 720  
tacatgaaat gttccataag ccatatatta aggaaggcaa gagcgtttta caatgagttt 780  
tgttgtgata cttatgctga gagtaacact atggctgtgg tagagccata tttttctatt 840  
ccggttaatta attaatacct ccaaatcgac gtaattaaaa attgtattta taattagtaa 900  
aatgtttcat tagttttggt gtgttgtaat gtgatgtgct ctctatatat gtcatatatg 960  
tgtaacaag acgtcaagtt atgtaattaa tggtatatga aaact

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498457

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Lys | Phe | Ile | Thr | Leu | Xaa | Gln | Ile | His | Arg | Pro | Lys | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Ser | Thr | Thr | Lys | Ser | Arg | Arg | Arg | Asn | Asn | Asn | Lys | Pro | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Lys | Thr | Ile | Ser | Glu | Asn | Met | Leu | Asn | Asn | Val | Phe | Ser | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Thr | Leu | Thr | Glu | Ile | Tyr | His | Asn | Lys | Ile | Asn | Ser | His | Pro | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Asn | Pro | Leu | Leu | Phe | Leu | Glu | Asp | Gln | Phe | Val | Lys | Glu | Glu | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Asn | Gln | Gln | Glu | His | Gly | Lys | Val | Ser | Asn | Lys | Asp | Gly | Lys | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Thr | Ala | Thr | Lys | Tyr | Gly | Asp | Leu | Arg | Arg | Asp | Val | Ala | Arg | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Leu | Leu | Trp | Tyr | Met | Lys | Cys | Ser | Ile | Ser | His | Ile | Leu | Arg | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Arg | Ala | Phe | Tyr | Asn | Glu | Phe | Cys | Cys | Asp | Thr | Tyr | Ala | Glu | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Thr | Met | Ala | Val | Val | Glu | Pro | Tyr | Phe | Ser | Ile | Pro | Val | Ile | Asn |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1498458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Asn | Val | Phe | Ser | Gly | Lys | Thr | Leu | Thr | Glu | Ile | Tyr | His |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn | Lys | Ile | Asn | Ser | His | Pro | Leu | Thr | Asn | Pro | Leu | Leu | Phe | Leu | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Gln | Phe | Val | Lys | Glu | Glu | Glu | Thr | Asn | Gln | Gln | Glu | His | Gly | Lys |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ser | Asn | Lys | Asp | Gly | Lys | Ser | Ile | Thr | Ala | Thr | Lys | Tyr | Gly | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Arg | Arg | Asp | Val | Ala | Arg | Leu | Ser | Leu | Leu | Trp | Tyr | Met | Lys | Cys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Ile | Ser | His | Ile | Leu | Arg | Lys | Ala | Arg | Ala | Phe | Tyr | Asn | Glu | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Cys | Cys | Asp | Thr | Tyr | Ala | Glu | Ser | Asn | Thr | Met | Ala | Val | Val | Glu | Pro |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Phe | Ser | Ile | Pro | Val | Ile | Asn |     |     |     |     |     |     |     |     |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1802 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1802

(D) OTHER INFORMATION: / Ceres Seq. ID 1498459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| aaacttagcc | aaacgtcaca  | aatccaaaac  | ccaaaaccga  | atcggtttttt | agcctccaag  | 60   |
| agagagatct | acagatagag  | aatgatagaa  | ccgtcgatgg  | agagagagaa  | tggtgcttta  | 120  |
| acggcggcga | caacaacgac  | gacggcgggtg | acttctctctc | ctccgatggc  | ttcttcaccg  | 180  |
| cgtcaagctt | tagttgagag  | attgaaagat  | tatggacaag  | aagatatttt  | ctctcttttg  | 240  |
| gatgaacttt | caccagacga  | gaaagatttt  | ctcgtagag   | atattgagaa  | tttggatctt  | 300  |
| ccaagaatag | atcggatcat  | tagatgttca  | cttcactctc  | aaggtttacc  | ggttgcgggc  | 360  |
| attgaaccgg | taccggagaa  | ttgggtttcg  | acagttagatg | gtagaacaat  | ggaagataga  | 420  |
| gagaaatggt | ggaaaatggg  | attaaaaact  | atctatgaag  | gcaaattagg  | tgttggtgctt | 480  |
| ttatctggtg | gacagggaac  | aaggcttgga  | agctcagatc  | caaaaggatg  | tttcaatatc  | 540  |
| ggattaccat | cagggaatc   | gctctttcag  | attcaagcag  | agagaatctt  | gtgtgttcaa  | 600  |
| agacttgctg | ctcaagtagt  | gagtgaaggt  | ccaattcgtc  | cagttacaaa  | tacatttggt  | 660  |
| tattatgact | tagtccattt  | actgatgaan  | gcgacacgaa  | aatattttctc | gangtcacaa  | 720  |
| gtactttggt | cttgaaccag  | atcaaatcag  | ttttttccaa  | caaggtactt  | tgccctgcgt  | 780  |
| tacaagtggt | ggaaagttaa  | ttatggagac  | acctttcagt  | ctagctaaag  | ctccagatgg  | 840  |
| taacggcgga | gtctatgcag  | cgctaaagt   | ttcaaggcta  | ttagaggata  | tggcttctag  | 900  |
| ggggattaaa | tacgtcgatt  | gctatggcgt  | tgacaatgtc  | ctggttcgag  | tagctgatcc  | 960  |
| tacttttctt | ggatacttca  | tcgataaagg  | ggctgcttcg  | gctgcaaaag  | ttgtgctggaa | 1020 |
| ggcatatyct | cmagaacagg  | taggagtgyt  | tgtagaaga   | ggtaaaggag  | gaccgttgac  | 1080 |
| agtagttgag | tatagtgagc  | ttgatcagtc  | tatggcttct  | gctattaatc  | aacgaacagg  | 1140 |
| acgtcttcaa | tattgctgga  | gtaacgtgtg  | cttacacatg  | tttacttttag | atttccttaa  | 1200 |
| tcaagtcgct | accggcctag  | aaaaagatat  | cgtgtaccat  | ttggcggaga  | agaagatacc  | 1260 |
| atctatgaat | ggatacacaa  | tgggactaaa  | actagaacaa  | ttcatttttg  | attcgtttcc  | 1320 |
| ttatgctcct | tcaaccgcac  | tttttgaggt  | tttaagggaa  | gaggagtgtg  | caccagtga   | 1380 |
| gaatgttaac | gggtcgaatt  | tcgatacacc  | ggaaagtgcg  | aggcttttg   | ttctaagggt  | 1440 |
| acacacacgt | tgggttatag  | cagctggtgg  | atttctaaca  | cattctgtgc  | ctttatatgc  | 1500 |
| tactggtgta | gaggtttcac  | ctttgtgctc  | atacgccgga  | gaaaatcttg  | aagctatttg  | 1560 |
| tcgaggaaga | acgtttcatg  | cacctgtgta  | aatttccttc  | taatggtttt  | tgtgtttttg  | 1620 |
| ttttggggtt | ttaaaatctt  | ttcttcattt  | ttatgtgatt  | tgttttcttt  | gtttccgggt  | 1680 |
| gtggtttata | tatataaaact | gattatcttc  | ccatgagaga  | gagaaagaga  | gagtcaaaaga | 1740 |
| ggtcttggcg | ttttgtatcc  | attaatgtaa  | catatcta    | aaaaatttta  | tgttggtttt  | 1800 |

tg

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1498460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Glu | Pro | Ser | Met | Glu | Arg | Glu | Asn | Gly | Ala | Leu | Thr | Ala | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Thr | Thr | Thr | Thr | Ala | Val | Thr | Ser | Pro | Pro | Pro | Met | Ala | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Arg | Gln | Ala | Leu | Val | Glu | Arg | Leu | Lys | Asp | Tyr | Gly | Gln | Glu | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Phe | Ser | Leu | Trp | Asp | Glu | Leu | Ser | Pro | Asp | Glu | Lys | Asp | Phe | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Val | Arg | Asp | Ile | Glu | Asn | Leu | Asp | Leu | Pro | Arg | Ile | Asp | Arg | Ile | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Cys | Ser | Leu | His | Ser | Gln | Gly | Leu | Pro | Val | Ala | Ala | Ile | Glu | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Pro | Glu | Asn | Trp | Val | Ser | Thr | Val | Asp | Gly | Arg | Thr | Met | Glu | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Glu | Lys | Trp | Trp | Lys | Met | Gly | Leu | Lys | Thr | Ile | Tyr | Glu | Gly | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

Leu Gly Val Val Leu Leu Ser Gly Gly Gln Gly Thr Arg Leu Gly Ser  
130 135 140  
Ser Asp Pro Lys Gly Cys Phe Asn Ile Gly Leu Pro Ser Gly Lys Ser  
145 150 155 160  
Leu Phe Gln Ile Gln Ala Glu Arg Ile Leu Cys Val Gln Arg Leu Ala  
165 170 175  
Ala Gln Val Val Ser Glu Gly Pro Ile Arg Pro Val Thr Asn Thr Leu  
180 185 190  
Val Tyr Tyr Asp Leu Val His Leu Leu Met Xaa Ala Thr Arg Lys Tyr  
195 200 205  
Phe Ser Xaa Ser Gln Val Leu Trp Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1498461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Met Glu Thr Pro Phe Ser Leu Ala Lys Ala Pro Asp Gly Asn Gly Gly  
1 5 10 15  
Val Tyr Ala Ala Leu Lys Cys Ser Arg Leu Leu Glu Asp Met Ala Ser  
20 25 30  
Arg Gly Ile Lys Tyr Val Asp Cys Tyr Gly Val Asp Asn Val Leu Val  
35 40 45  
Arg Val Ala Asp Pro Thr Phe Leu Gly Tyr Phe Ile Asp Lys Gly Ala  
50 55 60  
Ala Ser Ala Ala Lys Val Val Arg Lys Ala Tyr Xaa Xaa Glu Gln Val  
65 70 75 80  
Gly Val Xaa Val Arg Gly Lys Gly Gly Pro Leu Thr Val Val Glu  
85 90 95  
Tyr Ser Glu Leu Asp Gln Ser Met Ala Ser Ala Ile Asn Gln Arg Thr  
100 105 110  
Gly Arg Leu Gln Tyr Cys Trp Ser Asn Val Cys Leu His Met Phe Thr  
115 120 125  
Leu Asp Phe Leu Asn Gln Val Ala Thr Gly Leu Glu Lys Asp Ser Val  
130 135 140  
Tyr His Leu Ala Glu Lys Lys Ile Pro Ser Met Asn Gly Tyr Thr Met  
145 150 155 160  
Gly Leu Lys Leu Glu Gln Phe Ile Phe Asp Ser Phe Pro Tyr Ala Pro  
165 170 175  
Ser Thr Ala Leu Phe Glu Val Leu Arg Glu Glu Glu Phe Ala Pro Val  
180 185 190  
Lys Asn Val Asn Gly Ser Asn Phe Asp Thr Pro Glu Ser Ala Arg Leu  
195 200 205  
Leu Val Leu Arg Leu His Thr Arg Trp Val Ile Ala Ala Gly Gly Phe  
210 215 220  
Leu Thr His Ser Val Pro Leu Tyr Ala Thr Gly Val Glu Val Ser Pro  
225 230 235 240  
Leu Cys Ser Tyr Ala Gly Glu Asn Leu Glu Ala Ile Cys Arg Gly Arg  
245 250 255  
Thr Phe His Ala Pro Cys Glu Ile Ser Leu  
260 265

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..237  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498462  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met Ala Ser Arg Gly Ile Lys Tyr Val Asp Cys Tyr Gly Val Asp Asn  
1 5 10 15  
Val Leu Val Arg Val Ala Asp Pro Thr Phe Leu Gly Tyr Phe Ile Asp  
20 25 30  
Lys Gly Ala Ala Ser Ala Ala Lys Val Val Arg Lys Ala Tyr Xaa Xaa  
35 40 45  
Glu Gln Val Gly Val Xaa Val Arg Arg Gly Lys Gly Gly Pro Leu Thr  
50 55 60  
Val Val Glu Tyr Ser Glu Leu Asp Gln Ser Met Ala Ser Ala Ile Asn  
65 70 75 80  
Gln Arg Thr Gly Arg Leu Gln Tyr Cys Trp Ser Asn Val Cys Leu His  
85 90 95  
Met Phe Thr Leu Asp Phe Leu Asn Gln Val Ala Thr Gly Leu Glu Lys  
100 105 110  
Asp Ser Val Tyr His Leu Ala Glu Lys Lys Ile Pro Ser Met Asn Gly  
115 120 125  
Tyr Thr Met Gly Leu Lys Leu Glu Gln Phe Ile Phe Asp Ser Phe Pro  
130 135 140  
Tyr Ala Pro Ser Thr Ala Leu Phe Glu Val Leu Arg Glu Glu Glu Phe  
145 150 155 160  
Ala Pro Val Lys Asn Val Asn Gly Ser Asn Phe Asp Thr Pro Glu Ser  
165 170 175  
Ala Arg Leu Leu Val Leu Arg Leu His Thr Arg Trp Val Ile Ala Ala  
180 185 190  
Gly Gly Phe Leu Thr His Ser Val Pro Leu Tyr Ala Thr Gly Val Glu  
195 200 205  
Val Ser Pro Leu Cys Ser Tyr Ala Gly Glu Asn Leu Glu Ala Ile Cys  
210 215 220  
Arg Gly Arg Thr Phe His Ala Pro Cys Glu Ile Ser Leu  
225 230 235

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1359 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1359  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

ctaacttctc tgttcatctt tttctctctt tatttataaa tttatctgca tagtactctc 60  
tgaatctata tcttcaaaaa aaaaaaacgt ccaagatcaa atcaagaaac ccattaaaaa 120  
aaaaaatcag gttttggttt cagttttaag ggtttaaggt ttcttgggga agaaacgatg 180  
gagacttttt gtgggtttca aaaggaggaa gagcagatgg atttacctcc tgggttcagg 240  
tttcatccaa cagatgaaga actcataaac tcactatctc cataagaagg ttcttgacac 300  
cagctttctc gctaaagcta tcggtgaagt tgatttaaac aaatcagagc catgggagtt 360  
accatggatg gcaaaaatgg gtgagaaaga atggtatttt ttctgtgtga gagacagaaa 420  
gtatccacc ggtttaagaa ctaaccgagc aactgaagcc ggttattgga aggcgaccgg 480  
gaaggataaa gagatatacc gaggcaaadc acttggtggg atgaagaaga cacttgtttt 540  
ctatagagga agagctccta aaggtcagaa aaccaactgg gtgatgcatg agtacaggct 600

```
tgaaaaaaat tctctgccca taacttgccg aaaaccgcaa agaatgaatg ggtgatatgc 660
agggtgttcc aaaagagtgc tggagggaag aagatcccga tttcgagtct aatccgaatc 720
ggttcactcg gaaccgactt taacccttcg cttttgccct ctttaaccga ttcttcgcct 780
tacaacgata aaaccaaacc agaaccgggtc tacgtgccct gcttctccaa ccaaaccgat 840
caaaaccaag gaaccacact caattgcttc agcagccctg ttcttaactc gatccaagcc 900
gacatttttc acaggattcc actctatcaa actcagtcct tccaggtttc tatgaatcta 960
cagagcccgg ttctcacgca agaacactca gttctacatg ctatgatcga gaacaacaga 1020
agacaaagtc tcaaaacgat gagtgtctca caagaaaccg gagtttcaac tgacatgaac 1080
actgatattc catcggattt tgaatttggt aagaggcggg ttgattctca agaagatccg 1140
tcttcctcta ctggaccggg tgatcttgaa cctttctgga attactgaag atgattcaag 1200
attctcatgt ccattaattt actgtggtgt gttaaagttt gtataggcta ttgtcatata 1260
ctctcatatc aacttccact atatattata acaatttaaa gaaacttaaa aatatgattt 1320
gatatatgac taaagtatta taatacaatt ttgtacccc
```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```
Met Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val Arg Asp
1 5 10 15
Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly
 20 25 30
Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly Lys Ser
 35 40 45
Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro
 50 55 60
Lys Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Lys
65 70 75 80
Asn Ser Leu Pro Ile Thr Cys Arg Lys Pro Gln Arg Met Asn Gly
 85 90 95
```

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

```
Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val Arg Asp Arg Lys Tyr
1 5 10 15
Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly Tyr Trp Lys
 20 25 30
Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly Lys Ser Leu Val Gly
 35 40 45
Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys Gly Gln
 50 55 60
Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Lys Asn Ser Leu
65 70 75 80
Pro Ile Thr Cys Arg Lys Pro Gln Arg Met Asn Gly
 85 90
```

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Met Asn Leu Gln Ser Pro Val Leu Thr Gln Glu His Ser Val Leu His  
1 5 10 15  
Ala Met Ile Glu Asn Asn Arg Arg Gln Ser Leu Lys Thr Met Ser Val  
20 25 30  
Ser Gln Glu Thr Gly Val Ser Thr Asp Met Asn Thr Asp Ile Ser Ser  
35 40 45  
Asp Phe Glu Phe Gly Lys Arg Arg Phe Asp Ser Gln Glu Asp Pro Ser  
50 55 60  
Ser Ser Thr Gly Pro Val Asp Leu Glu Pro Phe Trp Asn Tyr  
65 70 75

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1879
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

acttctctct ctctctctct ctcttttctc aaatcttgga ggagaagaag caaagaatta 60  
gactactctg caacaatggc tatttattct gtccataacg gcgacaagaa gcattgggtgg 120  
ttcactcaca agaagattgt tgataagtac attaaggacg caagatcttt aatggagagt 180  
gaggagcaaa acgacgttgc ttcagccatt catttactag acgcggttt atcaatatcc 240  
ccgcgttcgg aaactgcgtt agaacttaaa gccagatctt tgctctttct acgtcgcttc 300  
aaagatgtag ttgatatgct tcaagattat atcccaagcc tcaagcttgc cgtgaacgag 360  
gaagatggat cttattcata cgaaggttct tcttactctt cctcctcttc tcagctctcc 420  
cggaaacttc tctctgactc atctcctcgc cgtgactcat ccttcaagtg cttctctggt 480  
tcttacctga aaaagaaaat tatggctggg atttgtaaaa atcgcgatca agataaacia 540  
tggagatacg ttgttttagg acaagcttgt tgccacctag gattaatgga ggacgcattg 600  
gttcttcttt aaaccggaaa acgtctcgca acagtcgagt tccgccgtct aagtgttaagc 660  
ttgtcagatg atagcgtctc actcctcctc tctgaatcgt catcatcatc atcctcatcc 720  
tcttatgctt ttctccacg caaagtctcc gaatgcgaaa ccgtcactaa ccttctcgcc 780  
cacacgaaaa atctcctcgc gcgtcgctcc gccggattcg ccgcctttga cgctggactt 840  
ttcgccgact cgatacgta cttctccaaa attctcgacg gtctgctgctg tcccgcgcca 900  
caaggattcc tcgctgattg ctatatgcac cgcgcgcgcg cttacaaatc cgccgggaaa 960  
atcgcggaag cgcgcgcgga ttgtaataaa accttagctc ttgagccgtc gtgtatocat 1020  
gcgttgagga ctagagccac tcttttgtaa acggttcggt gtctaccgga ttcgcttcac 1080  
gatttagagc atttgaagat actctacaac actatcttac gtgatcgga acttcccgga 1140  
ccaccgtgga aacgacacaa tgtgaaatac agagagatac cgggaaagt atgcgaactg 1200  
acgacgaaat cgaagaaact gaaagcaaaa atggcgaaat gagaaatcgg aaacggtgat 1260  
tattacggat tggtcggagt tagacgcggt tgcacgagat cggagcttga tcgagcaaat 1320  
ctcttgcctc gtctcaggca taaaccggac aaggctttag cattcatgga acgttgcgat 1380  
ttcttcgata agattgagat tagttccggt aaagatcgag cgaagatgtc ttctttgttg 1440  
ctttaccgat tgaattcagag aggttatata gctttggcgg cagcgatagc tgaggaggaa 1500  
cagaggaaga agatgatggt gttgactcaa atgtcaacga aaacggttga agaacaatgaa 1560  
ccggttgaaa aatccggttc aattacttta accgattttg cagaaattaa gccggggaat 1620



tcgaacgcgt accaaggagt tttctgccga ggtcttgctg ctggtgggag tttgttatct 1680  
aggaccggat ttaaccaacc gataccaatg aaatagcatg cgatcagttg ttaaccggga 1740  
atcttagttt gtatataatt aagaattttt tgtcacttta aaatattcgt ctcttttgag 1800  
ttaattctcc tactttctct ttatttctgt gcagaaaatg ctttacttgt cgaatatcaa 1860  
atcaaagtag tgtgagatt

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1498476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Thr Ser Leu Ser Leu Ser Leu Ser Phe Leu Lys Ser Trp Arg Arg Arg  
1 5 10 15  
Ser Lys Glu Leu Asp Tyr Ser Ala Thr Met Ala Ile Tyr Ser Val His  
20 25 30  
Asn Gly Asp Lys Lys His Trp Trp Phe Thr His Lys Lys Ile Val Asp  
35 40 45  
Lys Tyr Ile Lys Asp Ala Arg Ser Leu Met Glu Ser Glu Glu Gln Asn  
50 55 60  
Asp Val Ala Ser Ala Ile His Leu Leu Asp Ala Ala Leu Ser Ile Ser  
65 70 75 80  
Pro Arg Ser Glu Thr Ala Leu Glu Leu Lys Ala Arg Ser Leu Leu Phe  
85 90 95  
Leu Arg Arg Phe Lys Asp Val Val Asp Met Leu Gln Asp Tyr Ile Pro  
100 105 110  
Ser Leu Lys Leu Ala Val Asn Glu Glu Asp Gly Ser Tyr Ser Tyr Glu  
115 120 125  
Gly Ser Ser Tyr Ser Ser Ser Ser Ser Gln Leu Ser Arg Lys Leu Leu  
130 135 140  
Ser Asp Ser Ser Pro Arg Arg Asp Ser Ser Phe Lys Cys Phe Ser Val  
145 150 155 160  
Ser Tyr Leu Lys Lys Lys Ile Met Ala Gly Ile Cys Lys Asn Arg Asp  
165 170 175  
Gln Asp Lys Gln Trp Arg Tyr Val Val Leu Gly Gln Ala Cys Cys His  
180 185 190  
Leu Gly Leu Met Glu Asp Ala Leu Val Leu Leu  
195 200

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1498477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Met Ala Ile Tyr Ser Val His Asn Gly Asp Lys Lys His Trp Trp Phe  
1 5 10 15  
Thr His Lys Lys Ile Val Asp Lys Tyr Ile Lys Asp Ala Arg Ser Leu  
20 25 30  
Met Glu Ser Glu Glu Gln Asn Asp Val Ala Ser Ala Ile His Leu Leu  
35 40 45

Asp Ala Ala Leu Ser Ile Ser Pro Arg Ser Glu Thr Ala Leu Glu Leu  
50 55 60  
Lys Ala Arg Ser Leu Leu Phe Leu Arg Arg Phe Lys Asp Val Val Asp  
65 70 75 80  
Met Leu Gln Asp Tyr Ile Pro Ser Leu Lys Leu Ala Val Asn Glu Glu  
85 90 95  
Asp Gly Ser Tyr Ser Tyr Glu Gly Ser Ser Tyr Ser Ser Ser Ser Ser  
100 105 110  
Gln Leu Ser Arg Lys Leu Leu Ser Asp Ser Ser Pro Arg Asp Ser  
115 120 125  
Ser Phe Lys Cys Phe Ser Val Ser Tyr Leu Lys Lys Lys Ile Met Ala  
130 135 140  
Gly Ile Cys Lys Asn Arg Asp Gln Asp Lys Gln Trp Arg Tyr Val Val  
145 150 155 160  
Leu Gly Gln Ala Cys Cys His Leu Gly Leu Met Glu Asp Ala Leu Val  
165 170 175  
Leu Leu

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..269

(D) OTHER INFORMATION: / Ceres Seq. ID 1498478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met His Arg Ala Ala Tyr Lys Ser Ala Gly Lys Ile Ala Glu Ala  
1 5 10 15  
Ile Ala Asp Cys Asn Lys Thr Leu Ala Leu Glu Pro Ser Cys Ile His  
20 25 30  
Ala Leu Glu Thr Arg Ala Thr Leu Leu Glu Thr Val Arg Cys Leu Pro  
35 40 45  
Asp Ser Leu His Asp Leu Glu His Leu Lys Ile Leu Tyr Asn Thr Ile  
50 55 60  
Leu Arg Asp Arg Lys Leu Pro Gly Pro Pro Trp Lys Arg His Asn Val  
65 70 75 80  
Lys Tyr Arg Glu Ile Pro Gly Lys Leu Cys Glu Leu Thr Thr Lys Ser  
85 90 95  
Lys Lys Leu Lys Ala Lys Met Ala Asn Gly Glu Ile Gly Asn Val Asp  
100 105 110  
Tyr Tyr Gly Leu Val Gly Val Arg Arg Gly Cys Thr Arg Ser Glu Leu  
115 120 125  
Asp Arg Ala Asn Leu Leu Leu Cys Leu Arg His Lys Pro Asp Lys Ala  
130 135 140  
Leu Ala Phe Met Glu Arg Cys Asp Phe Phe Asp Gln Ser Glu Ile Ser  
145 150 155 160  
Ser Val Lys Asp Arg Ala Lys Met Ser Ser Leu Leu Leu Tyr Arg Leu  
165 170 175  
Ile Gln Arg Gly Tyr Thr Ala Leu Ala Ala Ile Ala Glu Glu Glu  
180 185 190  
Gln Arg Lys Lys Met Met Val Leu Thr Gln Met Ser Thr Lys Thr Val  
195 200 205  
Glu Glu His Glu Pro Val Glu Lys Ser Gly Ser Ile Thr Leu Thr Asp  
210 215 220  
Phe Ala Glu Ile Lys Pro Gly Asn Ser Asn Ala Tyr Gln Gly Val Phe  
225 230 235 240  
Cys Arg Gly Leu Ala Ala Val Gly Ser Leu Leu Ser Arg Thr Gly Phe

245 250 255  
Asn Gln Pro Ile Pro Met Lys Tyr Asp Ala Ile Ser Cys  
260 265

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1751
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```
aatctctctc cctctctatc tctctcttac aaaattccat ttcacgggga aaataataat 60
acgacttttg aaatctctcg ctaatatttc ccaagaaaac ctgatgaatt aaaagttcat 120
attttcttgg tgttggttgg tattagatga ctatttcttg gtattagtca attctctggt 180
tccatcttat atggatagtc tagacacaga gcaaagatcc ttctttggag aaaaagaaga 240
tgagagacga gagaggatcg tttcttcacg tattggtcgt agatagatct taatcgataa 300
ccatctaggc cttgatctaa ccattcaata taaactttat ttctttcttc ttttcgatct 360
caattgttcc gaccaaacaa gatgaagaga tcacgtggaa gctccgattc tttatccggt 420
ttcttaccaa ttcgccattc tacaacagac aaacaaataa gcccaagacc aacaactacc 480
ggctttctct attccggcgc cggagactac tcccagatgt ttgacgcatt agaagacgac 540
ggaagtctag aggacctcgg cggcggttga cacgcgtctt ctacggcggc ggagaaaaaa 600
cggcggttgg gtgtagagca agtgaaagcg ttagagaaga atttcgagat tgataacaag 660
ttagagccag agaggaaagt gaagctggct caagagcttg gggtgcagcc acgccaaagtc 720
gcgatctggt ttcaaaaaccg ccgtgctcgg tggaaaacaa agcagcttga acgtgattac 780
ggcgttctta agtcaaactt tgatgcactc aaacgcaacc gcgactcgct tcaacgcgat 840
aacgattcac tccttgacaa gattaaagag ctgaaagcaa aacttaacgt ggaaggggtt 900
aaaggtatag aagagaacgg cgctttaaaa gtagtggaag caaatcagac ggtgatggct 960
aataatgaag tcttagagct aagccaccgt tctccatcgc caccaccgca tattcctacg 1020
gaagctccga catcgagct cgcattcgaa atgttttagca tttttccacg cacggaaaac 1080
ttcagagaag atcctgccga tagcagcgac tcaagcgcgg ttttgaacga agagtatagt 1140
cccaatacgg ttgaagcagc gggcgcgagt gcgggccacga ctgtagaaat gtcgacgatg 1200
gattgtttta gccaatcgt gaaaatggaa gagcatgaag atctgttttag tggagaggaa 1260
gcttgcaagt tgtttgcgga caatgagcaa tggattgct ccgatcagtg gaattcgtaa 1320
aatgtggggg cagaaataaa aacatagaaa agtcgaagg gatatgtgga aatattactg 1380
aagtcataatt gggtcggaaa atgcattact caaaatatta ggggttttgt tgagaaaaatg 1440
gaatatgacg cgagagggtg gtaaaaacga gcgtgtggtg ttccatgcac gtgtggccgt 1500
aatcttttca aggttgaatg agagaggaca acaatgtctg aaatcatcgg gaataaaaaa 1560
aatatgtgac gaagaaatcg ttttttcgtc gtttataata ttatttgaat aattttactt 1620
aggtgaatgt aatcgtcaaa aatctttaa ttccgaaggg ttaaagattc tgagcacgac 1680
tatctatcta tcctcttcta ttgttctcgt cgtccattga cgactatgca caattcataa 1740
gattattccc t
```

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

```
Met Lys Arg Ser Arg Gly Ser Ser Asp Ser Leu Ser Gly Phe Leu Pro
1 5 10 15
Ile Arg His Ser Thr Thr Asp Lys Gln Ile Ser Pro Arg Pro Thr Thr
20 25 30
```

Thr Gly Phe Leu Tyr Ser Gly Ala Gly Asp Tyr Ser Gln Met Phe Asp  
35 40 45  
Ala Leu Glu Asp Asp Gly Ser Leu Glu Asp Leu Gly Gly Val Gly His  
50 55 60  
Ala Ser Ser Thr Ala Ala Glu Lys Lys Arg Arg Leu Gly Val Glu Gln  
65 70 75 80  
Val Lys Ala Leu Glu Lys Asn Phe Glu Ile Asp Asn Lys Leu Glu Pro  
85 90 95  
Glu Arg Lys Val Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln  
100 105 110  
Val Ala Ile Trp Phe Gln Asn Arg Ala Arg Trp Lys Thr Lys Gln  
115 120 125  
Leu Glu Arg Asp Tyr Gly Val Leu Lys Ser Asn Phe Asp Ala Leu Lys  
130 135 140  
Arg Asn Arg Asp Ser Leu Gln Arg Asp Asn Asp Ser Leu Leu Gly Gln  
145 150 155 160  
Ile Lys Glu Leu Lys Ala Lys Leu Asn Val Glu Gly Phe Lys Gly Ile  
165 170 175  
Glu Glu Asn Gly Ala Leu Lys Val Val Glu Ala Asn Gln Thr Val Met  
180 185 190  
Ala Asn Asn Glu Val Leu Glu Leu Ser His Arg Ser Pro Ser Pro Pro  
195 200 205  
Pro His Ile Pro Thr Glu Ala Pro Thr Ser Glu Leu Ala Phe Glu Met  
210 215 220  
Phe Ser Ile Phe Pro Arg Thr Glu Asn Phe Arg Glu Asp Pro Ala Asp  
225 230 235 240  
Ser Ser Asp Ser Ser Ala Val Leu Asn Glu Glu Tyr Ser Pro Asn Thr  
245 250 255  
Val Glu Ala Ala Gly Ala Val Ala Ala Thr Thr Val Glu Met Ser Thr  
260 265 270  
Met Asp Cys Phe Ser Gln Phe Val Lys Met Glu Glu His Glu Asp Leu  
275 280 285  
Phe Ser Gly Glu Glu Ala Cys Lys Leu Phe Ala Asp Asn Glu Gln Trp  
290 295 300  
Tyr Cys Ser Asp Gln Trp Asn Ser  
305 310

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1498489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Met Phe Asp Ala Leu Glu Asp Asp Gly Ser Leu Glu Asp Leu Gly Gly  
1 5 10 15  
Val Gly His Ala Ser Ser Thr Ala Ala Glu Lys Lys Arg Arg Leu Gly  
20 25 30  
Val Glu Gln Val Lys Ala Leu Glu Lys Asn Phe Glu Ile Asp Asn Lys  
35 40 45  
Leu Glu Pro Glu Arg Lys Val Lys Leu Ala Gln Glu Leu Gly Leu Gln  
50 55 60  
Pro Arg Gln Val Ala Ile Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys  
65 70 75 80  
Thr Lys Gln Leu Glu Arg Asp Tyr Gly Val Leu Lys Ser Asn Phe Asp  
85 90 95  
Ala Leu Lys Arg Asn Arg Asp Ser Leu Gln Arg Asp Asn Asp Ser Leu

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 100                                                             | 105 | 110 |
| Leu Gly Gln Ile Lys Glu Leu Lys Ala Lys Leu Asn Val Glu Gly Phe |     |     |
| 115                                                             | 120 | 125 |
| Lys Gly Ile Glu Glu Asn Gly Ala Leu Lys Val Val Glu Ala Asn Gln |     |     |
| 130                                                             | 135 | 140 |
| Thr Val Met Ala Asn Asn Glu Val Leu Glu Leu Ser His Arg Ser Pro |     |     |
| 145                                                             | 150 | 155 |
| Ser Pro Pro Pro His Ile Pro Thr Glu Ala Pro Thr Ser Glu Leu Ala |     |     |
| 165                                                             | 170 | 175 |
| Phe Glu Met Phe Ser Ile Phe Pro Arg Thr Glu Asn Phe Arg Glu Asp |     |     |
| 180                                                             | 185 | 190 |
| Pro Ala Asp Ser Ser Asp Ser Ser Ala Val Leu Asn Glu Glu Tyr Ser |     |     |
| 195                                                             | 200 | 205 |
| Pro Asn Thr Val Glu Ala Ala Gly Ala Val Ala Ala Thr Thr Val Glu |     |     |
| 210                                                             | 215 | 220 |
| Met Ser Thr Met Asp Cys Phe Ser Gln Phe Val Lys Met Glu Glu His |     |     |
| 225                                                             | 230 | 235 |
| Glu Asp Leu Phe Ser Gly Glu Glu Ala Cys Lys Leu Phe Ala Asp Asn |     |     |
| 245                                                             | 250 | 255 |
| Glu Gln Trp Tyr Cys Ser Asp Gln Trp Asn Ser                     |     |     |
| 260                                                             | 265 |     |

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atttttcttg agagatccaa aaaaagtatc agaaagaaga agaagacgac tccaaaaawc  | 60   |
| gatgccgtat tacaccaacg acgacaatga cgctcgacgat ttcaccgaat acgatccgat | 120  |
| gccttatagt ggaggctacg acatcacctg gacatacggc cggttcaattc caccgtccga | 180  |
| cgagacttgt taccctctct cctctctctc cggcgacgcc tttgagtatc agcgacctaa  | 240  |
| tttctcttct aacaacgatt cttctgctta tgacgaccaa gctcttaaaa ccgagtacag  | 300  |
| tagctatgca cgaccgagac cggttggatc tggatctgat tttggccgga aacctaatc   | 360  |
| tggatatgga gggagaacgg aggttgagta tggccggaaa actgaatcgg agcatggatc  | 420  |
| tggctatggt gggagaattg agagcgatta cgtgaagcct agctatggcg gtcacgagga  | 480  |
| tgatggtgac gatggtcaca aaaaacatag tggtaaggat tatgatgatg gagatgagaa  | 540  |
| gagtaagaag aaggagaagg agaagaagaa ggataagaag aaagatggta ataactctga  | 600  |
| agatgatgag tttaagaaga agaagaagaa atagcagtac aaggagcatc atgatgatga  | 660  |
| tgattatgat gagaagaaga agaagaagaa agactataat gatgatgatg agaagaagaa  | 720  |
| gaagaagcat tataatgatg atgatgatga gaagaagaag aagcattaca atgatgatga  | 780  |
| tgatgagaag aagaagaaga aggagtatca tgatgatgag gataagaaga agaagaagca  | 840  |
| ctatgataat gatgatgatg agaagaagaa gaagaaggat catcgtgatg atgatgatga  | 900  |
| gaagaagaag aagaaggata accaccacaa gggacatgac taaaaaagggt ttatgatttg | 960  |
| ggatttgcat tcttatgact aaataagtaa caacaactta agcacacttc tgctctctac  | 1020 |
| gtttatgtca attgttggtt tgtttttgct tcgtgttttt gctgctaact tcaatgagat  | 1080 |
| cttcataagt catatgtaat atgttttagtg tacgtgtttt ctagtgatgt cgtttgggtc | 1140 |

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1498494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Phe Phe Leu Arg Asp Pro Lys Lys Val Ser Glu Arg Arg Arg Arg Arg  
1 5 10 15  
Leu Gln Lys Xaa Met Pro Tyr Tyr Thr Asn Asp Asp Asn Asp Val Asp  
20 25 30  
Asp Phe Thr Glu Tyr Asp Pro Met Pro Tyr Ser Gly Gly Tyr Asp Ile  
35 40 45  
Thr Val Thr Tyr Gly Arg Ser Ile Pro Pro Ser Asp Glu Thr Cys Tyr  
50 55 60  
Pro Leu Ser Ser Leu Ser Gly Asp Ala Phe Glu Tyr Gln Arg Pro Asn  
65 70 75 80  
Phe Ser Ser Asn Asn Asp Ser Ser Ala Tyr Asp Asp Gln Ala Leu Lys  
85 90 95  
Thr Glu Tyr Ser Ser Tyr Ala Arg Pro Gly Pro Val Gly Ser Gly Ser  
100 105 110  
Asp Phe Gly Arg Lys Pro Asn Ser Gly Tyr Gly Gly Arg Thr Glu Val  
115 120 125  
Glu Tyr Gly Arg Lys Thr Glu Ser Glu His Gly Ser Gly Tyr Gly Gly  
130 135 140  
Arg Ile Glu Ser Asp Tyr Val Lys Pro Ser Tyr Gly Gly His Glu Asp  
145 150 155 160  
Asp Gly Asp Asp Gly His Lys Lys His Ser Gly Lys Asp Tyr Asp Asp  
165 170 175  
Gly Asp Glu Lys Ser Lys Lys Lys Glu Lys Glu Lys Lys Lys Asp Lys  
180 185 190  
Lys Lys Asp Gly Asn Asn Ser Glu Asp Asp Glu Phe Lys Lys Lys Lys  
195 200 205  
Lys Lys  
210

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..190

(D) OTHER INFORMATION: / Ceres Seq. ID 1498495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

Met Pro Tyr Tyr Thr Asn Asp Asp Asn Asp Val Asp Asp Phe Thr Glu  
1 5 10 15  
Tyr Asp Pro Met Pro Tyr Ser Gly Gly Tyr Asp Ile Thr Val Thr Tyr  
20 25 30  
Gly Arg Ser Ile Pro Pro Ser Asp Glu Thr Cys Tyr Pro Leu Ser Ser  
35 40 45  
Leu Ser Gly Asp Ala Phe Glu Tyr Gln Arg Pro Asn Phe Ser Ser Asn  
50 55 60  
Asn Asp Ser Ser Ala Tyr Asp Asp Gln Ala Leu Lys Thr Glu Tyr Ser  
65 70 75 80  
Ser Tyr Ala Arg Pro Gly Pro Val Gly Ser Gly Ser Asp Phe Gly Arg  
85 90 95  
Lys Pro Asn Ser Gly Tyr Gly Gly Arg Thr Glu Val Glu Tyr Gly Arg  
100 105 110  
Lys Thr Glu Ser Glu His Gly Ser Gly Tyr Gly Gly Arg Ile Glu Ser  
115 120 125  
Asp Tyr Val Lys Pro Ser Tyr Gly Gly His Glu Asp Asp Gly Asp Asp

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 130 |     | 135 |     | 140 |     |     |     |     |     |     |     |     |     |     |     |
| Gly | His | Lys | Lys | His | Ser | Gly | Lys | Asp | Tyr | Asp | Asp | Gly | Asp | Glu | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Lys | Lys | Lys | Glu | Lys | Glu | Lys | Lys | Lys | Asp | Lys | Lys | Lys | Asp | Gly |
|     |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |
| Asn | Asn | Ser | Glu | Asp | Asp | Glu | Phe | Lys | Lys | Lys | Lys | Lys | Lys |     |     |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1498496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Tyr | Ser | Gly | Gly | Tyr | Asp | Ile | Thr | Val | Thr | Tyr | Gly | Arg | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Pro | Pro | Ser | Asp | Glu | Thr | Cys | Tyr | Pro | Leu | Ser | Ser | Leu | Ser | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Asp | Ala | Phe | Glu | Tyr | Gln | Arg | Pro | Asn | Phe | Ser | Ser | Asn | Asn | Asp | Ser |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Tyr | Asp | Asp | Gln | Ala | Leu | Lys | Thr | Glu | Tyr | Ser | Ser | Tyr | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Arg | Pro | Gly | Pro | Val | Gly | Ser | Gly | Ser | Asp | Phe | Gly | Arg | Lys | Pro | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Gly | Tyr | Gly | Gly | Arg | Thr | Glu | Val | Glu | Tyr | Gly | Arg | Lys | Thr | Glu |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     | 95  |     |
| Ser | Glu | His | Gly | Ser | Gly | Tyr | Gly | Gly | Arg | Ile | Glu | Ser | Asp | Tyr | Val |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Pro | Ser | Tyr | Gly | Gly | His | Glu | Asp | Asp | Gly | Asp | Asp | Gly | His | Lys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys | His | Ser | Gly | Lys | Asp | Tyr | Asp | Asp | Gly | Asp | Glu | Lys | Ser | Lys | Lys |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Lys | Glu | Lys | Glu | Lys | Lys | Lys | Asp | Lys | Lys | Lys | Asp | Gly | Asn | Asn | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Asp | Asp | Glu | Phe | Lys | Lys | Lys | Lys | Lys |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1332

(D) OTHER INFORMATION: / Ceres Seq. ID 1498497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| gatacatctc  | ctcgctcgccg | ttcttcggat  | tttcaactctt | ctgctcgaaa  | ggtctctcac  | 60  |
| tcttctcttt  | tttaattctat | tgaaattgaa  | acttcccttc  | tcttctcttc  | tcttctctgt  | 120 |
| agcaactcctg | cttctagttt  | agctgctctt  | cttcttctac  | ttgctgcaac  | aactccaaat  | 180 |
| catcatttct  | cttggtccag  | gcagtgcttg  | agaatcattg  | aagaagggtga | tcgctgggtgc | 240 |
| tggttttgata | actcaaagcc  | gttttgctga  | aagagggtta  | ccaaagttag  | aagctcaaga  | 300 |
| acttgaggct  | gtgtcttctt  | tttgtatcat  | gccatatttt  | attcagaggc  | ttttcaatac  | 360 |
| ttgcaagtca  | tctctctcac  | ctaattggtcc | tgtgtctgag  | gaggccttag  | acaagggttcg | 420 |
| caatgtcttg  | gagaaaatca  | agccgtctga  | tgttgggtctc | gaacaggaag  | ctcaattggt  | 480 |

|            |             |            |             |             |            |      |
|------------|-------------|------------|-------------|-------------|------------|------|
| gcgtaattgg | cctgggtcctg | ggaacgagcg | taatggaaac  | aatcattctc  | tgccagcaat | 540  |
| aaaatacctt | cagttacatg  | agtgtgacag | cttctcgatt  | ggaattttct  | gcatgccacc | 600  |
| tgggtctatc | ataccacttc  | ataatcatcc | aggcatgaca  | gtgctaagca  | agcttgttta | 660  |
| tggttcaatg | cacgttaagt  | catatgattg | ggctgagcct  | gaccaatcag  | agctagacga | 720  |
| tccattacaa | gcaagaccg   | cgaagctggt | caaggatatt  | gatatgactt  | cccctagccc | 780  |
| agcaaccact | ctatatccaa  | caaccggtgg | caacattcat  | tgtttcaaag  | ccattactca | 840  |
| ttgtgcaatc | tttgacatct  | tatctcctcc | atactcttct  | actcatggca  | gacactgcaa | 900  |
| ctacttcgga | aaatccccaa  | tgctagactt | acctgggtgag | attgaagtga  | tgaatggaga | 960  |
| agtgatctca | aatgtgacat  | ggcttgaaga | gtatcaacct  | ccagataact  | ttgtgatatg | 1020 |
| gagagttccg | tacagaggtc  | cagtgmttag | aaaatgagaa  | atacaaaaag  | gattaaacat | 1080 |
| attaaaaaag | agcagaaaga  | gaaaggtgct | tatgatcagg  | agaataattg  | gtaaaccatt | 1140 |
| cagaggctgg | ctgcataatg  | gtcgagggtc | ttacataatt  | gtgaccacat  | taagttccag | 1200 |
| cctatgtcgt | tgtatgataa  | tgattacttc | actagtttaa  | tattataatt  | tttttcccct | 1260 |
| atttttatat | gcagctacac  | aaaaaattgc | tcataaacag  | tgttatatatt | agttatcata | 1320 |
| aattttgttt | cc          |            |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Tyr | Phe | Ile | Gln | Arg | Leu | Phe | Asn | Thr | Cys | Lys | Ser | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Asn | Gly | Pro | Val | Ser | Glu | Glu | Ala | Leu | Asp | Lys | Val | Arg | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Glu | Lys | Ile | Lys | Pro | Ser | Asp | Val | Gly | Leu | Glu | Gln | Glu | Ala |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Gln | Leu | Val | Arg | Asn | Trp | Pro | Gly | Pro | Gly | Asn | Glu | Arg | Asn | Gly | Asn |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Asn | His | Ser | Leu | Pro | Ala | Ile | Lys | Tyr | Leu | Gln | Leu | His | Glu | Cys | Asp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Phe | Ser | Ile | Gly | Ile | Phe | Cys | Met | Pro | Pro | Gly | Ser | Ile | Ile | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | His | Asn | His | Pro | Gly | Met | Thr | Val | Leu | Ser | Lys | Leu | Val | Tyr | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Met | His | Val | Lys | Ser | Tyr | Asp | Trp | Ala | Glu | Pro | Asp | Gln | Ser | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Asp | Asp | Pro | Leu | Gln | Ala | Arg | Pro | Ala | Lys | Leu | Val | Lys | Asp | Ile |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asp | Met | Thr | Ser | Pro | Ser | Pro | Ala | Thr | Thr | Leu | Tyr | Pro | Thr | Thr | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Asn | Ile | His | Cys | Phe | Lys | Ala | Ile | Thr | His | Cys | Ala | Ile | Phe | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Leu | Ser | Pro | Pro | Tyr | Ser | Ser | Thr | His | Gly | Arg | His | Cys | Asn | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Arg | Lys | Ser | Pro | Met | Leu | Asp | Leu | Pro | Gly | Glu | Ile | Glu | Val | Met |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Gly | Glu | Val | Ile | Ser | Asn | Val | Thr | Trp | Leu | Glu | Glu | Tyr | Gln | Pro |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Pro | Asp | Asn | Phe | Val | Ile | Trp | Arg | Val | Pro | Tyr | Arg | Gly | Pro | Val | Xaa |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..154
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498499
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Pro | Gly | Ser | Ile | Ile | Pro | Leu | His | Asn | His | Pro | Gly | Met | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Ser | Lys | Leu | Val | Tyr | Gly | Ser | Met | His | Val | Lys | Ser | Tyr | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Ala | Glu | Pro | Asp | Gln | Ser | Glu | Leu | Asp | Asp | Pro | Leu | Gln | Ala | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ala | Lys | Leu | Val | Lys | Asp | Ile | Asp | Met | Thr | Ser | Pro | Ser | Pro | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Thr | Leu | Tyr | Pro | Thr | Thr | Gly | Gly | Asn | Ile | His | Cys | Phe | Lys | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Thr | His | Cys | Ala | Ile | Phe | Asp | Ile | Leu | Ser | Pro | Pro | Tyr | Ser | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | His | Gly | Arg | His | Cys | Asn | Tyr | Phe | Arg | Lys | Ser | Pro | Met | Leu | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Pro | Gly | Glu | Ile | Glu | Val | Met | Asn | Gly | Glu | Val | Ile | Ser | Asn | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Trp | Leu | Glu | Glu | Tyr | Gln | Pro | Pro | Asp | Asn | Phe | Val | Ile | Trp | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Pro | Tyr | Arg | Gly | Pro | Val | Xaa | Arg | Lys |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:469:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 140 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..140
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1498500
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Val | Leu | Ser | Lys | Leu | Val | Tyr | Gly | Ser | Met | His | Val | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Asp | Trp | Ala | Glu | Pro | Asp | Gln | Ser | Glu | Leu | Asp | Asp | Pro | Leu | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Arg | Pro | Ala | Lys | Leu | Val | Lys | Asp | Ile | Asp | Met | Thr | Ser | Pro | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ala | Thr | Thr | Leu | Tyr | Pro | Thr | Thr | Gly | Gly | Asn | Ile | His | Cys | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ala | Ile | Thr | His | Cys | Ala | Ile | Phe | Asp | Ile | Leu | Ser | Pro | Pro | Tyr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Ser | Thr | His | Gly | Arg | His | Cys | Asn | Tyr | Phe | Arg | Lys | Ser | Pro | Met |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Asp | Leu | Pro | Gly | Glu | Ile | Glu | Val | Met | Asn | Gly | Glu | Val | Ile | Ser |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asn | Val | Thr | Trp | Leu | Glu | Glu | Tyr | Gln | Pro | Pro | Asp | Asn | Phe | Val | Ile |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Trp | Arg | Val | Pro | Tyr | Arg | Gly | Pro | Val | Xaa | Arg | Lys |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:470:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 984 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..984  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

```
agattcgcgga gttcttctggt cttcgtttctg cctttwtttt ttttattttt tttgtgtggt 60
tgagagatgt ctgcctttga agacgattcc ttcgtcatat tcaacgatga tgcgtctgag 120
tctgttccag tctcaggctc ttttgacgcc actgattctt tctcagcttt cgacgggtca 180
ctccaagtcg aggactccgt cgacgatgtt tttgcagcgc cgtcttctga ctacggtgct 240
tactccaacg gtgacggcat cttcggatcc aacggggatc acgacggtcc tatcttgcca 300
ccaccgtcgg agatggaatc agatgaggga tttgctctta gagaatggag aagacaaaat 360
gcaattcaac ttgaggagaa ggagaagaga gaaaaggaaat tggtgaagca aattattgag 420
gaagctgata aatacaaaaga agagtttcat aagaagattg aagtaacttg tgaatacaac 480
aaagcagcta acagagagaa ggaaaagctg tatctggaga accaagagaa gttctacgcg 540
gaatccagca agaattactg gaaggcaata gcagagctag ttcctaaaga agttccaaca 600
atagagaaaa ggagaggaaa aaaagagcaa caagatccta agaagccaac agtctctgtg 660
attcaaggta caaagcccggt taagccaacc gatctaaca gaatgagaca aatattggtg 720
aagctcaaac acaaccaccc ttctcacctg aaactcactt ctcaacctcc atcggaggag 780
gcggtctgct ctccaaagaa tgttcccgaa accaagccca ctgaggcagt tactgctgct 840
taaaaacctc ttttgttttc ttattcgttg cttacatctg tgtgaattca gtctttgcat 900
ttcattatgt gttataaaca gctgagagat tttatggttc atgtgtgtta ttaacataat 960
tatgtcatat tggaatgata actt
```

(2) INFORMATION FOR SEQ ID NO:471:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 134 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..134  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```
Asp Ser Arg Val Leu Arg Ser Ser Phe Cys Leu Xaa Phe Phe Tyr Phe
1 5 10 15
Phe Cys Val Phe Glu Arg Cys Leu Pro Leu Lys Thr Ile Pro Ser Ser
20 25 30
Tyr Ser Thr Met Met Arg Leu Ser Leu Phe Gln Ser Gln Ala Leu Leu
35 40 45
Thr Pro Leu Ile Leu Ser Gln Leu Ser Thr Ala His Ser Lys Ser Arg
50 55 60
Thr Pro Ser Thr Met Phe Leu Gln Arg Arg Leu Thr Thr Val Leu
65 70 75 80
Thr Pro Thr Val Thr Ala Ser Ser Asp Pro Thr Gly Ile Thr Thr Val
85 90 95
Leu Ser Cys His His Arg Arg Arg Trp Asn Gln Met Arg Asp Leu Leu
100 105 110
Leu Glu Asn Gly Glu Asp Lys Met Gln Phe Asn Leu Arg Arg Arg Arg
115 120 125
Arg Glu Lys Arg Asn Cys
130
```

(2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 258 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..258
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498503
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Phe | Glu | Asp | Asp | Ser | Phe | Val | Ile | Leu | Asn | Asp | Asp | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Glu | Ser | Val | Pro | Val | Ser | Gly | Ser | Phe | Asp | Ala | Thr | Asp | Ser | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ala | Phe | Asp | Gly | Ser | Leu | Gln | Val | Glu | Asp | Ser | Val | Asp | Asp | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Ala | Ala | Pro | Ser | Ser | Asp | Tyr | Gly | Ala | Tyr | Ser | Asn | Gly | Asp | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Phe | Gly | Ser | Asn | Gly | Asp | His | Asp | Gly | Pro | Ile | Leu | Pro | Pro | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Glu | Met | Glu | Ser | Asp | Glu | Gly | Phe | Ala | Leu | Arg | Glu | Trp | Arg | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Asn | Ala | Ile | Gln | Leu | Glu | Glu | Lys | Glu | Lys | Arg | Glu | Lys | Glu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | Gln | Ile | Ile | Glu | Glu | Ala | Asp | Gln | Tyr | Lys | Glu | Glu | Phe | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Lys | Ile | Glu | Val | Thr | Cys | Glu | Asn | Asn | Lys | Ala | Ala | Asn | Arg | Glu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Glu | Lys | Leu | Tyr | Leu | Glu | Asn | Gln | Glu | Lys | Phe | Tyr | Ala | Glu | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Lys | Asn | Tyr | Trp | Lys | Ala | Ile | Ala | Glu | Leu | Val | Pro | Lys | Glu | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Thr | Ile | Glu | Lys | Arg | Arg | Gly | Lys | Lys | Glu | Gln | Gln | Asp | Pro | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Pro | Thr | Val | Ser | Val | Ile | Gln | Gly | Pro | Lys | Pro | Gly | Lys | Pro | Thr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Leu | Thr | Arg | Met | Arg | Gln | Ile | Leu | Val | Lys | Leu | Lys | His | Asn | Pro |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Ser | His | Leu | Lys | Leu | Thr | Ser | Gln | Pro | Pro | Ser | Glu | Glu | Ala | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ala | Pro | Pro | Lys | Asn | Val | Pro | Glu | Thr | Lys | Pro | Thr | Glu | Ala | Val | Thr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:473:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 176 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..176
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498504
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Asp | Glu | Gly | Phe | Ala | Leu | Arg | Glu | Trp | Arg | Arg | Gln | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ile | Gln | Leu | Glu | Glu | Lys | Glu | Lys | Arg | Glu | Lys | Glu | Leu | Leu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ile | Ile | Glu | Glu | Ala | Asp | Gln | Tyr | Lys | Glu | Glu | Phe | His | Lys | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Glu | Val | Thr | Cys | Glu | Asn | Asn | Lys | Ala | Ala | Asn | Arg | Glu | Lys | Glu |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Leu | Tyr | Leu | Glu | Asn | Gln | Glu | Lys | Phe | Tyr | Ala | Glu | Ser | Ser | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Tyr | Trp | Lys | Ala | Ile | Ala | Glu | Leu | Val | Pro | Lys | Glu | Val | Pro | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Glu | Lys | Arg | Arg | Gly | Lys | Lys | Glu | Gln | Gln | Asp | Pro | Lys | Lys | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Val | Ser | Val | Ile | Gln | Gly | Pro | Lys | Pro | Gly | Lys | Pro | Thr | Asp | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Arg | Met | Arg | Gln | Ile | Leu | Val | Lys | Leu | Lys | His | Asn | Pro | Pro | Ser |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Leu | Lys | Leu | Thr | Ser | Gln | Pro | Pro | Ser | Glu | Glu | Ala | Ala | Ala | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Lys | Asn | Val | Pro | Glu | Thr | Lys | Pro | Thr | Glu | Ala | Val | Thr | Ala | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1308
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| catctttttc  | tctcttttatt | tataaattta  | tctgcatagt  | actctctgaa  | tctatatctt  | 60   |
| caaaaaaaaa  | aaacgtccaa  | gatcaaata   | agaaacccat  | taaaaaaaaa  | aatcagggtt  | 120  |
| tgggtttcagt | tttaagggtt  | taagggtttct | tggggaagaa  | acgatggaga  | ctttttgtgg  | 180  |
| gtttcaaaaag | gaggaagagc  | agatggattt  | acctcctggg  | ttcagggttc  | atccaacaga  | 240  |
| tgaagaactc  | ataactcact  | atctccataa  | gaaggttctt  | gacaccagct  | tctcagctaa  | 300  |
| agctatcggt  | gaagttgatt  | taaacaatc   | agagccatgg  | gagttacat   | ggatggcaaa  | 360  |
| aatgggtgag  | aaagaatggt  | attttttctg  | tgtgagagac  | agaaagtatc  | ccaccgggtt  | 420  |
| aagaactaac  | cgagcaactg  | aagccggtta  | ttggaaggcg  | accgggaagg  | ataaagagat  | 480  |
| ataccgaggc  | aaatcacttg  | ttgggatgaa  | gaagacactt  | gttttctata  | gaggaagagc  | 540  |
| tcctaaaggt  | cagaaaacca  | actgggtgat  | gcatgagtac  | aggcttgaag  | gaaaattctc  | 600  |
| tgcccataac  | ttgccgaaaa  | ccgcaaagaa  | tgaatgggtg  | atatgcaggg  | tgwtccaaaa  | 660  |
| gagtgtctgga | gggcaagaag  | atcccgat    | cgagtcta    | ccgaatcggt  | tcactcggaa  | 720  |
| ccgactttta  | cccttcgctt  | ttgccctctt  | taaccgattc  | ttcgccctac  | aacgataaar  | 780  |
| ccraaacaga  | ascggtctac  | gtgccctgct  | tctccaacca  | aacggatcaa  | aaccaaggaa  | 840  |
| ccacactcaa  | ttgcttcagc  | agccctgttc  | ttaactcgat  | ccaagccgac  | atttttcmca  | 900  |
| ggattccact  | ctatcaaact  | cagtccctcc  | aggtttctat  | gaatctacag  | agcccgggtc  | 960  |
| tcacgcaaga  | acactcagtt  | ctacatgcta  | tgatcgagaa  | caacagaaga  | caaagtctca  | 1020 |
| aaacgatgag  | tgtctcacia  | gaaaccggag  | tttcaactga  | catgaacact  | gatattctcat | 1080 |
| cggattttga  | atttggttaag | agacggtttg  | attctcaaga  | agatccgtct  | tcctctactg  | 1140 |
| gaccggttga  | tcttgaacct  | ttctggaatt  | actgaagatg  | attcaagatt  | ctcatgtcca  | 1200 |
| tttaatttact | gtggtgtgtt  | aaagtttgta  | taggctattg  | tcataatactc | tcataatcaac | 1260 |
| ttccactata  | tattataaca  | atttaaagaa  | acttaaaaaat | atgatttg    |             |      |

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1498510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Thr | Phe | Cys | Gly | Phe | Gln | Lys | Glu | Glu | Glu | Gln | Met | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Pro | Gly | Phe | Arg | Phe | His | Pro | Thr | Asp | Glu | Glu | Leu | Ile | Thr | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Leu | His | Lys | Lys | Val | Leu | Asp | Thr | Ser | Phe | Ser | Ala | Lys | Ala | Ile |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Gly | Glu | Val | Asp | Leu | Asn | Lys | Ser | Glu | Pro | Trp | Glu | Leu | Pro | Trp | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Lys | Met | Gly | Glu | Lys | Glu | Trp | Tyr | Phe | Phe | Cys | Val | Arg | Asp | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Tyr | Pro | Thr | Gly | Leu | Arg | Thr | Asn | Arg | Ala | Thr | Glu | Ala | Gly | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Trp | Lys | Ala | Thr | Gly | Lys | Asp | Lys | Glu | Ile | Tyr | Arg | Gly | Lys | Ser | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Gly | Met | Lys | Lys | Thr | Leu | Val | Phe | Tyr | Arg | Gly | Arg | Ala | Pro | Lys |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Gln | Lys | Thr | Asn | Trp | Val | Met | His | Glu | Tyr | Arg | Leu | Glu | Gly | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Ser | Ala | His | Asn | Leu | Pro | Lys | Thr | Ala | Lys | Asn | Glu | Trp | Val | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Cys | Arg | Val | Xaa | Gln | Lys | Ser | Ala | Gly | Gly | Gln | Glu | Asp | Pro | Asp | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Ser | Asn | Pro | Asn | Arg | Phe | Thr | Arg | Asn | Arg | Leu |     |     |     |     |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Leu | Pro | Pro | Gly | Phe | Arg | Phe | His | Pro | Thr | Asp | Glu | Glu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Thr | His | Tyr | Leu | His | Lys | Lys | Val | Leu | Asp | Thr | Ser | Phe | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ala | Ile | Gly | Glu | Val | Asp | Leu | Asn | Lys | Ser | Glu | Pro | Trp | Glu | Leu |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Trp | Met | Ala | Lys | Met | Gly | Glu | Lys | Glu | Trp | Tyr | Phe | Phe | Cys | Val |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Arg | Asp | Arg | Lys | Tyr | Pro | Thr | Gly | Leu | Arg | Thr | Asn | Arg | Ala | Thr | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Gly | Tyr | Trp | Lys | Ala | Thr | Gly | Lys | Asp | Lys | Glu | Ile | Tyr | Arg | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Ser | Leu | Val | Gly | Met | Lys | Lys | Thr | Leu | Val | Phe | Tyr | Arg | Gly | Arg |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Pro | Lys | Gly | Gln | Lys | Thr | Asn | Trp | Val | Met | His | Glu | Tyr | Arg | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Glu | Gly | Lys | Phe | Ser | Ala | His | Asn | Leu | Pro | Lys | Thr | Ala | Lys | Asn | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Trp | Val | Ile | Cys | Arg | Val | Xaa | Gln | Lys | Ser | Ala | Gly | Gly | Gln | Glu | Asp |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Pro | Asp | Phe | Glu | Ser | Asn | Pro | Asn | Arg | Phe | Thr | Arg | Asn | Arg | Leu |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Met Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val Arg Asp  
1 5 10 15  
Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly  
20 25 30  
Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly Lys Ser  
35 40 45  
Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro  
50 55 60  
Lys Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly  
65 70 75 80  
Lys Phe Ser Ala His Asn Leu Pro Lys Thr Ala Lys Asn Glu Trp Val  
85 90 95  
Ile Cys Arg Val Xaa Gln Lys Ser Ala Gly Gly Gln Glu Asp Pro Asp  
100 105 110  
Phe Glu Ser Asn Pro Asn Arg Phe Thr Arg Asn Arg Leu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

attctctaga tgcttgaaag ctgtgtaggg attgtagaag aggaggcgat atttttcaat 60  
cgctcgctcgt ttgggaaatt cctcacatct cagatgaact ccaatcgctt cgagaaactc 120  
taattcctcg ggagttttcg atagcatcat cgagaaattg ttttcccggt gaacaatgga 180  
tggttaacaaa gatgacgcgt tgaaatgcct aaaaatcggc aaggatgcta taaaagcagg 240  
agatagatct cgcgctttga aatttcttga gaaagcttgt cgtcttgatc caaatcttct 300  
gatcgatgat cttgttttcg atctgaagaa gcaatcggat gaaccagcgg cggaggagga 360  
ttcgcttga tctggcgcca acgagtcctt taagccgctg gatcgacctt ctcttcgtca 420  
acgtggatct tcgtcatcag ccgcgggatc gtcacatct tcgtcttcca cggaagaaca 480  
acgaacgatc gtgagggaga taaagtcgaa gaaggattac tatgagatcc ttggattgaa 540  
aagaaactgt tcagtggaa atttgaggaa atcttatcgg aaactctcgt tgaaagtcca 600  
tcccataag aataaagctc ctgcttctga agaagctttt aaattcgtct ctaaagcttt 660  
ccaatgctta aagcaacaaa gacactagcc gaaagtacga cgtcagtggg tccgatgagc 720  
ctgcttatca accatgccga gctgcgagaa gaaacaacgg attcaacggc ttctctgatg 780  
atgaatttga tgctgatgag attttcagaa gcttcttttg tgggtgggga atgaatcctg 840  
ctactactca attccgatca ttcaatttcg gtggaggaac tagaacagct aattaagctt 900  
ctgatacagg attcaatcct cgtgtactcc ttcaaatact tcctgtttgt ttcatactac 960  
ttctcaactt tttgccttct cctcaaccaa ttactcgtt ttctccatcg tataactagc 1020  
agcaciaaatt caccactcat aggggtgtca attactttgt gagatcagcc aagttcgagc 1080  
aggaataccc gataagtagc ttctagagac agagggttga agagcaagtt gatagagatt 1140  
acttgcttat acttgccag aattgtcgcc atgagcttca gagacaacaa tggggatata 1200  
tccgcgaagc gccacattgt gacatgatga agagggttga tgcagctgct gcataaacca 1260

tccatgtcag agagagactg aagcaccaag ttagtaaact caaatccaag aaacttggtt 1320  
ggattgttct gagacatagc tatggtactt actaacttct gagcattttt gttgatgctt 1380  
cagtgaagttt gatttctaag tcccaaactc atatacgttg attactgtgc tccttatgat 1440  
gttagtatga aacatattat gtgtg

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1498518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Met Asp Gly Asn Lys Asp Asp Ala Leu Lys Cys Leu Lys Ile Gly Lys  
1 5 10 15  
Asp Ala Ile Lys Ala Gly Asp Arg Ser Arg Ala Leu Lys Phe Leu Glu  
20 25 30  
Lys Ala Cys Arg Leu Asp Pro Asn Leu Leu Ile Asp Asp Leu Val Ser  
35 40 45  
Asp Leu Lys Lys Gln Ser Asp Glu Pro Ala Ala Glu Glu Asp Ser Pro  
50 55 60  
Gly Ser Gly Ala Asn Glu Ser Ser Lys Pro Ser Asp Arg Pro Ser Leu  
65 70 75 80  
Arg Gln Arg Gly Ser Ser Ser Ser Ala Ala Gly Ser Ser Ser Ser Ser  
85 90 95  
Ser Ser Thr Glu Gln Arg Thr Ile Val Arg Glu Ile Lys Ser Lys  
100 105 110  
Lys Asp Tyr Tyr Glu Ile Leu Gly Leu Lys Arg Asn Cys Ser Val Glu  
115 120 125  
Asp Leu Arg Lys Ser Tyr Arg Lys Leu Ser Leu Lys Val His Pro Asp  
130 135 140  
Lys Asn Lys Ala Pro Ala Ser Glu Glu Ala Phe Lys Phe Val Ser Lys  
145 150 155 160  
Ala Phe Gln Cys Leu Lys Gln Gln Arg His  
165 170

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 778 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..778

(D) OTHER INFORMATION: / Ceres Seq. ID 1498519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

ctctctctta ggtttttttt cccttctccc aatctcatct tctccgaaaa cctttcttct 60  
ctcaaatttc tggtagaaac atgtctgacg acgagcacca ctttgaggcc agcgaatccg 120  
gagcttccaa gacctatcct caatcagccg gtaacatccg taaagggtgt cacatcgatca 180  
tcaaaaaccg tccctgcaag gttgttgagg ttctgacttc caaaactggc aagcacggtc 240  
acgccaaatg tcactttgtt gctattgata tcttcaactgc taagaagctt gaagatattg 300  
ttccatcttc ccacaattgt gatgttccac atgtgaaccg tgttgattac cagttgattg 360  
atatcactga gtagggcttc gtgagccttc tcaactgacag tggtaggcacc aaggatgatc 420  
tcaagcttcc caccgatgat ggtctcaccg nccagttgtt gtgttttgtt aatgcacatg 480  
agscttgatg tcgatgaggg aaaggatatt gtgggtgtctg tcatgtcttc catgggagag 540  
gagcagatct gtgccgtcaa ggaagttggt ggtggcaagt aaacaagtat cattcgatat 600  
attattacca gtttgacaac ggacgtcaat gttataagaa ccaaagatg tttttctttt 660

tcctaattta gaccctttgt gtgtgtttct tgttgcaaga caaccatata tattggtttt 720  
ggattgttg aaaagtttgt gttgaaacat tcaaagtttc ttatgagatg ttattctc

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1498520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Leu | Arg | Phe | Phe | Phe | Pro | Ser | Pro | Asn | Leu | Ile | Phe | Ser | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Leu | Ser | Ser | Leu | Lys | Phe | Leu | Val | Lys | Thr | Cys | Leu | Thr | Thr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Thr | Leu | Arg | Pro | Ala | Asn | Pro | Glu | Leu | Pro | Arg | Pro | Ile | Leu | Asn |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gln | Pro | Val | Thr | Ser | Val | Lys | Val | Val | Thr | Ser | Ser | Ser | Lys | Thr | Val |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Pro | Ala | Arg | Leu | Leu | Arg | Phe | Arg | Leu | Pro | Lys | Leu | Ala | Ser | Thr | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Pro | Asn | Val | Thr | Leu | Leu | Leu | Leu | Ile | Ser | Ser | Leu | Leu | Arg | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Lys | Ile | Leu | Phe | His | Leu | Pro | Thr | Ile | Val | Met | Phe | His | Met |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1498521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asp | Asp | Glu | His | His | Phe | Glu | Ala | Ser | Glu | Ser | Gly | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Thr | Tyr | Pro | Gln | Ser | Ala | Gly | Asn | Ile | Arg | Lys | Gly | Gly | His | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ile | Lys | Asn | Arg | Pro | Cys | Lys | Val | Val | Glu | Val | Ser | Thr | Ser | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr | Gly | Lys | His | Gly | His | Ala | Lys | Cys | His | Phe | Val | Ala | Ile | Asp | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Phe | Thr | Ala | Lys | Lys | Leu | Glu | Asp | Ile | Val | Pro | Ser | Ser | His | Asn | Cys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Val | Pro | His | Val | Asn | Arg | Val | Asp | Tyr | Gln | Leu | Ile | Asp | Ile | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Asp | Gly | Phe | Val | Ser | Leu | Leu | Thr | Asp | Ser | Gly | Gly | Thr | Lys | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Leu | Lys | Leu | Pro | Thr | Asp | Asp | Gly | Leu | Thr | Xaa | Gln | Leu | Leu | Cys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Phe | Val | Asn | Ala | His | Glu | Xaa | Trp | Ile | Arg |     |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1212
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

|            |            |            |            |            |             |            |      |
|------------|------------|------------|------------|------------|-------------|------------|------|
| ctgtctctct | tca        | gtgacac    | aaacccaaag | aaaagtagtg | agaaacaaaa  | tcgaggtaac | 60   |
| tactagatga | agac       | gatgac     | gcaattaaat | attgcggttg | trgttgtagt  | gacgggtctt | 120  |
| attggaatgt | tgag       | atcatc     | ggaggctcaa | cttcaaata  | atttctacgc  | gaagagctgt | 180  |
| ccaaacgcag | agaaa      | atcat      | ttcagatcat | attcaaaatc | atatccacaa  | tggtccttct | 240  |
| cttgacgctc | ctctc      | atccg      | aatgcacttc | catgattgct | tcgttagggg  | atgtgacgga | 300  |
| tcgggtgttg | taaatt     | caac       | atctggtaac | gcagagagag | atgcaccacc  | gaatctaaca | 360  |
| cttagaggat | tcggtttc   | gt         | ggaaaggatt | aaggctcttc | ttgaaaaagt  | gtgtcctaag | 420  |
| actgtttctt | gcgcag     | atat       | cattgctttg | actgctagag | acacagttgt  | cgccaccgga | 480  |
| ggtccttcat | ggagtgttc  | c          | aacgggaaga | agagacggta | ggatctcaaa  | tttgaaggag | 540  |
| gctacgaata | acattccacc | tccaac     | gagt       | aatttcacga | ctttacgacg  | acttttcaaa | 600  |
| aaccaaggcc | ttaatctcaa | ggaccttg   | tt         | ctgctctctg | gggctcacac  | gattgggtgc | 660  |
| tcacattgtt | cttccatgaa | tactcgtctc | tacaacttct | cgactacagt | caaacaagat  |            | 720  |
| ccatctctcg | atagccagta | cgcagcta   | ctaaaggcta | acaaatgtaa | gagcctaaac  |            | 780  |
| gacaatagca | ccatcctgga | gatggatccc | ggtagtagca | gaagcttcga | tctcagttat  |            | 840  |
| tataggcttg | tcttgaagag | gagaggcttg | ttccaatctg | attctgcctt | gacaacgaac  |            | 900  |
| tcagcgacgt | tgaaggtgat | caacgacttg | gtcaacgggt | ctgaaaagaa | gtttttcaaa  |            | 960  |
| gcttttgcta | agtcaatgrg | agaagatggg | gagagttaaw | gtgacagact | ggctcagctg  |            | 1020 |
| gtgtgatcag | gacacggtgt | tctgtcgtcg | gaagttagta | agcttggtcg | gaatgtgggtg |            | 1080 |
| tgttatggtc | attgtttgtt | tgtgtgactt | tcggaaaaaa | caaagtgtgt | taatttaatt  |            | 1140 |
| ttgttgttgt | ttgatttgtg | tttatgcacc | caagaatgat | gtgttatggt | tcaattaata  |            | 1200 |
| tgtgaatcat | tt         |            |            |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 310 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..310
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1498523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Met | Thr | Gln | Leu | Asn | Ile | Ala | Val | Xaa | Val | Val | Val | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Leu | Ile | Gly | Met | Leu | Arg | Ser | Ser | Glu | Ala | Gln | Leu | Gln | Met | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Tyr | Ala | Lys | Ser | Cys | Pro | Asn | Ala | Glu | Lys | Ile | Ile | Ser | Asp | His |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ile | Gln | Asn | His | Ile | His | Asn | Gly | Pro | Ser | Leu | Ala | Ala | Pro | Leu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Met | His | Phe | His | Asp | Cys | Phe | Val | Arg | Gly | Cys | Asp | Gly | Ser | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ile | Asn | Ser | Thr | Ser | Gly | Asn | Ala | Glu | Arg | Asp | Ala | Pro | Pro | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Thr | Leu | Arg | Gly | Phe | Gly | Phe | Val | Glu | Arg | Ile | Lys | Ala | Leu | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Lys | Val | Cys | Pro | Lys | Thr | Val | Ser | Cys | Ala | Asp | Ile | Ile | Ala | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Ala | Arg | Asp | Thr | Val | Val | Ala | Thr | Gly | Gly | Pro | Ser | Trp | Ser | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Thr | Gly | Arg | Arg | Asp | Gly | Arg | Ile | Ser | Asn | Leu | Lys | Glu | Ala | Thr |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asn | Asn | Ile | Pro | Pro | Pro | Thr | Ser | Asn | Phe | Thr | Thr | Leu | Arg | Arg | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Lys | Asn | Gln | Gly | Leu | Asn | Leu | Lys | Asp | Leu | Val | Leu | Leu | Ser | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | His | Thr | Ile | Gly | Val | Ser | His | Cys | Ser | Ser | Met | Asn | Thr | Arg | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Asn | Phe | Ser | Thr | Thr | Val | Lys | Gln | Asp | Pro | Ser | Leu | Asp | Ser | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Ala | Ala | Asn | Leu | Lys | Ala | Asn | Lys | Cys | Lys | Ser | Leu | Asn | Asp | Asn |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Thr | Ile | Leu | Glu | Met | Asp | Pro | Gly | Ser | Ser | Arg | Ser | Phe | Asp | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Tyr | Tyr | Arg | Leu | Val | Leu | Lys | Arg | Arg | Gly | Leu | Phe | Gln | Ser | Asp |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ser | Ala | Leu | Thr | Thr | Asn | Ser | Ala | Thr | Leu | Lys | Val | Ile | Asn | Asp | Leu |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Val | Asn | Gly | Ser | Glu | Lys | Lys | Phe | Phe | Lys | Ala | Phe | Ala | Lys | Ser | Met |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Xaa | Glu | Asp | Gly | Glu | Ser |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..307

(D) OTHER INFORMATION: / Ceres Seq. ID 1498524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Gln | Leu | Asn | Ile | Ala | Val | Xaa | Val | Val | Thr | Val | Leu | Ile |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly | Met | Leu | Arg | Ser | Ser | Glu | Ala | Gln | Leu | Gln | Met | Asn | Phe | Tyr | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ser | Cys | Pro | Asn | Ala | Glu | Lys | Ile | Ile | Ser | Asp | His | Ile | Gln | Asn |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| His | Ile | His | Asn | Gly | Pro | Ser | Leu | Ala | Ala | Pro | Leu | Ile | Arg | Met | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | His | Asp | Cys | Phe | Val | Arg | Gly | Cys | Asp | Gly | Ser | Val | Leu | Ile | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Thr | Ser | Gly | Asn | Ala | Glu | Arg | Asp | Ala | Pro | Pro | Asn | Leu | Thr | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Gly | Phe | Gly | Phe | Val | Glu | Arg | Ile | Lys | Ala | Leu | Leu | Glu | Lys | Val |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Pro | Lys | Thr | Val | Ser | Cys | Ala | Asp | Ile | Ile | Ala | Leu | Thr | Ala | Arg |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Thr | Val | Val | Ala | Thr | Gly | Gly | Pro | Ser | Trp | Ser | Val | Pro | Thr | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Arg | Asp | Gly | Arg | Ile | Ser | Asn | Leu | Lys | Glu | Ala | Thr | Asn | Asn | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Pro | Pro | Thr | Ser | Asn | Phe | Thr | Thr | Leu | Arg | Arg | Leu | Phe | Lys | Asn |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Gly | Leu | Asn | Leu | Lys | Asp | Leu | Val | Leu | Leu | Ser | Gly | Ala | His | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Gly | Val | Ser | His | Cys | Ser | Ser | Met | Asn | Thr | Arg | Leu | Tyr | Asn | Phe |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ser | Thr | Thr | Val | Lys | Gln | Asp | Pro | Ser | Leu | Asp | Ser | Gln | Tyr | Ala | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

Asn Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile  
225 230 235 240  
Leu Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr  
245 250 255  
Arg Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu  
260 265 270  
Thr Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly  
275 280 285  
Ser Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp  
290 295 300  
Gly Glu Ser  
305

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1498525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Met Leu Arg Ser Ser Glu Ala Gln Leu Gln Met Asn Phe Tyr Ala Lys  
1 5 10 15  
Ser Cys Pro Asn Ala Glu Lys Ile Ile Ser Asp His Ile Gln Asn His  
20 25 30  
Ile His Asn Gly Pro Ser Leu Ala Ala Pro Leu Ile Arg Met His Phe  
35 40 45  
His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Ile Asn Ser  
50 55 60  
Thr Ser Gly Asn Ala Glu Arg Asp Ala Pro Pro Asn Leu Thr Leu Arg  
65 70 75 80  
Gly Phe Gly Phe Val Glu Arg Ile Lys Ala Leu Leu Glu Lys Val Cys  
85 90 95  
Pro Lys Thr Val Ser Cys Ala Asp Ile Ile Ala Leu Thr Ala Arg Asp  
100 105 110  
Thr Val Val Ala Thr Gly Gly Pro Ser Trp Ser Val Pro Thr Gly Arg  
115 120 125  
Arg Asp Gly Arg Ile Ser Asn Leu Lys Glu Ala Thr Asn Asn Ile Pro  
130 135 140  
Pro Pro Thr Ser Asn Phe Thr Thr Leu Arg Arg Leu Phe Lys Asn Gln  
145 150 155 160  
Gly Leu Asn Leu Lys Asp Leu Val Leu Leu Ser Gly Ala His Thr Ile  
165 170 175  
Gly Val Ser His Cys Ser Ser Met Asn Thr Arg Leu Tyr Asn Phe Ser  
180 185 190  
Thr Thr Val Lys Gln Asp Pro Ser Leu Asp Ser Gln Tyr Ala Ala Asn  
195 200 205  
Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile Leu  
210 215 220  
Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr Arg  
225 230 235 240  
Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu Thr  
245 250 255  
Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly Ser  
260 265 270  
Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp Gly  
275 280 285  
Glu Ser

290

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1734 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1734
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

```
atcaatggct ctggatgcat tcttcttcat cgtctctcta tttcttctgt ttccgtcacc 60
atccgcgtca gaatccacta ctcagttttg tagtgcaggg agagagaatg gtgtgggac 120
ttgtgggggt tcatcgacga ggattttgat taaaggaggt actgttgta atgcacacca 180
tcaagaactt gctgatgttt atgtggaaaa tggtattatt gtcgctgtgc agccaaacat 240
taaggttggg gatgaagtca ctgtcctcga tgctactgga aagtttgta tgccaggagg 300
aattgacccc cacacgcacc tcgccatgga atttatgggt accgagacta ttgatgattt 360
cttcagtggg caggcagcgg cattagctgg tggacaacta atgcatatag actttgttat 420
acctgtcaat gggaaatctgg tggctgggtt tgaagcctat gaaaacaaat ctagagaatc 480
ttgtatggat tacggttttc atatggcaat cacaagtgg gatgaagggtg tttccaggga 540
catggagatg ttgggtcaagg aaaagggtat caactctttc aagtttttcc tagcgtataa 600
aggatctctt atggtaactg atgacctact cctagaagga cttaaaagat gcaaaccctt 660
cggtgccctg gccatggttc atgctgaaaa tggagatgca gtattcgaag gacagaaaag 720
aatgattgar ctgggcattt acaggtccag agggatcatg tcttttcaag gcctcctgtg 780
ctcgagggag agggcactgc tagagcaatt cgtttggtc gttttattaa cacgcctctc 840
tatgttgttc atgtgatgag tgttgatgca atggacgaga ttgctaaagc tcgaaaatca 900
ggacagaagg ttattggaga gcctgttgtg tctggattaa tccttgatga tcattggcct 960
tgggatcctg acttcacaat tgcgtccaag tatgtcatga gtccacctat cagaccagta 1020
ggacatggga aagccctaca agatgccctt tccacaggaa tccttcagct tgtaggaact 1080
gatcactgca ctttcaattc tacacaaaaa gctctaggac ttgatgattt ccgcaaaata 1140
cctaattggtg ttaatggcct tgaggaacgg atgcacttga tatgggacac gatggtggag 1200
tctggccaac tctcagctac tgattatgtt cgaataacca gcactgagtg tgctagaatt 1260
ttcaacatat attccaggaa aggagctatc cttgctgggt cggatgcaga tattatcata 1320
ttgaatccaa actcaagcta cgagattagc tcaaagtctc atcattcaag atcagacaca 1380
aacgtctacg agggcagaag aggaaaggga aaagttgaag tgacaatagc aggaggacga 1440
attgtgtggg aaaacgagga acttaaagtt gttccaagaa gtggcaagta tatagagatg 1500
cctcctttca gttacctttt cgatggtatt gagaaatcag atgctaatta tctatcttct 1560
cttcgagctc cagttaagcg tgtcagaact gaagctacgt aaagtgcagg tatctatctt 1620
tcgtgattct gtaagaacaa ttgtacataa tttgtattaa aagtattgaa agagcgatta 1680
tgaataatgt gcatgtagtc tggttttgag aaaaaataaa agattgtaaa attt
```

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..284
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

```
Ser Met Ala Leu Asp Ala Phe Phe Phe Ile Val Ser Leu Phe Leu Leu
1 5 10 15
Phe Pro Ser Pro Ser Ala Ser Glu Ser Thr Thr Gln Phe Cys Ser Ala
20 25 30
Gly Arg Glu Asn Gly Val Gly Ser Cys Gly Val Ser Ser Thr Arg Ile
35 40 45
Leu Ile Lys Gly Gly Thr Val Val Asn Ala His His Gln Glu Leu Ala
```

|                     |                     |                         |
|---------------------|---------------------|-------------------------|
| 50                  | 55                  | 60                      |
| Asp Val Tyr Val Glu | Asn Gly Ile Ile Val | Ala Val Gln Pro Asn Ile |
| 65                  | 70                  | 75                      |
| Lys Val Gly Asp Glu | Val Thr Val Leu Asp | Ala Thr Gly Lys Phe Val |
| 85                  | 90                  | 95                      |
| Met Pro Gly Gly Ile | Asp Pro His Thr His | Leu Ala Met Glu Phe Met |
| 100                 | 105                 | 110                     |
| Gly Thr Glu Thr Ile | Asp Asp Phe Ser Gly | Gln Ala Ala Leu         |
| 115                 | 120                 | 125                     |
| Ala Gly Gly Thr Thr | Met His Ile Asp Phe | Val Ile Pro Val Asn Gly |
| 130                 | 135                 | 140                     |
| Asn Leu Val Ala Gly | Phe Glu Ala Tyr Glu | Asn Lys Ser Arg Glu Ser |
| 145                 | 150                 | 155                     |
| Cys Met Asp Tyr Gly | Phe His Met Ala Ile | Thr Lys Trp Asp Glu Gly |
| 165                 | 170                 | 175                     |
| Val Ser Arg Asp Met | Glu Met Leu Val Lys | Glu Lys Gly Ile Asn Ser |
| 180                 | 185                 | 190                     |
| Phe Lys Phe Phe Leu | Ala Tyr Lys Gly Ser | Leu Met Val Thr Asp Asp |
| 195                 | 200                 | 205                     |
| Leu Leu Leu Glu Gly | Leu Lys Arg Cys Lys | Ser Leu Gly Ala Leu Ala |
| 210                 | 215                 | 220                     |
| Met Val His Ala Glu | Asn Gly Asp Ala Val | Phe Glu Gly Gln Lys Arg |
| 225                 | 230                 | 235                     |
| Met Ile Xaa Leu Gly | Ile Tyr Arg Ser Arg | Gly Ser Cys Ser Phe Gln |
| 245                 | 250                 | 255                     |
| Gly Leu Leu Cys Ser | Arg Glu Arg Pro Leu | Leu Glu Gln Phe Val Trp |
| 260                 | 265                 | 270                     |
| Leu Val Leu Leu Thr | Arg Leu Ser Met Leu | Phe Met                 |
| 275                 | 280                 |                         |

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..283

(D) OTHER INFORMATION: / Ceres Seq. ID 1498528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Asp | Ala | Phe | Phe | Phe | Ile | Val | Ser | Leu | Phe | Leu | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Pro | Ser | Ala | Ser | Glu | Ser | Thr | Thr | Gln | Phe | Cys | Ser | Ala | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Glu | Asn | Gly | Val | Gly | Ser | Cys | Gly | Val | Ser | Ser | Thr | Arg | Ile | Leu |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Lys | Gly | Gly | Thr | Val | Val | Asn | Ala | His | His | Gln | Glu | Leu | Ala | Asp |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Tyr | Val | Glu | Asn | Gly | Ile | Ile | Val | Ala | Val | Gln | Pro | Asn | Ile | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Gly | Asp | Glu | Val | Thr | Val | Leu | Asp | Ala | Thr | Gly | Lys | Phe | Val | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Gly | Gly | Ile | Asp | Pro | His | Thr | His | Leu | Ala | Met | Glu | Phe | Met | Gly |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Glu | Thr | Ile | Asp | Asp | Phe | Phe | Ser | Gly | Gln | Ala | Ala | Ala | Leu | Ala |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Gly | Gly | Thr | Thr | Met | His | Ile | Asp | Phe | Val | Ile | Pro | Val | Asn | Gly | Asn |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Leu | Val | Ala | Gly | Phe | Glu | Ala | Tyr | Glu | Asn | Lys | Ser | Arg | Glu | Ser | Cys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Met Asp Tyr Gly Phe His Met Ala Ile Thr Lys Trp Asp Glu Gly Val  
165 170 175  
Ser Arg Asp Met Glu Met Leu Val Lys Glu Lys Gly Ile Asn Ser Phe  
180 185 190  
Lys Phe Phe Leu Ala Tyr Lys Gly Ser Leu Met Val Thr Asp Asp Leu  
195 200 205  
Leu Leu Glu Gly Leu Lys Arg Cys Lys Ser Leu Gly Ala Leu Ala Met  
210 215 220  
Val His Ala Glu Asn Gly Asp Ala Val Phe Glu Gly Gln Lys Arg Met  
225 230 235 240  
Ile Xaa Leu Gly Ile Tyr Arg Ser Arg Gly Ser Cys Ser Phe Gln Gly  
245 250 255  
Leu Leu Cys Ser Arg Glu Arg Pro Leu Leu Glu Gln Phe Val Trp Leu  
260 265 270  
Val Leu Leu Thr Arg Leu Ser Met Leu Phe Met  
275 280

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1498529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Met Leu Phe Ser Arg Pro Pro Val Leu Glu Gly Glu Ala Thr Ala Arg  
1 5 10 15  
Ala Ile Arg Leu Ala Arg Phe Ile Asn Thr Pro Leu Tyr Val Val His  
20 25 30  
Val Met Ser Val Asp Ala Met Asp Glu Ile Ala Lys Ala Arg Lys Ser  
35 40 45  
Gly Gln Lys Val Ile Gly Glu Pro Val Val Ser Gly Leu Ile Leu Asp  
50 55 60  
Asp His Trp Leu Trp Asp Pro Asp Phe Thr Ile Ala Ser Lys Tyr Val  
65 70 75 80  
Met Ser Pro Pro Ile Arg Pro Val Gly His Gly Lys Ala Leu Gln Asp  
85 90 95  
Ala Leu Ser Thr Gly Ile Leu Gln Leu Val Gly Thr Asp His Cys Thr  
100 105 110  
Phe Asn Ser Thr Gln Lys Ala Leu Gly Leu Asp Asp Phe Arg Lys Ile  
115 120 125  
Pro Asn Gly Val Asn Gly Leu Glu Glu Arg Met His Leu Ile Trp Asp  
130 135 140  
Thr Met Val Glu Ser Gly Gln Leu Ser Ala Thr Asp Tyr Val Arg Ile  
145 150 155 160  
Thr Ser Thr Glu Cys Ala Arg Ile Phe Asn Ile Tyr Pro Arg Lys Gly  
165 170 175  
Ala Ile Leu Ala Gly Ser Asp Ala Asp Ile Ile Ile Leu Asn Pro Asn  
180 185 190  
Ser Ser Tyr Glu Ile Ser Ser Lys Ser His His Ser Arg Ser Asp Thr  
195 200 205  
Asn Val Tyr Glu Gly Arg Arg Gly Lys Gly Lys Val Glu Val Thr Ile  
210 215 220  
Ala Gly Gly Arg Ile Val Trp Glu Asn Glu Glu Leu Lys Val Val Pro  
225 230 235 240  
Arg Ser Gly Lys Tyr Ile Glu Met Pro Pro Phe Ser Tyr Leu Phe Asp  
245 250 255  
Gly Ile Glu Lys Ser Asp Ala Asn Tyr Leu Ser Ser Leu Arg Ala Pro

260 265 270  
Val Lys Arg Val Arg Thr Glu Ala Thr  
275 280  
(2) INFORMATION FOR SEQ ID NO:491:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1193 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1193  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498530  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:  
atcacttact taacatacta agagagtatt tagaacttgc aaaaaatggc ttccaaggct 60  
ttgattctgt taggtctctt ctcagttctt ctcgtcgtct ccgaagtgtc tgccgcaagg 120  
maatcgggca tgggtgaagcc agagagtgtg gaaactgtgc aacctgaagg ttatggcggt 180  
ggccacggag gacatggtgg tcacggaggg ggaggaggcc acggacatgg aggacacaac 240  
ggaggagggg gccacggact tgacggatac rgaggagggt gagggcacta tggaggaggt 300  
ggaggacact acggagggtg tggaggagga tacggagggt gagggaggaca ccacgggaag 360  
gcggaaagca ctcccctaaa gcccctaagc taccagttcc tccggtgacc gtcccctaagc 420  
taccagttcc tccggtgacc gtcccctaagc taccagttcc taagctaccc gttcccccg 480  
taactgtacc taagctaccc gttcctccag tgaccgtccc taagctaccc ctctctccga 540  
tttcagggtt acccatacct ccagtggtag gtcccaatct gccattgcc cctttgccaa 600  
ttgtagggtc tattcttcca ccgggaacaa ccccaccagc cacaggaggg aaggactgtc 660  
ctccaccgcc agggagcgta aagccaccat cagggggcgg gaaggcgaca tgtccaatag 720  
acacgtcgaa gttaggtgct tgcgtcgact tggtggagg tttagtaaag atagggttg 780  
gggatccagc agttaacaaa tggtgtccgt tacttaaagg cctcgttgaa atcgaagccg 840  
cggcttgtct ctgcaactacc ctcaagctca aagctcttga cctcaatctt tatgtccctg 900  
ttgctcttca gcttctcctt acctgtggca aaaatccacc tccgggctac acttggtcca 960  
tatgataaac tcactccact tataaaggat gctttggaaa aaaaagtgtg aagagaatgg 1020  
cagagctcca atctttcctg tcttggttta ccaaatacat catatcaaat cctatccctt 1080  
tgattctttt ctctatcggt cccttatgct tgtatcatta attaatgtgt gctttttaga 1140  
ttaatgattc ttctcttgta ttaaagtatg atttgaaatc cttttttttt ctc

(2) INFORMATION FOR SEQ ID NO:492:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498531  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:  
Met Ala Ser Lys Ala Leu Ile Leu Leu Gly Leu Phe Ser Val Leu Leu  
1 5 10 15  
Val Val Ser Glu Val Ser Ala Ala Arg Xaa Ser Gly Met Val Lys Pro  
20 25 30  
Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly Gly Gly His Gly  
35 40 45  
Gly His Gly Gly His Gly Gly Gly Gly His Gly His Gly Gly His  
50 55 60  
Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Xaa Gly Gly Gly Gly  
65 70 75 80  
His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Tyr  
85 90 95  
Gly Gly Gly Gly Gly His His Gly Arg Ala Glu Ser Thr Pro Leu Lys  
100 105 110

Pro Leu Ser Tyr Gln Phe Leu Arg  
115 120

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly  
1 5 10 15  
Gly Gly His Gly Gly His Gly Gly His Gly Gly Gly Gly His Gly  
20 25 30  
His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Xaa  
35 40 45  
Gly Gly Gly Gly His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly  
50 55 60  
Gly Gly Gly Tyr Gly Gly Gly Gly Gly His His Gly Arg Ala Glu Ser  
65 70 75 80  
Thr Pro Leu Lys Pro Leu Ser Tyr Gln Phe Leu Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

Met Ala Val Ala Thr Glu Asp Met Val Val Thr Glu Gly Glu Glu Ala  
1 5 10 15  
Thr Asp Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp  
20 25 30  
Xaa Glu Glu Val Glu Gly Thr Met Glu Glu Val Glu Asp Thr Thr Glu  
35 40 45  
Val Val Glu Glu Asp Thr Glu Val Glu Glu Asp Thr Thr Glu Gly Arg  
50 55 60  
Lys Ala Leu Pro  
65

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1669
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

accgtgatta ctgattactg tggttaattat ttttattctg cgtacgttac gtaagagaga



|             |            |             |             |            |             |      |
|-------------|------------|-------------|-------------|------------|-------------|------|
| tattgaggaa  | tggctgcgaa | gaagggttttt | ggatcgggcg  | aagcgagtaa | tttgggtgacg | 120  |
| gagcttcgtc  | ggagttttga | tgatgggtgtg | acacgtgggt  | atgaatggag | agtgactcag  | 180  |
| cttaagaaac  | tgatgattat | ttgtgataat  | catgagcctg  | agatcgctgc | ggctcttcgc  | 240  |
| gatgatcttg  | gtaagcctga | gcttgaatct  | tctgtttatg  | aggtatctct | actgagaaac  | 300  |
| tctatcaagt  | tggctcttaa | gcagctaaaag | aactggatgg  | ctccggagaa | ggcaaagact  | 360  |
| tctctaacaa  | cgtttctctg | atccgcggag  | attgtgtctg  | agcctcttgg | tgttggtgcta | 420  |
| gtgatctcgg  | cttggaacta | tccttttctg  | ttgtctattg  | atcctgttat | tgggtgcaatt | 480  |
| tctgctggga  | atgctgttgt | tttaaagcca  | tcagaattgg  | ctccagcttc | gtcagctctg  | 540  |
| ctcactaagt  | tactggaaca | gtatcttgat  | ccttctgctg  | tgcgagttgt | cgaaggagct  | 600  |
| gttaccgaaa  | caagtgtctc | gctagagcag  | aagtgggaca  | agatattcta | cacaggtagt  | 660  |
| tcaaaaatcg  | gacgtgtcat | aatggcggca  | gctgcgaagc  | atctcacacc | ggttggttcta | 720  |
| gagcttggag  | gaaaatctcc | tgtcgttgta  | gactcggata  | ccgatttgaa | agttaccgtc  | 780  |
| aggcggataa  | tcgtaggcaa | atgggggttg  | aacaacggac  | aggcgtgcgt | ttcgccggac  | 840  |
| tatatcttga  | cgacaaaaga | atatgctcct  | aaattgattg  | atgccatgaa | gcttgaattg  | 900  |
| gagaaatttt  | atgggaagaa | ccctatagag  | tcgaaagata  | tgtcacgtat | cgtaaactcg  | 960  |
| aatcaccttg  | atcgcttgct | taagttgtta  | gacgagaagg  | aagtttctga | caaaattgtc  | 1020 |
| tatgggtgtg  | aaaaggacag | agaaaacttg  | aaaattgtct  | cgacaatctt | gctcgatgta  | 1080 |
| ccattagatt  | ctctgatcat | gagtgaagaa  | atatttggcc  | ctctccttcc | aatcctcacg  | 1140 |
| cttaacaact  | tggaagagag | ctttgacgtg  | attcgttctc  | gacctaagcc | acttgccgca  | 1200 |
| tacttgttta  | cacataacaa | gaagttgaaa  | gagagattca  | cagcgacagt | ctccgctgga  | 1260 |
| ggcatagtag  | tcaatgacat | agctgttcat  | cttgcaattc  | acacattgcc | attcggagga  | 1320 |
| gttgggtgaaa | gtggaatggg | tgcttaccat  | ggtaaattct  | catttgatgc | ttttagtcac  | 1380 |
| aagaaggcgg  | ttctctacag | aagccttttc  | ggtgattcag  | ccgtcaggta | tcgccatac   | 1440 |
| tcgagaggaa  | agcttagatt | gttaaaagcc  | cttgctcgaca | gcaatatatt | cgatttattc  | 1500 |
| aaagtccttc  | tcggtttagc | ttaaacggta  | aaaagaccga  | ggacacttcc | ctttgtacct  | 1560 |
| tatttacttg  | ttttattttt | caaacatgga  | cttagttggg  | taatatgttt | tggtttggtg  | 1620 |
| ttgattctat  | gaatattgaa | gttgataaat  | aaaagatttt  | cggttgggtt |             |      |

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 484 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..484

(D) OTHER INFORMATION: / Ceres Seq. ID 1498535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Lys | Lys | Val | Phe | Gly | Ser | Ala | Glu | Ala | Ser | Asn | Leu | Val |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Thr | Glu | Leu | Arg | Arg | Ser | Phe | Asp | Asp | Gly | Val | Thr | Arg | Gly | Tyr | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Trp | Arg | Val | Thr | Gln | Leu | Lys | Lys | Leu | Met | Ile | Ile | Cys | Asp | Asn | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Glu | Pro | Glu | Ile | Val | Ala | Ala | Leu | Arg | Asp | Asp | Leu | Gly | Lys | Pro | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Leu | Glu | Ser | Ser | Val | Tyr | Glu | Val | Ser | Leu | Leu | Arg | Asn | Ser | Ile | Lys |
|     |     |     |     |     | 70  |     |     |     |     |     | 75  |     |     | 80  |     |
| Leu | Ala | Leu | Lys | Gln | Leu | Lys | Asn | Trp | Met | Ala | Pro | Glu | Lys | Ala | Lys |
|     |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |
| Thr | Ser | Leu | Thr | Thr | Phe | Pro | Ala | Ser | Ala | Glu | Ile | Val | Ser | Glu | Pro |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Leu | Gly | Val | Val | Leu | Val | Ile | Ser | Ala | Trp | Asn | Tyr | Pro | Phe | Leu | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Ile | Asp | Pro | Val | Ile | Gly | Ala | Ile | Ser | Ala | Gly | Asn | Ala | Val | Val |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Leu | Lys | Pro | Ser | Glu | Leu | Ala | Pro | Ala | Ser | Ser | Ala | Leu | Leu | Thr | Lys |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Leu | Glu | Gln | Tyr | Leu | Asp | Pro | Ser | Ala | Val | Arg | Val | Val | Glu | Gly |
|     |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |

Ala Val Thr Glu Thr Ser Ala Leu Leu Glu Gln Lys Trp Asp Lys Ile  
180 185 190  
Phe Tyr Thr Gly Ser Ser Lys Ile Gly Arg Val Ile Met Ala Ala Ala  
195 200 205  
Ala Lys His Leu Thr Pro Val Val Leu Glu Leu Gly Gly Lys Ser Pro  
210 215 220  
Val Val Val Asp Ser Asp Thr Asp Leu Lys Val Thr Val Arg Arg Ile  
225 230 235 240  
Ile Val Gly Lys Trp Gly Cys Asn Asn Gly Gln Ala Cys Val Ser Pro  
245 250 255  
Asp Tyr Ile Leu Thr Thr Lys Glu Tyr Ala Pro Lys Leu Ile Asp Ala  
260 265 270  
Met Lys Leu Glu Leu Glu Lys Phe Tyr Gly Lys Asn Pro Ile Glu Ser  
275 280 285  
Lys Asp Met Ser Arg Ile Val Asn Ser Asn His Phe Asp Arg Leu Ser  
290 295 300  
Lys Leu Leu Asp Glu Lys Glu Val Ser Asp Lys Ile Val Tyr Gly Gly  
305 310 315 320  
Glu Lys Asp Arg Glu Asn Leu Lys Ile Ala Pro Thr Ile Leu Leu Asp  
325 330 335  
Val Pro Leu Asp Ser Leu Ile Met Ser Glu Glu Ile Phe Gly Pro Leu  
340 345 350  
Leu Pro Ile Leu Thr Leu Asn Asn Leu Glu Glu Ser Phe Asp Val Ile  
355 360 365  
Arg Ser Arg Pro Lys Pro Leu Ala Ala Tyr Leu Phe Thr His Asn Lys  
370 375 380  
Lys Leu Lys Glu Arg Phe Thr Ala Thr Val Ser Ala Gly Gly Ile Val  
385 390 395 400  
Val Asn Asp Ile Ala Val His Leu Ala Leu His Thr Leu Pro Phe Gly  
405 410 415  
Gly Val Gly Glu Ser Gly Met Gly Ala Tyr His Gly Lys Phe Ser Phe  
420 425 430  
Asp Ala Phe Ser His Lys Lys Ala Val Leu Tyr Arg Ser Leu Phe Gly  
435 440 445  
Asp Ser Ala Val Arg Tyr Pro Pro Tyr Ser Arg Gly Lys Leu Arg Leu  
450 455 460  
Leu Lys Ala Leu Val Asp Ser Asn Ile Phe Asp Leu Phe Lys Val Leu  
465 470 475 480  
Leu Gly Leu Ala

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..443

(D) OTHER INFORMATION: / Ceres Seq. ID 1498536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

Met Ile Ile Cys Asp Asn His Glu Pro Glu Ile Val Ala Ala Leu Arg  
1 5 10 15  
Asp Asp Leu Gly Lys Pro Glu Leu Glu Ser Ser Val Tyr Glu Val Ser  
20 25 30  
Leu Leu Arg Asn Ser Ile Lys Leu Ala Leu Lys Gln Leu Lys Asn Trp  
35 40 45  
Met Ala Pro Glu Lys Ala Lys Thr Ser Leu Thr Thr Phe Pro Ala Ser  
50 55 60  
Ala Glu Ile Val Ser Glu Pro Leu Gly Val Val Leu Val Ile Ser Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Trp | Asn | Tyr | Pro | Phe | Leu | Leu | Ser | Ile | Asp | Pro | Val | Ile | Gly | Ala | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ala | Gly | Asn | Ala | Val | Val | Leu | Lys | Pro | Ser | Glu | Leu | Ala | Pro | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Ala | Leu | Leu | Thr | Lys | Leu | Glu | Gln | Tyr | Leu | Asp | Pro | Ser |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ala | Val | Arg | Val | Val | Glu | Gly | Ala | Val | Thr | Glu | Thr | Ser | Ala | Leu | Leu |
|     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Glu | Gln | Lys | Trp | Asp | Lys | Ile | Phe | Tyr | Thr | Gly | Ser | Ser | Lys | Ile | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | Val | Ile | Met | Ala | Ala | Ala | Ala | Lys | His | Leu | Thr | Pro | Val | Val | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Leu | Gly | Gly | Lys | Ser | Pro | Val | Val | Val | Asp | Ser | Asp | Thr | Asp | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Val | Thr | Val | Arg | Arg | Ile | Ile | Val | Gly | Lys | Trp | Gly | Cys | Asn | Asn |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Gly | Gln | Ala | Cys | Val | Ser | Pro | Asp | Tyr | Ile | Leu | Thr | Thr | Lys | Glu | Tyr |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Pro | Lys | Leu | Ile | Asp | Ala | Met | Lys | Leu | Glu | Leu | Glu | Lys | Phe | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Lys | Asn | Pro | Ile | Glu | Ser | Lys | Asp | Met | Ser | Arg | Ile | Val | Asn | Ser |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Asn | His | Phe | Asp | Arg | Leu | Ser | Lys | Leu | Leu | Asp | Glu | Lys | Glu | Val | Ser |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Asp | Lys | Ile | Val | Tyr | Gly | Gly | Glu | Lys | Asp | Arg | Glu | Asn | Leu | Lys | Ile |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ala | Pro | Thr | Ile | Leu | Leu | Asp | Val | Pro | Leu | Asp | Ser | Leu | Ile | Met | Ser |
|     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Glu | Glu | Ile | Phe | Gly | Pro | Leu | Leu | Pro | Ile | Leu | Thr | Leu | Asn | Asn | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Glu | Glu | Ser | Phe | Asp | Val | Ile | Arg | Ser | Arg | Pro | Lys | Pro | Leu | Ala | Ala |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Tyr | Leu | Phe | Thr | His | Asn | Lys | Lys | Leu | Lys | Glu | Arg | Phe | Thr | Ala | Thr |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Val | Ser | Ala | Gly | Gly | Ile | Val | Val | Asn | Asp | Ile | Ala | Val | His | Leu | Ala |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Leu | His | Thr | Leu | Pro | Phe | Gly | Gly | Val | Gly | Glu | Ser | Gly | Met | Gly | Ala |
|     |     | 370 |     |     |     | 375 |     |     |     | 380 |     |     |     |     |     |
| Tyr | His | Gly | Lys | Phe | Ser | Phe | Asp | Ala | Phe | Ser | His | Lys | Lys | Ala | Val |
| 385 |     |     |     |     | 390 |     |     |     | 395 |     |     |     |     | 400 |     |
| Leu | Tyr | Arg | Ser | Leu | Phe | Gly | Asp | Ser | Ala | Val | Arg | Tyr | Pro | Pro | Tyr |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |
| Ser | Arg | Gly | Lys | Leu | Arg | Leu | Leu | Lys | Ala | Leu | Val | Asp | Ser | Asn | Ile |
|     |     |     | 420 |     |     |     | 425 |     |     |     |     | 430 |     |     |     |
| Phe | Asp | Leu | Phe | Lys | Val | Leu | Gly | Leu | Ala |     |     |     |     |     |     |
|     |     | 435 |     |     |     | 440 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..395
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Pro | Glu | Lys | Ala | Lys | Thr | Ser | Leu | Thr | Thr | Phe | Pro | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Glu | Ile | Val | Ser | Glu | Pro | Leu | Gly | Val | Val | Leu | Val | Ile | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Asn | Tyr | Pro | Phe | Leu | Leu | Ser | Ile | Asp | Pro | Val | Ile | Gly | Ala | Ile |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Gly | Asn | Ala | Val | Val | Leu | Lys | Pro | Ser | Glu | Leu | Ala | Pro | Ala |
|     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Ala | Leu | Leu | Thr | Lys | Leu | Leu | Glu | Gln | Tyr | Leu | Asp | Pro | Ser |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Val | Arg | Val | Val | Glu | Gly | Ala | Val | Thr | Glu | Thr | Ser | Ala | Leu | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Gln | Lys | Trp | Asp | Lys | Ile | Phe | Tyr | Thr | Gly | Ser | Ser | Lys | Ile | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Val | Ile | Met | Ala | Ala | Ala | Ala | Lys | His | Leu | Thr | Pro | Val | Val | Leu |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Leu | Gly | Gly | Lys | Ser | Pro | Val | Val | Val | Asp | Ser | Asp | Thr | Asp | Leu |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Lys | Val | Thr | Val | Arg | Arg | Ile | Ile | Val | Gly | Lys | Trp | Gly | Cys | Asn | Asn |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Gln | Ala | Cys | Val | Ser | Pro | Asp | Tyr | Ile | Leu | Thr | Thr | Lys | Glu | Tyr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Pro | Lys | Leu | Ile | Asp | Ala | Met | Lys | Leu | Glu | Leu | Glu | Lys | Phe | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Lys | Asn | Pro | Ile | Glu | Ser | Lys | Asp | Met | Ser | Arg | Ile | Val | Asn | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | His | Phe | Asp | Arg | Leu | Ser | Lys | Leu | Leu | Asp | Glu | Lys | Glu | Val | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Lys | Ile | Val | Tyr | Gly | Gly | Glu | Lys | Asp | Arg | Glu | Asn | Leu | Lys | Ile |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ala | Pro | Thr | Ile | Leu | Leu | Asp | Val | Pro | Leu | Asp | Ser | Leu | Ile | Met | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Glu | Ile | Phe | Gly | Pro | Leu | Leu | Pro | Ile | Leu | Thr | Leu | Asn | Asn | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Glu | Ser | Phe | Asp | Val | Ile | Arg | Ser | Arg | Pro | Lys | Pro | Leu | Ala | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Tyr | Leu | Phe | Thr | His | Asn | Lys | Lys | Leu | Lys | Glu | Arg | Phe | Thr | Ala | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Ser | Ala | Gly | Gly | Ile | Val | Val | Asn | Asp | Ile | Ala | Val | His | Leu | Ala |
|     |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Leu | His | Thr | Leu | Pro | Phe | Gly | Gly | Val | Gly | Glu | Ser | Gly | Met | Gly | Ala |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Tyr | His | Gly | Lys | Phe | Ser | Phe | Asp | Ala | Phe | Ser | His | Lys | Lys | Ala | Val |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Tyr | Arg | Ser | Leu | Phe | Gly | Asp | Ser | Ala | Val | Arg | Tyr | Pro | Pro | Tyr |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Arg | Gly | Lys | Leu | Arg | Leu | Leu | Lys | Ala | Leu | Val | Asp | Ser | Asn | Ile |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Phe | Asp | Leu | Phe | Lys | Val | Leu | Leu | Gly | Leu | Ala |     |     |     |     |     |
|     | 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

aggaattcgc acaagaccat tacystagaa catcmtaatc acaaaaatca aatccatctc

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| ccactcttct  | agcatcttga  | agcttaaatc  | tcagccgtcc  | gatcatgccg  | atcagaaaca  | 120  |
| tcgccattgg  | ccgtccagat  | gaagcaaccc  | gtcccgatgc  | cttaaaggcg  | gcgttggtg   | 180  |
| agttcatttc  | aactttgatc  | tttgctcgtc  | ccggttcagg  | ctctggcatg  | gctttcaaca  | 240  |
| agctcactga  | aaacggagcc  | accactcctt  | ctgggtctcgt | agctgctgca  | ctgggtcatg  | 300  |
| ccttttgact  | cttcgtcgtc  | gtctcagttg  | gtgccaacat  | ctctgggtgga | cacgttaacc  | 360  |
| ctgccgtcac  | tttcgggtgct | ttcattgggtg | gtaacatcac  | tctcctccgt  | ggatatcctt  | 420  |
| actggattgc  | tcagctttctc | ggctccgtcg  | tcgcttgccct | catccttaaa  | ttcgccaccg  | 480  |
| gtgggcttggc | tgtgccggct  | tttgggtctct | ctgctggagt  | aggagtgttg  | aacgctttcg  | 540  |
| ttttcgagat  | cgtgatgaca  | ttcggggcttg | tttacaccgt  | ctacgctaca  | gccattgacc  | 600  |
| ctggaaccat  | taccttgctg  | ctacaagacc  | aagtcgggtg  | attacaagcc  | acacgtgaca  | 660  |
| atggcaagac  | ctggattacg  | gttcagcctg  | ttgaaggagc  | gtttgtcgtc  | aatctcggcg  | 720  |
| accacgggtca | ttttttgagc  | aatgggaggt  | tcaagaatgc  | tgatcatcag  | gccgtgggtga | 780  |
| actctaactc  | gagcagatta  | tccatagcca  | cgttccagaa  | ccccgcgccg  | gatgccacag  | 840  |
| tgtatccact  | gaaagtaaga  | gaaggagaga  | aggcaatatt  | ggaggagcca  | atcacgtttg  | 900  |
| ccgagatgta  | taagagaaag  | atgggaagag  | atttggagct  | tgctcgcctc  | aagaagctgg  | 960  |
| ctaaagagga  | gcgtgaccac  | aaagaagttg  | ccaagcctgt  | cgaccaaata  | ttcgcttaga  | 1020 |
| atctctgtgt  | tcttgcttac  | ttgttggtgc  | gttggttctg  | ttttgtacgt  | tggtactgaa  | 1080 |
| aattatgcta  | ggctcgggtg  | gttttggtgt  | c           |             |             |      |

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1498543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ile | Arg | Asn | Ile | Ala | Ile | Gly | Arg | Pro | Asp | Glu | Ala | Thr | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Asp | Ala | Leu | Lys | Ala | Ala | Leu | Ala | Glu | Phe | Ile | Ser | Thr | Leu | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Val | Val | Ala | Gly | Ser | Gly | Ser | Gly | Met | Ala | Phe | Asn | Lys | Leu | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Asn | Gly | Ala | Thr | Thr | Pro | Ser | Gly | Leu | Val | Ala | Ala | Ala | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Ala | Phe | Gly | Leu | Phe | Val | Ala | Val | Ser | Val | Gly | Ala | Asn | Ile | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Gly | His | Val | Asn | Pro | Ala | Val | Thr | Phe | Gly | Ala | Phe | Ile | Gly | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Ile | Thr | Leu | Leu | Arg | Gly | Ile | Leu | Tyr | Trp | Ile | Ala | Gln | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ser | Val | Val | Ala | Cys | Leu | Ile | Leu | Lys | Phe | Ala | Thr | Gly | Gly | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Val | Pro | Ala | Phe | Gly | Leu | Ser | Ala | Gly | Val | Gly | Val | Leu | Asn | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Val | Phe | Glu | Ile | Val | Met | Thr | Phe | Gly | Leu | Val | Tyr | Thr | Val | Tyr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Thr | Ala | Ile | Asp | Pro | Gly | Thr | Ile | Thr | Leu | Leu | Leu | Gln | Asp | Gln |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Val | Gly | Gly | Leu | Gln | Ala | Thr | Arg | Asp | Asn | Gly | Lys | Thr | Trp | Ile | Thr |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Gln | Pro | Val | Glu | Gly | Ala | Phe | Val | Val | Asn | Leu | Gly | Asp | His | Gly |
|     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| His | Phe | Leu | Ser | Asn | Gly | Arg | Phe | Lys | Asn | Ala | Asp | His | Gln | Ala | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Asn | Ser | Asn | Ser | Ser | Arg | Leu | Ser | Ile | Ala | Thr | Phe | Gln | Asn | Pro |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Ala | Pro | Asp | Ala | Thr | Val | Tyr | Pro | Leu | Lys | Val | Arg | Glu | Gly | Glu | Lys |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ala | Ile | Leu | Glu | Glu | Pro | Ile | Thr | Phe | Ala | Glu | Met | Tyr | Lys | Arg | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Met | Gly | Arg | Asp | Leu | Glu | Leu | Ala | Arg | Leu | Lys | Lys | Leu | Ala | Lys | Glu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Arg | Asp | His | Lys | Glu | Val | Ala | Lys | Pro | Val | Asp | Gln | Ile | Phe | Ala |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1498544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Phe | Asn | Lys | Leu | Thr | Glu | Asn | Gly | Ala | Thr | Thr | Pro | Ser | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Val | Ala | Ala | Ala | Leu | Ala | His | Ala | Phe | Gly | Leu | Phe | Val | Ala | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Val | Gly | Ala | Asn | Ile | Ser | Gly | Gly | His | Val | Asn | Pro | Ala | Val | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Gly | Ala | Phe | Ile | Gly | Gly | Asn | Ile | Thr | Leu | Leu | Arg | Gly | Ile | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Tyr | Trp | Ile | Ala | Gln | Leu | Leu | Gly | Ser | Val | Val | Ala | Cys | Leu | Ile | Leu |
|     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Phe | Ala | Thr | Gly | Gly | Leu | Ala | Val | Pro | Ala | Phe | Gly | Leu | Ser | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Val | Gly | Val | Leu | Asn | Ala | Phe | Val | Phe | Glu | Ile | Val | Met | Thr | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Leu | Val | Tyr | Thr | Val | Tyr | Ala | Thr | Ala | Ile | Asp | Pro | Gly | Thr | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Leu | Leu | Leu | Gln | Asp | Gln | Val | Gly | Gly | Leu | Gln | Ala | Thr | Arg | Asp |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Asn | Gly | Lys | Thr | Trp | Ile | Thr | Val | Gln | Pro | Val | Glu | Gly | Ala | Phe | Val |
|     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Val | Asn | Leu | Gly | Asp | His | Gly | His | Phe | Leu | Ser | Asn | Gly | Arg | Phe | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Ala | Asp | His | Gln | Ala | Val | Val | Asn | Ser | Asn | Ser | Ser | Arg | Leu | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Ala | Thr | Phe | Gln | Asn | Pro | Ala | Pro | Asp | Ala | Thr | Val | Tyr | Pro | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Val | Arg | Glu | Gly | Glu | Lys | Ala | Ile | Leu | Glu | Glu | Pro | Ile | Thr | Phe |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Ala | Glu | Met | Tyr | Lys | Arg | Lys | Met | Gly | Arg | Asp | Leu | Glu | Leu | Ala | Arg |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Leu | Lys | Lys | Leu | Ala | Lys | Glu | Glu | Arg | Asp | His | Lys | Glu | Val | Ala | Lys |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Pro | Val | Asp | Gln | Ile | Phe | Ala |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 260 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1498545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

```
Met Thr Phe Gly Leu Val Tyr Thr Val Tyr Ala Thr Ala Ile Asp Pro
1 5 10 15
Gly Thr Ile Thr Leu Leu Leu Gln Asp Gln Val Gly Gly Leu Gln Ala
20 25 30
Thr Arg Asp Asn Gly Lys Thr Trp Ile Thr Val Gln Pro Val Glu Gly
35 40 45
Ala Phe Val Val Asn Leu Gly Asp His Gly His Phe Leu Ser Asn Gly
50 55 60
Arg Phe Lys Asn Ala Asp His Gln Ala Val Val Asn Ser Asn Ser Ser
65 70 75 80
Arg Leu Ser Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Thr Val
85 90 95
Tyr Pro Leu Lys Val Arg Glu Gly Glu Lys Ala Ile Leu Glu Glu Pro
100 105 110
Ile Thr Phe Ala Glu Met Tyr Lys Arg Lys Met Gly Arg Asp Leu Glu
115 120 125
Leu Ala Arg Leu Lys Lys Leu Ala Lys Glu Glu Arg Asp His Lys Glu
130 135 140
Val Ala Lys Pro Val Asp Gln Ile Phe Ala
145 150
```

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..382

(D) OTHER INFORMATION: / Ceres Seq. ID 1498550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

```
aaacacaaac aaaactcata ttttcaatct ccaggtgctt tacaccaaca gagtcgcaag 60
aaaacaaaaa ccaaactcgg atttagtttg acagaagaag gaatcgagag tcgggtatgc 120
attatcctaa caacagaacc gaattcgtcg gagctccagc cccaaccggg tatcaaaagg 180
agcagttgtc accggagcaa gagctttcag ttattgtctc tgctttgcaa cacgtgatct 240
caggggaaaa cgaaacggcg csgtgtcagg gtttttccag tgacagcaca gtgataagcg 300
cggggaatgcs tcggttggat tcagacactt gtcaagtctg taggatcgaa ggaatgtctcg 360
gctgtaacta ctttttcgcg cc
```

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1498551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

```
Lys His Lys Gln Asn Ser Tyr Phe Gln Ser Pro Gly Ala Leu His Gln
1 5 10 15
Gln Ser Arg Lys Lys Thr Lys Thr Lys Leu Gly Phe Ser Leu Thr Glu
20 25 30
```

Glu Gly Ile Glu Ser Arg Val Cys Ile Ile Leu Thr Thr Glu Pro Asn  
35 40 45  
Ser Ser Glu Leu Gln Pro Gln Pro Gly Ile Lys Arg Ser Ser Cys His  
50 55 60  
Arg Ser Lys Ser Phe Gln Leu Leu Ser Leu Leu Cys Asn Thr  
65 70 75

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1498552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

Met His Tyr Pro Asn Asn Arg Thr Glu Phe Val Gly Ala Pro Ala Pro  
1 5 10 15  
Thr Arg Tyr Gln Lys Glu Gln Leu Ser Pro Glu Gln Glu Leu Ser Val  
20 25 30  
Ile Val Ser Ala Leu Gln His Val Ile Ser Gly Glu Asn Glu Thr Ala  
35 40 45  
Xaa Cys Gln Gly Phe Ser Ser Asp Ser Thr Val Ile Ser Ala Gly Met  
50 55 60  
Xaa Arg Leu Asp Ser Asp Thr Cys Gln Val Cys Arg Ile Glu Gly Cys  
65 70 75 80  
Leu Gly Cys Asn Tyr Phe Phe Ala  
85

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1396

(D) OTHER INFORMATION: / Ceres Seq. ID 1498553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| attattattt  | ccagagaagc  | ttctcttttg | attctctcgc | tctctctttc  | ttcatcgcoct | 60   |
| cttcgagctt  | cgatggtttg  | gaatattctg | gtgaccggtg | gtgctgggta  | catcggaagt  | 120  |
| cacacggttc  | ttcagcttct  | tctcggaggc | tataacaccg | tcgttataga  | caacctcgac  | 180  |
| aattcctctc  | tcgtttcgat  | ccaacgcgtc | aaggatctcg | ccggagatca  | tggacaaaat  | 240  |
| ctcacgcgtc  | accaggtgga  | ccttcgcgat | aaaccgcac  | ttgagaaggt  | tttctccgaa  | 300  |
| acaaagtttg  | atgcagtaat  | gcattttgct | ggattgaaag | cagttgggtga | gagcgtggcg  | 360  |
| aaaccacttc  | tgtattataa  | caataacttg | attgcgacta | ttacactttt  | ggaagtaatg  | 420  |
| gctgcacacg  | gatgtaaaaa  | gcttgtatgt | tcttcgtccg | ctactgtgta  | tggctggcca  | 480  |
| aaggagggtc  | cttgtagaca  | agagtctccc | ctgtctggaa | tgagtcctta  | tggacggaca  | 540  |
| aagctgttca  | tagaggacat  | ttgccgtgat | gtacaacgtg | gtgatcctga  | atggagaatc  | 600  |
| ataatgctga  | ggtactttta  | ccctgtggga | gctcacccta | gcggtcgcat  | tggtaggat   | 660  |
| ccttggtgga  | ctccaaataa  | tctcatgcct | tatgtccagc | aagtcgttgt  | tgggaggcta  | 720  |
| cctaacctaa  | aaatttatgg  | aactgactat | accactaaag | atggcactgg  | tgtacgagac  | 780  |
| tatattcatg  | ttgttgatct  | agcagatggc | catatatttg | cgcttcaaaa  | gctagacgat  | 840  |
| actgaaatag  | gttggtgaggt | atacaacctg | ggaaccggaa | aaggaacaac  | agtgttgag   | 900  |
| atggttgatg  | catttgagaa  | agcttctgga | atgaaaatcc | cactggtgaa  | ggttggaagg  | 960  |
| agaccaggtg  | atgcagaaac  | cgtctatgcg | tcaacagaaa | aagctgaacg  | cgaactaaac  | 1020 |
| tgggaaggcaa | atgtttggaat | cgaagaaatg | tgtagggatc | agtggaaactg | ggcaagcaac  | 1080 |
| aatccttttcg | gttacgggttc | ttcaccaaac | tcaacataac | gaagctaacg  | tatccaacac  | 1140 |



|                   |            |            |            |            |             |      |
|-------------------|------------|------------|------------|------------|-------------|------|
| tccattcttt        | ttcttttggg | tcgtcggtg  | ttatctttat | gttacacact | cagggttttag | 1200 |
| ctttaaagcc        | taaacacagt | gagggagaag | ttactttctt | attcatatat | ctgctttctc  | 1260 |
| cttttgtaat        | ttatatatat | cttatatacg | cataggttta | acttaagcgg | atccttttgt  | 1320 |
| tttttggaat        | tgtataatct | ctcttaggaa | attaattgtc | atgggattat | atttgtatta  | 1380 |
| aatagaaact gaattc |            |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..372

(D) OTHER INFORMATION: / Ceres Seq. ID 1498554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Ile | Ile | Ser | Arg | Glu | Ala | Ser | Leu | Leu | Ile | Leu | Ser | Leu | Ser | Leu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ser | Ser | Ser | Pro | Leu | Arg | Ala | Ser | Met | Val | Gly | Asn | Ile | Leu | Val | Thr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Gly | Ala | Gly | Tyr | Ile | Gly | Ser | His | Thr | Val | Leu | Gln | Leu | Leu | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Gly | Tyr | Asn | Thr | Val | Val | Ile | Asp | Asn | Leu | Asp | Asn | Ser | Ser | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Val | Ser | Ile | Gln | Arg | Val | Lys | Asp | Leu | Ala | Gly | Asp | His | Gly | Gln | Asn |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu | Thr | Val | His | Gln | Val | Asp | Leu | Arg | Asp | Lys | Pro | Ala | Leu | Glu | Lys |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Val | Phe | Ser | Glu | Thr | Lys | Phe | Asp | Ala | Val | Met | His | Phe | Ala | Gly | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Lys | Ala | Val | Gly | Glu | Ser | Val | Ala | Lys | Pro | Leu | Leu | Tyr | Tyr | Asn | Asn |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Asn | Leu | Ile | Ala | Thr | Ile | Thr | Leu | Leu | Glu | Val | Met | Ala | Ala | His | Gly |  |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Cys | Lys | Lys | Leu | Val | Phe | Ser | Ser | Ser | Ala | Thr | Val | Tyr | Gly | Trp | Pro |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Lys | Glu | Val | Pro | Cys | Thr | Glu | Glu | Ser | Pro | Leu | Ser | Gly | Met | Ser | Pro |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Tyr | Gly | Arg | Thr | Lys | Leu | Phe | Ile | Glu | Asp | Ile | Cys | Arg | Asp | Val | Gln |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Arg | Gly | Asp | Pro | Glu | Trp | Arg | Ile | Met | Leu | Arg | Tyr | Phe | Asn | Pro |     |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Val | Gly | Ala | His | Pro | Ser | Gly | Arg | Ile | Gly | Glu | Asp | Pro | Cys | Gly | Thr |  |
|     |     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |  |
| Pro | Asn | Asn | Leu | Met | Pro | Tyr | Val | Gln | Gln | Val | Val | Val | Gly | Arg | Leu |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Pro | Asn | Leu | Lys | Ile | Tyr | Gly | Thr | Asp | Tyr | Thr | Thr | Lys | Asp | Gly | Thr |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Gly | Val | Arg | Asp | Tyr | Ile | His | Val | Val | Asp | Leu | Ala | Asp | Gly | His | Ile |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Phe | Ala | Leu | Gln | Lys | Leu | Asp | Asp | Thr | Glu | Ile | Gly | Cys | Glu | Val | Tyr |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Asn | Leu | Gly | Thr | Gly | Lys | Gly | Thr | Thr | Val | Leu | Glu | Met | Val | Asp | Ala |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Phe | Glu | Lys | Ala | Ser | Gly | Met | Lys | Ile | Pro | Leu | Val | Lys | Val | Gly | Arg |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Arg | Pro | Gly | Asp | Ala | Glu | Thr | Val | Tyr | Ala | Ser | Thr | Glu | Lys | Ala | Glu |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Arg | Glu | Leu | Asn | Trp | Lys | Ala | Asn | Phe | Gly | Ile | Glu | Glu | Met | Cys | Arg |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |  |

Asp Gln Trp Asn Trp Ala Ser Asn Asn Pro Phe Gly Tyr Gly Ser Ser  
355 360 365  
Pro Asn Ser Thr  
370

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1498555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

Met Val Gly Asn Ile Leu Val Thr Gly Gly Ala Gly Tyr Ile Gly Ser  
1 5 10 15  
His Thr Val Leu Gln Leu Leu Leu Gly Gly Tyr Asn Thr Val Val Ile  
20 25 30  
Asp Asn Leu Asp Asn Ser Ser Leu Val Ser Ile Gln Arg Val Lys Asp  
35 40 45  
Leu Ala Gly Asp His Gly Gln Asn Leu Thr Val His Gln Val Asp Leu  
50 55 60  
Arg Asp Lys Pro Ala Leu Glu Lys Val Phe Ser Glu Thr Lys Phe Asp  
65 70 75 80  
Ala Val Met His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val Ala  
85 90 95  
Lys Pro Leu Leu Tyr Tyr Asn Asn Asn Leu Ile Ala Thr Ile Thr Leu  
100 105 110  
Leu Glu Val Met Ala Ala His Gly Cys Lys Lys Leu Val Phe Ser Ser  
115 120 125  
Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro Cys Thr Glu Glu  
130 135 140  
Ser Pro Leu Ser Gly Met Ser Pro Tyr Gly Arg Thr Lys Leu Phe Ile  
145 150 155 160  
Glu Asp Ile Cys Arg Asp Val Gln Arg Gly Asp Pro Glu Trp Arg Ile  
165 170 175  
Ile Met Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro Ser Gly Arg  
180 185 190  
Ile Gly Glu Asp Pro Cys Gly Thr Pro Asn Asn Leu Met Pro Tyr Val  
195 200 205  
Gln Gln Val Val Val Gly Arg Leu Pro Asn Leu Lys Ile Tyr Gly Thr  
210 215 220  
Asp Tyr Thr Thr Lys Asp Gly Thr Gly Val Arg Asp Tyr Ile His Val  
225 230 235 240  
Val Asp Leu Ala Asp Gly His Ile Phe Ala Leu Gln Lys Leu Asp Asp  
245 250 255  
Thr Glu Ile Gly Cys Glu Val Tyr Asn Leu Gly Thr Gly Lys Gly Thr  
260 265 270  
Thr Val Leu Glu Met Val Asp Ala Phe Glu Lys Ala Ser Gly Met Lys  
275 280 285  
Ile Pro Leu Val Lys Val Gly Arg Arg Pro Gly Asp Ala Glu Thr Val  
290 295 300  
Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Asn Trp Lys Ala Asn  
305 310 315 320  
Phe Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Ser Asn  
325 330 335  
Asn Pro Phe Gly Tyr Gly Ser Ser Pro Asn Ser Thr  
340 345

(2) INFORMATION FOR SEQ ID NO:509:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 266 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..266  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498556  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Phe | Ala | Gly | Leu | Lys | Ala | Val | Gly | Glu | Ser | Val | Ala | Lys | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Tyr | Tyr | Asn | Asn | Asn | Leu | Ile | Ala | Thr | Ile | Thr | Leu | Leu | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Val | Met | Ala | Ala | His | Gly | Cys | Lys | Leu | Val | Phe | Ser | Ser | Ser | Ala |     |
|     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |     |
| Thr | Val | Tyr | Gly | Trp | Pro | Lys | Glu | Val | Pro | Cys | Thr | Glu | Glu | Ser | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Ser | Gly | Met | Ser | Pro | Tyr | Gly | Arg | Thr | Lys | Leu | Phe | Ile | Glu | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Cys | Arg | Asp | Val | Gln | Arg | Gly | Asp | Pro | Glu | Trp | Arg | Ile | Ile | Met |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Leu | Arg | Tyr | Phe | Asn | Pro | Val | Gly | Ala | His | Pro | Ser | Gly | Arg | Ile | Gly |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Glu | Asp | Pro | Cys | Gly | Thr | Pro | Asn | Asn | Leu | Met | Pro | Tyr | Val | Gln | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Val | Val | Val | Gly | Arg | Leu | Pro | Asn | Leu | Lys | Ile | Tyr | Gly | Thr | Asp | Tyr |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Thr | Thr | Lys | Asp | Gly | Thr | Gly | Val | Arg | Asp | Tyr | Ile | His | Val | Val | Asp |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Leu | Ala | Asp | Gly | His | Ile | Phe | Ala | Leu | Gln | Lys | Leu | Asp | Asp | Thr | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ile | Gly | Cys | Glu | Val | Tyr | Asn | Leu | Gly | Thr | Gly | Lys | Gly | Thr | Thr | Val |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |
| Leu | Glu | Met | Val | Asp | Ala | Phe | Glu | Lys | Ala | Ser | Gly | Met | Lys | Ile | Pro |
|     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |
| Leu | Val | Lys | Val | Gly | Arg | Arg | Pro | Gly | Asp | Ala | Glu | Thr | Val | Tyr | Ala |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ser | Thr | Glu | Lys | Ala | Glu | Arg | Glu | Leu | Asn | Trp | Lys | Ala | Asn | Phe | Gly |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Ile | Glu | Glu | Met | Cys | Arg | Asp | Gln | Trp | Asn | Trp | Ala | Ser | Asn | Asn | Pro |
|     |     |     | 245 |     |     |     | 250 |     |     |     |     |     |     | 255 |     |
| Phe | Gly | Tyr | Gly | Ser | Ser | Pro | Asn | Ser | Thr |     |     |     |     |     |     |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:510:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 558 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..558  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498561  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| rysgtgcgtt | attgccggga | gattaccggg | aagaacagat | aacgagataa | agaactattg | 60  |
| gaacacacat | atacgaagaa | agcttataaa | cagagggatt | gatccaacga | gtcacagacc | 120 |
| aatccaagaa | tcatcagctt | ctcaagattc | taaacctaca | caactagaac | cagttacgag | 180 |
| taacaccatt | aatatctcat | tcacttctgc | tccaaaggtc | gaaacgttcc | atgaaagtat | 240 |

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| aagctttccg  | ggaaaatcag | aaaaaatctc | aatgcttacg | ttcaaagaag | aaaaagatga | 300 |
| gtgtccagtt  | caagaaaagt | tcccagattt | gaatcttgag | ctcagaatca | gtcttcctga | 360 |
| tgatgttgat  | cgtcttcaag | gacatggaaa | gtcaacaacg | ccacgttggt | tcaagtgcag | 420 |
| cttaggggatg | ataaacggca | tggagtgcag | atgcggaaga | atgagatgcg | atgtagtcgg | 480 |
| aggtagcagc  | aaggggagtg | acatgagcaa | tggatttgat | tttttagggg | tggcaaagaa | 540 |
| agagaccact  | tctctttt   |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1498562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Xaa | Ser | Leu | Ile | Ala | Gly | Arg | Leu | Pro | Gly | Arg | Thr | Asp | Asn | Glu | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Asn | Tyr | Trp | Asn | Thr | His | Ile | Arg | Arg | Lys | Leu | Ile | Asn | Arg | Gly |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Asp | Pro | Thr | Ser | His | Arg | Pro | Ile | Gln | Glu | Ser | Ser | Ala | Ser | Gln |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asp | Ser | Lys | Pro | Thr | Gln | Leu | Glu | Pro | Val | Thr | Ser | Asn | Thr | Ile | Asn |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Ser | Phe | Thr | Ser | Ala | Pro | Lys | Val | Glu | Thr | Phe | His | Glu | Ser | Ile |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ser | Phe | Pro | Gly | Lys | Ser | Glu | Lys | Ile | Ser | Met | Leu | Thr | Phe | Lys | Glu |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Glu | Lys | Asp | Glu | Cys | Pro | Val | Gln | Glu | Lys | Phe | Pro | Asp | Leu | Asn | Leu |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Leu | Arg | Ile | Ser | Leu | Pro | Asp | Val | Asp | Arg | Leu | Gln | Gly | His |     |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Lys | Ser | Thr | Thr | Pro | Arg | Cys | Phe | Lys | Cys | Ser | Leu | Gly | Met | Ile |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Asn | Gly | Met | Glu | Cys | Arg | Cys | Gly | Arg | Met | Arg | Cys | Asp | Val | Val | Gly |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Gly | Ser | Ser | Lys | Gly | Ser | Asp | Met | Ser | Asn | Gly | Phe | Asp | Phe | Leu | Gly |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Leu | Ala | Lys | Lys | Glu | Thr | Thr | Ser | Leu |     |     |     |     |     |     |     |  |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1498563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Thr | Phe | Lys | Glu | Glu | Lys | Asp | Glu | Cys | Pro | Val | Gln | Glu | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Phe | Pro | Asp | Leu | Asn | Leu | Glu | Leu | Arg | Ile | Ser | Leu | Pro | Asp | Asp | Val |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Arg | Leu | Gln | Gly | His | Gly | Lys | Ser | Thr | Thr | Pro | Arg | Cys | Phe | Lys |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Cys | Ser | Leu | Gly | Met | Ile | Asn | Gly | Met | Glu | Cys | Arg | Cys | Gly | Arg | Met |  |

50 55 60  
Arg Cys Asp Val Val Gly Gly Ser Ser Lys Gly Ser Asp Met Ser Asn  
65 70 75 80  
Gly Phe Asp Phe Leu Gly Leu Ala Lys Lys Glu Thr Thr Ser Leu  
85 90 95

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..802  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

aacacatttc aagcatttga ttaatcaaag acaaagaaaa cgaaaatggt ggcaatattt 60  
cagaaagctt ttgtcacccc accggaagaa ctcaacagtc cggcttctca tttctccggc 120  
aaaactccta aacttcccg gaaactctc tccgacttcc tctctcatca ccaaaacaat 180  
gctttctcta tgaacttcgg cgactccgcc gtcttagctt acgctcgcca agaaacctct 240  
cttcgtcaaa ggttgttctg tggactagat gggatctact gtatgtttct agggagattg 300  
aataatctct gtacattgaa tcgacaatac ggtttatctg ggaagaagat tgagaaggag 360  
cccaagttct tgaagaatgg tgatgctggt atggtgaaga tgactccaac caagcccatg 420  
gttggtggaga ctttctctga gtacccacca cttggacgtt tcgctgtgca gggacatgag 480  
gcagactgtt gcagtcggtg ttatcaagag tgttgacaag aaggacccaa ccggagccaa 540  
ggttaccaag gctgccgtca agaagggtgc gaagtgaacc atcctcaaaa ctctatctgc 600  
cgcaggtgaa tcaaaggaca gtgttagttt tattacaata gtttggtatt tggtcgctg 660  
tctgtgttct tgtttcggtt tctccccgtc agagcgttgt tctcgtaatt gggttcttga 720  
tcggaggtgg cggatctaca cacacattct tcctgttttt tgctttttat ttgttttctc 780  
atattgaact gtttaaaatg ag

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..156  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

Met Leu Ala Ile Phe Gln Lys Ala Phe Ala His Pro Pro Glu Glu Leu  
1 5 10 15  
Asn Ser Pro Ala Ser His Phe Ser Gly Lys Thr Pro Lys Leu Pro Gly  
20 25 30  
Glu Thr Leu Ser Asp Phe Leu Ser His His Gln Asn Asn Ala Phe Ser  
35 40 45  
Met Asn Phe Gly Asp Ser Ala Val Leu Ala Tyr Ala Arg Gln Glu Thr  
50 55 60  
Ser Leu Arg Gln Arg Leu Phe Cys Gly Leu Asp Gly Ile Tyr Cys Met  
65 70 75 80  
Phe Leu Gly Arg Leu Asn Asn Leu Cys Thr Leu Asn Arg Gln Tyr Gly  
85 90 95  
Leu Ser Gly Lys Lys Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly  
100 105 110  
Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu  
115 120 125  
Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Gln Gly His  
130 135 140

Glu Ala Asp Cys Cys Ser Arg Cys Tyr Gln Glu Cys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

Met Asn Phe Gly Asp Ser Ala Val Leu Ala Tyr Ala Arg Gln Glu Thr  
1 5 10 15  
Ser Leu Arg Gln Arg Leu Phe Cys Gly Leu Asp Gly Ile Tyr Cys Met  
20 25 30  
Phe Leu Gly Arg Leu Asn Asn Leu Cys Thr Leu Asn Arg Gln Tyr Gly  
35 40 45  
Leu Ser Gly Lys Lys Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly  
50 55 60  
Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu  
65 70 75 80  
Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Gln Gly His  
85 90 95  
Glu Ala Asp Cys Cys Ser Arg Cys Tyr Gln Glu Cys  
100 105

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..534
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

aaaccaagtt ttcttctaag ctgtatttga aagggatat atttcacaca ccaaacagat 60  
cagaagcnaa aaggtaataa tataatggcg gatttgaggg acgaaaaagg taaccctaac 120  
catctaaccg acacacaggg aaacccaatt gtcgacctga ctgatgagca cggtaacccc 180  
atgtacctaa ccggtgttgt tagctccact cctcagcagt aaggagagna ctaccagcga 240  
cattgcagag caccctacta gcaccgttgg agaaacacat ccggcagctg ctccagctgg 300  
tgctggtgct gccaccgctg ccaactgcgac aggagtctct gctggtactg gagcaaccac 360  
cacagggcag caacaccatg ggctcgcttga agagcatctt cgtcggctctg gaagttcatc 420  
tagctctagc tcggaggatg acgggcaagg agggaggagg aagaagagca taaaggagaa 480  
aattaaagag aagctcaaag ccgccaacga attccaagaa actgattgtt ggat

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

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Met Ala Asp Leu Arg Asp Glu Lys Gly Asn Pro Ile His Leu Thr Asp  
1 5 10 15  
Thr Gln Gly Asn Pro Ile Val Asp Leu Thr Asp Glu His Gly Asn Pro  
20 25 30  
Met Tyr Leu Thr Gly Val Val Ser Thr Pro Gln Gln  
35 40 45

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..31

(D) OTHER INFORMATION: / Ceres Seq. ID 1498569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

Met Gly Arg Leu Lys Ser Ile Phe Val Gly Leu Glu Val His Leu Ala  
1 5 10 15  
Leu Ala Arg Arg Met Thr Gly Lys Glu Gly Gly Arg Arg Ala  
20 25 30

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1548 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1548

(D) OTHER INFORMATION: / Ceres Seq. ID 1498574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

|              |             |             |             |             |             |      |
|--------------|-------------|-------------|-------------|-------------|-------------|------|
| aaaattagg    | ctttatctta  | tcttcgcgat  | tctctcatct  | cctccctcta  | aaattctccg  | 60   |
| jcgacacagt   | tcaccggaaa  | tcgtagacga  | aatcagattc  | tttctcttta  | gtatgaaaca  | 120  |
| atgaatttga   | tctcaagaac  | attgacaaga  | gcagtgtctt  | cgtcactata  | ccactcaaaa  | 180  |
| gcagcgaagc   | tccccactca  | aaaatggata  | atctcgcagc  | aaatccgtgt  | tttctccgcc  | 240  |
| acagtcacatca | gcggtggagg  | aaagaaacct  | ctggcaaaaag | tatccgtgaa  | accaccgcta  | 300  |
| aatgtagcga   | cggagaaaaga | atcgactccg  | ccgaagacaa  | ttgagtacaa  | accggaaatt  | 360  |
| tcaaactgga   | tcaacctaat  | cggattcggt  | gaacaaccag  | ttcaattcgg  | tccttgctcc  | 420  |
| gatggaaaat   | tctgggctgg  | aacagttatt  | tctcagcggt  | ctgggtcaaa  | atcatctaatt | 480  |
| ttctggattc   | cgattatatt  | cgaaggagat  | ttagctaaaa  | ttgcagttca  | acatgtaaag  | 540  |
| aaagaagatc   | ggattcatgt  | ttccgggaag  | ctgtttattg  | attcgctcc   | tccaaatgtg  | 600  |
| acatattctc   | aatccaatgt  | tcaggttatg  | gttcagaatc  | ttaaacttct  | acaagctgct  | 660  |
| acttctacga   | ctaagacgat  | ctcaccacct  | gaaaaagaag  | ttaccagcat  | caagaaaaag  | 720  |
| cccgaagat    | ccaaaaaggt  | taaagtcata  | gatgaagaaa  | cctctaattc  | ttggaagcat  | 780  |
| cttattgaaa   | atcctaaaga  | gtgggttgat  | caccgtggga  | ataaagctaa  | cggattggta  | 840  |
| aagccaggac   | atcccgatct  | caagatgaag  | gttggtggtt  | tgctccctgtg | gctcagcaca  | 900  |
| gctcctgatt   | gggctttgct  | aaaactcgaa  | gagcttaagt  | ttgatgtctt  | agtcctctaaa | 960  |
| ggaaacatca   | aactgaatca  | acttaaagga  | gaggaatctt  | ggaaggattt  | gggttcagaac | 1020 |
| ccagacaaat   | ggttagacaa  | cagatcagat  | aagacaaacg  | tgaaataccc  | tgacttcaag  | 1080 |
| cataaagaga   | ctggtgaagc  | actgtggatg  | accaattctc  | ctatttgggt  | actgtcaaaag | 1140 |
| ttaccacctc   | taaagaagaa  | ccaagaaaaga | cctctcatgt  | ctaataaagt  | ctcgcagctt  | 1200 |
| gagcttgacg   | ttgaagtacc  | taaaggaaat  | ctgaaacagc  | ttaaaagaga  | ggaaatttgg  | 1260 |
| aagaacttgg   | ttgagaaccc  | cagtaaattg  | tgggataaca  | gattagacaa  | gagaaaccct  | 1320 |
| aaaggccctg   | actttaagca  | taaggagacc  | ggtgaagcac  | tgtggatagg  | tgattctccg  | 1380 |
| acttgggcgc   | tgtaaaagt   | accacctcta  | aagaaaaacc  | aagaaagacc  | tgatcatggc  | 1440 |
| taagcttctc   | tagcagcctt  | atgttaattt  | tggcccccac  | tatgtaaaaa  | ggccctatga  | 1500 |
| ctttattatc   | cagtcttata  | caaagagaat  | tgctatagta  | tcagtgc     |             |      |

(2) INFORMATION FOR SEQ ID NO:520:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 440 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..440  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498575  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Leu | Ile | Ser | Arg | Thr | Leu | Thr | Arg | Ala | Val | Ser | Ser | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | His | Ser | Lys | Ala | Ala | Lys | Leu | Pro | Thr | Gln | Lys | Trp | Ile | Ile | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Gln | Ile | Arg | Val | Phe | Ser | Ala | Thr | Val | Ile | Ser | Gly | Gly | Gly | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Pro | Leu | Ala | Lys | Val | Ser | Val | Lys | Pro | Pro | Leu | Asn | Val | Ala | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Lys | Glu | Ser | Thr | Pro | Pro | Lys | Thr | Ile | Glu | Tyr | Lys | Pro | Glu | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Asn | Trp | Ile | Asn | Leu | Ile | Gly | Phe | Val | Glu | Gln | Pro | Val | Gln | Phe |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Pro | Cys | Ser | Asp | Gly | Lys | Phe | Trp | Ala | Gly | Thr | Val | Ile | Ser | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ser | Gly | Ser | Lys | Ser | Ser | Asn | Phe | Trp | Ile | Pro | Ile | Ile | Phe | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Asp | Leu | Ala | Lys | Ile | Ala | Val | Gln | His | Val | Lys | Lys | Glu | Asp | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | His | Val | Ser | Gly | Lys | Leu | Phe | Ile | Asp | Ser | Pro | Pro | Pro | Asn | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Tyr | Ser | Gln | Ser | Asn | Val | Gln | Val | Met | Val | Gln | Asn | Leu | Asn | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Val | Gln | Ala | Ala | Thr | Ser | Thr | Thr | Lys | Thr | Ile | Ser | Pro | Pro | Glu | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Val | Thr | Ser | Ile | Lys | Lys | Lys | Pro | Ala | Arg | Ser | Lys | Lys | Val | Lys |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Ile | Asp | Glu | Glu | Thr | Ser | Asn | Ser | Trp | Lys | His | Leu | Ile | Glu | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Lys | Glu | Trp | Leu | Asp | His | Arg | Gly | Asn | Lys | Ala | Asn | Gly | Leu | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Lys | Pro | Gly | His | Pro | Asp | Phe | Lys | Met | Lys | Val | Gly | Gly | Leu | Ser | Leu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Trp | Leu | Ser | Thr | Ala | Pro | Asp | Trp | Ala | Leu | Leu | Lys | Leu | Glu | Glu | Leu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Phe | Asp | Val | Leu | Val | Pro | Lys | Gly | Asn | Ile | Lys | Leu | Asn | Gln | Leu |
|     | 275 |     |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Lys | Gly | Glu | Glu | Ser | Trp | Lys | Asp | Leu | Val | Gln | Asn | Pro | Asp | Lys | Trp |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Asp | Asn | Arg | Ser | Asp | Lys | Thr | Asn | Val | Lys | Tyr | Pro | Asp | Phe | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| His | Lys | Glu | Thr | Gly | Glu | Ala | Leu | Trp | Met | Thr | Asn | Ser | Pro | Ile | Trp |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Val | Leu | Ser | Lys | Leu | Pro | Pro | Leu | Lys | Lys | Asn | Gln | Glu | Arg | Pro | Leu |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Met | Ser | Asn | Lys | Val | Ser | Gln | Leu | Glu | Leu | Asp | Val | Glu | Val | Pro | Lys |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Gly | Asn | Leu | Lys | Gln | Leu | Lys | Arg | Glu | Glu | Ile | Trp | Lys | Asn | Leu | Val |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Glu | Asn | Pro | Ser | Lys | Trp | Trp | Asp | Asn | Arg | Leu | Asp | Lys | Arg | Asn | Pro |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |



Lys Gly Pro Asp Phe Lys His Lys Glu Thr Gly Glu Ala Leu Trp Ile  
                                  405                                  410                                  415  
Gly Asp Ser Pro Thr Trp Ala Leu Ser Lys Leu Pro Pro Leu Lys Lys  
                                  420                                  425                                  430  
Asn Gln Glu Arg Pro Val Met Ala  
                                  435                                  440

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1498576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

Met Val Gln Asn Leu Asn Phe Val Gln Ala Ala Thr Ser Thr Thr Lys  
1                                  5                                  10                                  15  
Thr Ile Ser Pro Pro Glu Lys Glu Val Thr Ser Ile Lys Lys Lys Pro  
                                  20                                  25                                  30  
Ala Arg Ser Lys Lys Val Lys Val Ile Asp Glu Glu Thr Ser Asn Ser  
                                  35                                  40                                  45  
Trp Lys His Leu Ile Glu Asn Pro Lys Glu Trp Leu Asp His Arg Gly  
                                  50                                  55                                  60  
Asn Lys Ala Asn Gly Leu Val Lys Pro Gly His Pro Asp Phe Lys Met  
65                                  70                                  75                                  80  
Lys Val Gly Gly Leu Ser Leu Trp Leu Ser Thr Ala Pro Asp Trp Ala  
                                  85                                  90                                  95  
Leu Leu Lys Leu Glu Glu Leu Lys Phe Asp Val Leu Val Pro Lys Gly  
                                  100                                  105                                  110  
Asn Ile Lys Leu Asn Gln Leu Lys Gly Glu Glu Ser Trp Lys Asp Leu  
                                  115                                  120                                  125  
Val Gln Asn Pro Asp Lys Trp Leu Asp Asn Arg Ser Asp Lys Thr Asn  
                                  130                                  135                                  140  
Val Lys Tyr Pro Asp Phe Lys His Lys Glu Thr Gly Glu Ala Leu Trp  
145                                  150                                  155                                  160  
Met Thr Asn Ser Pro Ile Trp Val Leu Ser Lys Leu Pro Pro Leu Lys  
                                  165                                  170                                  175  
Lys Asn Gln Glu Arg Pro Leu Met Ser Asn Lys Val Ser Gln Leu Glu  
                                  180                                  185                                  190  
Leu Asp Val Glu Val Pro Lys Gly Asn Leu Lys Gln Leu Lys Arg Glu  
                                  195                                  200                                  205  
Glu Ile Trp Lys Asn Leu Val Glu Asn Pro Ser Lys Trp Trp Asp Asn  
                                  210                                  215                                  220  
Arg Leu Asp Lys Arg Asn Pro Lys Gly Pro Asp Phe Lys His Lys Glu  
225                                  230                                  235                                  240  
Thr Gly Glu Ala Leu Trp Ile Gly Asp Ser Pro Thr Trp Ala Leu Ser  
                                  245                                  250                                  255  
Lys Leu Pro Pro Leu Lys Lys Asn Gln Glu Arg Pro Val Met Ala  
                                  260                                  265                                  270

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..607

(D) OTHER INFORMATION: / Ceres Seq. ID 1498577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

|            |             |            |             |             |            |     |
|------------|-------------|------------|-------------|-------------|------------|-----|
| atcaacttca | gatacctttca | ccagcaacac | aagttatattt | caaaagatga  | tgccaaattc | 60  |
| tagatcggcg | acaataactc  | cgacgacaga | atcaaccacc  | acgacaacaa  | caacaacaac | 120 |
| gactctaag  | acgtcgtatt  | ggtgttacag | ttgtacacga  | ttcatcagcg  | tttgggaaga | 180 |
| tcaagacgca | aacgctggag  | tcttatgtcc | ttattgcaac  | ggtggattca  | tcgaagagat | 240 |
| tgaagattct | tctaattcca  | ccgtcgcggc | gattccggct  | tcgactccgg  | aagttagatc | 300 |
| ggttgaggaa | acacatagat  | ctataattag | acgtcgtaga  | tctaatacgcc | ggacgtcctt | 360 |
| taatccggta | atcgtcttac  | acggcggagg | aggaggagga  | gccggtgaga  | gagttgagaa | 420 |
| cgaagaaggt | gacggagcta  | ctagagaacg | acgagcttat  | gagtyttatt  | acgatgatgg | 480 |
| atctggttca | ggtctaagac  | ctcttctcta | ttctgtatct  | gagatcttga  | ttggatctgg | 540 |
| attcgaacgg | ttacttgaac  | aattgagtca | gatcgaagcg  | tcaggtaacg  | gaatcggtag | 600 |
| atctggg    |             |            |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1498578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Ser | Asp | Pro | Phe | Thr | Ser | Asn | Thr | Ser | Tyr | Phe | Gln | Lys | Met |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Met | Pro | Asn | Ser | Arg | Ser | Ala | Thr | Ile | Thr | Pro | Thr | Thr | Glu | Ser | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Thr | Thr | Thr | Thr | Thr | Thr | Thr | Leu | Thr | Thr | Ser | Tyr | Trp | Cys |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Ser | Cys | Thr | Arg | Phe | Ile | Ser | Val | Trp | Glu | Asp | Gln | Asp | Ala | Asn |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Gly | Val | Leu | Cys | Pro | Tyr | Cys | Asn | Gly | Gly | Phe | Ile | Glu | Glu | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Asp | Ser | Ser | Asn | Ser | Thr | Val | Ala | Ala | Ile | Pro | Ala | Ser | Thr | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Val | Arg | Ser | Val | Glu | Glu | Thr | His | Arg | Ser | Ile | Ile | Arg | Arg | Arg |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ser | Asn | Arg | Arg | Thr | Ser | Phe | Asn | Pro | Val | Ile | Val | Leu | His | Gly |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Gly | Gly | Gly | Gly | Ala | Gly | Glu | Arg | Val | Glu | Asn | Glu | Glu | Gly | Asp |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ala | Thr | Arg | Glu | Arg | Arg | Ala | Tyr | Glu | Xaa | Tyr | Tyr | Asp | Asp | Gly |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ser | Gly | Ser | Gly | Leu | Arg | Pro | Leu | Pro | Asp | Ser | Val | Ser | Glu | Ile | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Gly | Ser | Gly | Phe | Glu | Arg | Leu | Leu | Glu | Gln | Leu | Ser | Gln | Ile | Glu |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ser | Gly | Asn | Gly | Ile | Gly | Arg | Ser | Gly |     |     |     |     |     |     |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1498579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Pro | Asn | Ser | Arg | Ser | Ala | Thr | Ile | Thr | Pro | Thr | Thr | Glu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Thr | Thr | Thr | Thr | Thr | Thr | Thr | Thr | Thr | Leu | Thr | Thr | Ser | Tyr | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Tyr | Ser | Cys | Thr | Arg | Phe | Ile | Ser | Val | Trp | Glu | Asp | Gln | Asp | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Ala | Gly | Val | Leu | Cys | Pro | Tyr | Cys | Asn | Gly | Gly | Phe | Ile | Glu | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Glu | Asp | Ser | Ser | Asn | Ser | Thr | Val | Ala | Ala | Ile | Pro | Ala | Ser | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Glu | Val | Arg | Ser | Val | Glu | Glu | Thr | His | Arg | Ser | Ile | Ile | Arg | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Arg | Ser | Asn | Arg | Arg | Thr | Ser | Phe | Asn | Pro | Val | Ile | Val | Leu | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Gly | Gly | Gly | Gly | Ala | Gly | Glu | Arg | Val | Glu | Asn | Glu | Glu | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Gly | Ala | Thr | Arg | Glu | Arg | Arg | Ala | Tyr | Glu | Xaa | Tyr | Tyr | Asp | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Gly | Ser | Gly | Ser | Gly | Leu | Arg | Pro | Leu | Pro | Asp | Ser | Val | Ser | Glu | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Ile | Gly | Ser | Gly | Phe | Glu | Arg | Leu | Leu | Glu | Gln | Leu | Ser | Gln | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Ala | Ser | Gly | Asn | Gly | Ile | Gly | Arg | Ser | Gly |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1498580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Asn | Ser | Arg | Ser | Ala | Thr | Ile | Thr | Pro | Thr | Thr | Glu | Ser | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Thr | Thr | Thr | Thr | Thr | Thr | Thr | Thr | Leu | Thr | Thr | Ser | Tyr | Trp | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Tyr | Ser | Cys | Thr | Arg | Phe | Ile | Ser | Val | Trp | Glu | Asp | Gln | Asp | Ala | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Gly | Val | Leu | Cys | Pro | Tyr | Cys | Asn | Gly | Gly | Phe | Ile | Glu | Glu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Asp | Ser | Ser | Asn | Ser | Thr | Val | Ala | Ala | Ile | Pro | Ala | Ser | Thr | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Val | Arg | Ser | Val | Glu | Glu | Thr | His | Arg | Ser | Ile | Ile | Arg | Arg | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Ser | Asn | Arg | Arg | Thr | Ser | Phe | Asn | Pro | Val | Ile | Val | Leu | His | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Gly | Gly | Gly | Gly | Gly | Ala | Gly | Glu | Arg | Val | Glu | Asn | Glu | Glu | Gly | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Ala | Thr | Arg | Glu | Arg | Arg | Ala | Tyr | Glu | Xaa | Tyr | Tyr | Asp | Asp | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ser | Gly | Ser | Gly | Leu | Arg | Pro | Leu | Pro | Asp | Ser | Val | Ser | Glu | Ile | Leu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Gly | Ser | Gly | Phe | Glu | Arg | Leu | Leu | Glu | Gln | Leu | Ser | Gln | Ile | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

Ala Ser Gly Asn Gly Ile Gly Arg Ser Gly  
180 185

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1303
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| aaagctcaga  | tatctgaata  | actcgcttgc  | gtgcctctct | ctctctaaaa  | gcccattctct | 60   |
| ttctcctcct  | cctcctccat  | tgaagaagaa  | acctaccttc | gtaatatattc | ctcaattacg  | 120  |
| atcatggtga  | atgttaaagg  | gtcaacccaaa | aaatcgaatc | ttgatcgatt  | ccttcattgc  | 180  |
| ataacaccct  | tagtgccacc  | ccaatctctc  | ccaagacgg  | agattagaac  | cctaaatcga  | 240  |
| ttgtggcatc  | catgggagag  | acaaaagggt  | gagtttttca | ggttgagtga  | tttgtgggat  | 300  |
| tgttatgatg  | aatggagcgc  | ttatggagct  | agcgttccta | ttcatgttac  | caacggagaa  | 360  |
| tctcttggtc  | aatactatgt  | tccttatctc  | tctgccatcc | agattttcac  | ctctcattcc  | 420  |
| tccttgatcc  | gcttaaggga  | agagtctgaa  | gatggggaat | gtgagggtag  | agatccggtt  | 480  |
| agcgattcag  | gtagcgatga  | gagtgctctc  | gaggaaggac | ttgagaacaa  | cacgctcttg  | 540  |
| catccaagtg  | atcgtttggg  | ttatctttat  | ctccaatact | ttgagagatc  | agctccttat  | 600  |
| accagagttc  | ctctgatgga  | taagatcaat  | gaattggctc | aaagataccc  | gggattgatg  | 660  |
| tcgttgagaa  | gcgttgatct  | ttctccagct  | agttggatgt | cagtagcatg  | gtacccgatt  | 720  |
| taccatatac  | caatgggaag  | aaccattaaa  | gacttatcca | cgtgtttcct  | cacttatcac  | 780  |
| actctttcct  | cttcttttca  | agatatggaa  | ccggaagaaa | atgggtggga  | caaggagaga  | 840  |
| gtgcggaggg  | aaggggaaga  | tataactctg  | ctcccatttg | ggatggctac  | ttacaagatg  | 900  |
| caaggcgatg  | tttggctttc  | gcaggaccac  | gatgatcaag | agagattggc  | ttcgtctttc  | 960  |
| agtggttcgg  | attccttggt  | taaacagctc  | agggtccaac | atcatgactt  | caactacttc  | 1020 |
| tgcaatatgt  | caatgactca  | tcgtggctaa  | acctcggttg | gatgacacca  | tgatgtttgc  | 1080 |
| ttgtttcctc  | atatatagtc  | taattcttgc  | tttgttctgg | aaccgcttgc  | gttttgtaaa  | 1140 |
| acgcaatgga  | gcgattcgct  | ttgcagtgtt  | ttggttagaa | tagcgttttg  | agtcttctaa  | 1200 |
| cctttgagag  | agtatatgtc  | gtatatagag  | ttttgttgct | tgttgaaaca  | gagtacaatt  | 1260 |
| gttggttgctt | gttaaaaaaca | gagtgattgt  | ttcttataag | ttg         |             |      |

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..308
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asn | Val | Lys | Gly | Ser | Thr | Lys | Lys | Ser | Asn | Leu | Asp | Arg | Phe |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | His | Cys | Ile | Thr | Pro | Leu | Val | Pro | Pro | Gln | Ser | Leu | Pro | Lys | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ile | Arg | Thr | Leu | Asn | Arg | Leu | Trp | His | Pro | Trp | Glu | Arg | Gln | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Glu | Phe | Phe | Arg | Leu | Ser | Asp | Leu | Trp | Asp | Cys | Tyr | Asp | Glu | Trp |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Ala | Tyr | Gly | Ala | Ser | Val | Pro | Ile | His | Val | Thr | Asn | Gly | Glu | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Val | Gln | Tyr | Tyr | Val | Pro | Tyr | Leu | Ser | Ala | Ile | Gln | Ile | Phe | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | His | Ser | Ser | Leu | Ile | Arg | Leu | Arg | Glu | Glu | Ser | Glu | Asp | Gly | Glu |

100 105 110  
Cys Glu Gly Arg Asp Pro Phe Ser Asp Ser Gly Ser Asp Glu Ser Val  
115 120 125  
Ser Glu Gly Leu Glu Asn Asn Thr Leu Leu His Pro Ser Asp Arg  
130 135 140  
Leu Gly Tyr Leu Tyr Leu Gln Tyr Phe Glu Arg Ser Ala Pro Tyr Thr  
145 150 155 160  
Arg Val Pro Leu Met Asp Lys Ile Asn Glu Leu Ala Gln Arg Tyr Pro  
165 170 175  
Gly Leu Met Ser Leu Arg Ser Val Asp Leu Ser Pro Ala Ser Trp Met  
180 185 190  
Ser Val Ala Trp Tyr Pro Ile Tyr His Ile Pro Met Gly Arg Thr Ile  
195 200 205  
Lys Asp Leu Ser Thr Cys Phe Leu Thr Tyr His Thr Leu Ser Ser Ser  
210 215 220  
Phe Gln Asp Met Glu Pro Glu Glu Asn Gly Gly Asp Lys Glu Arg Val  
225 230 235 240  
Arg Arg Glu Gly Glu Asp Ile Thr Leu Leu Pro Phe Gly Met Ala Thr  
245 250 255  
Tyr Lys Met Gln Gly Asp Val Trp Leu Ser Gln Asp His Asp Asp Gln  
260 265 270  
Glu Arg Leu Ala Ser Leu Tyr Ser Val Ala Asp Ser Trp Leu Lys Gln  
275 280 285  
Leu Arg Val Gln His His Asp Phe Asn Tyr Phe Cys Asn Met Ser Met  
290 295 300  
Thr His Arg Gly  
305

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gtccgagtca cgatgagtca actcggagat ttgcttagag aatcagaaga tggacaaga  | 60  |
| agtgagagga cgatgatgat gagtttgctc gaagaagatc aaatcaacgg tggagataga | 120 |
| acgatgagca aatggactac gttaaagcaa cggctgagat ttgattgggt tggttgtwgt | 180 |
| ggtaagcctc ttactctgcg tctcagacaa gcggagacac caatcgtcgt cgatgatgat | 240 |
| gacgacgaag aagaaagtca aaaccaggtc gttgactttt cggatccggg tacgggtacg | 300 |
| gagttggatt gtttgagacg cagagtaaga ggcttaccac aacaaccaac ccaatcaa   | 360 |
| ctcagccgtt gctttaacgt agtactttgg tggtttatgt tttggggcca tgtacagcct | 420 |
| ctgataaata attgatcgac tatgtttccg tttctttcat ctctcttttc tttcaa     | 480 |
| caaatcgaac ttattctcta ttgcaattat ctctttcg                         |     |

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

Val Arg Val Thr Met Ser Gln Leu Gly Asp Leu Leu Arg Glu Ser Glu

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Asp Gly Thr Arg Ser Glu Arg Thr Met Met Met Ser Leu Leu Glu Glu |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Asp Gln Ile Asn Gly Gly Asp Arg Thr Met Ser Lys Trp Thr Thr Leu |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Lys Gln Arg Leu Arg Phe Asp Trp Val Gly Cys Xaa Gly Lys Pro Leu |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Thr Leu Arg Leu Arg Gln Ala Glu Thr Pro Ile Val Val Asp Asp Asp |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Asp Asp Glu Glu Glu Ser Gln Asn Gln Val Val Asp Phe Ser Asp Pro |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Gly Thr Gly Thr Glu Leu Asp Cys Leu Arg Arg Arg Val Arg Gly Leu |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Pro Gln Gln Pro Thr Gln Ser Asn Leu Ser Arg Cys Phe Asn Val Val |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Leu Trp Trp Phe Met Phe Trp Gly His Val Gln Pro Leu Ile Asn Asn |     |     |     |
|                                                                 | 130 | 135 | 140 |

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1498597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| Met Ser Gln Leu Gly Asp Leu Leu Arg Glu Ser Glu Asp Gly Thr Arg |     |     |     |
| 1                                                               | 5   | 10  | 15  |
| Ser Glu Arg Thr Met Met Met Ser Leu Leu Glu Glu Asp Gln Ile Asn |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Gly Gly Asp Arg Thr Met Ser Lys Trp Thr Thr Leu Lys Gln Arg Leu |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Arg Phe Asp Trp Val Gly Cys Xaa Gly Lys Pro Leu Thr Leu Arg Leu |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Arg Gln Ala Glu Thr Pro Ile Val Val Asp Asp Asp Asp Asp Glu Glu |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Glu Ser Gln Asn Gln Val Val Asp Phe Ser Asp Pro Gly Thr Gly Thr |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Glu Leu Asp Cys Leu Arg Arg Arg Val Arg Gly Leu Pro Gln Gln Pro |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Thr Gln Ser Asn Leu Ser Arg Cys Phe Asn Val Val Leu Trp Trp Phe |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Met Phe Trp Gly His Val Gln Pro Leu Ile Asn Asn                 |     |     |     |
|                                                                 | 130 | 135 | 140 |

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1498598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

Met Met Met Ser Leu Leu Glu Glu Asp Gln Ile Asn Gly Gly Asp Arg  
1 5 10 15  
Thr Met Ser Lys Trp Thr Thr Leu Lys Gln Arg Leu Arg Phe Asp Trp  
20 25 30  
Val Gly Cys Xaa Gly Lys Pro Leu Thr Leu Arg Leu Arg Gln Ala Glu  
35 40 45  
Thr Pro Ile Val Val Asp Asp Asp Asp Glu Glu Glu Ser Gln Asn  
50 55 60  
Gln Val Val Asp Phe Ser Asp Pro Gly Thr Gly Thr Glu Leu Asp Cys  
65 70 75 80  
Leu Arg Arg Arg Val Arg Gly Leu Pro Gln Gln Pro Thr Gln Ser Asn  
85 90 95  
Leu Ser Arg Cys Phe Asn Val Val Leu Trp Trp Phe Met Phe Trp Gly  
100 105 110  
His Val Gln Pro Leu Ile Asn Asn  
115 120

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1919
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| cattaagagc  | aaaaactagt  | tttgctttca  | tttttttttg  | gtaggaaagg  | gttaattata  | 60   |
| cgtaacacag  | aaacaaaaac  | aattctcttt  | tcctctagaa  | aaagagatta  | aaaaaaaaaat | 120  |
| ggagggggagg | ttattgacgg  | tggttggtctg | cctcgctctct | acggtggcga  | tcgtgaacgc  | 180  |
| cggtgatcct  | tacttcttcc  | atacatggaa  | cgtgacttac  | ggaactgcct  | cacctctcgg  | 240  |
| tgttcctcaa  | aaggtgattc  | tcatacaacg  | tcaattccct  | ggtcctaacc  | ttaaactcaac | 300  |
| ctctaacaac  | aacgtcgtca  | tcaatgtctt  | caaccaccta  | gacgaacctt  | tcctcttgac  | 360  |
| ctggagtggg  | attcagcatc  | ggaagaactg  | ctggcaagat  | ggtgtggctg  | gaacttcatg  | 420  |
| ccccatccca  | gctggacaga  | actttactta  | ccatttccaa  | cctaaggacc  | agattgggtc  | 480  |
| ctacttctat  | tacccaacca  | cttctctcca  | ccgctttgct  | ggtggttttg  | gtgggtctccg | 540  |
| tgtcaacagc  | cgtctcctaa  | ttcccggttc  | ttatgctgat  | cctgaagatg  | actacactgt  | 600  |
| ccttctcggg  | gactgggtaca | cagctggcca  | cactgctctc  | aagaacttcc  | ttgacagttg  | 660  |
| acgcaccctt  | ggattgccta  | acggtgtttt  | gatcaatgga  | aagtctggaa  | aggttggagg  | 720  |
| aaagaacgag  | cctttgttca  | caatgaagcc  | tggaaagact  | tacaagtaca  | ggctctgcaa  | 780  |
| tgttgggttc  | aagtctacac  | ttaaacttcag | gatccagaac  | cacaagatga  | agctcgtgga  | 840  |
| gatggaagga  | tcccatgtta  | ttcagaacga  | ctatgactct  | ctcgatgtcc  | atggttgcca  | 900  |
| gtgcttttca  | gttcttgtga  | ctgctaacca  | agcagctaag  | gattactaca  | tggttgcatc  | 960  |
| gactagggtc  | ctcaagaagg  | agttgagcac  | cgtgggtgtg  | atccggtatg  | aggggaagcaa | 1020 |
| cgttcagggt  | tcaactgagc  | tacccaaggc  | tcctgttgga  | tgggcttggt  | ctttgaacca  | 1080 |
| gttcagggtc  | ttcagggtga  | accttaacct  | taacgctgca  | aggcctaacc  | cccaaggctc  | 1140 |
| ataccattac  | ggaaagatca  | atattaccgg  | tagcatcaag  | cttgtcaact  | ctaaaagtgt  | 1200 |
| ggttgacggg  | aaagtccggg  | ttggtttcaa  | tgggttatca  | cacgttgaca  | ccgagactcc  | 1260 |
| tttgaagcct  | gctgagtact  | tccaaatgtc  | agagaagggt  | ttcaagtaca  | atgtgatcaa  | 1320 |
| ggacgagcct  | gcagccaaaa  | tcacagcatt  | gactgtacaa  | cctaattgtc  | tcaacatcac  | 1380 |
| tttccgtacc  | tttgtagaga  | tcattttcga  | gaaccacgag  | aagaccatgc  | agtcattcca  | 1440 |
| tttggtatgg  | tactccttct  | tcgctgtcgc  | ttctgagcca  | gggaggtgga  | cgcctgaaaa  | 1500 |
| gagagagaac  | tacaacttgc  | tcgatgcggg  | tagcagacac  | accgtgcaag  | tctaccccaa  | 1560 |
| gtcttggtca  | gctatccttt  | tgacattcga  | caacgccggg  | atgtggaaca  | tcagggtctga | 1620 |
| gaacttggag  | aggaaatacc  | taggcgagca  | attgtatgtc  | agtgttctat  | caccggagaa  | 1680 |
| atcgctaagg  | gacgagtaca  | acatccccct  | caacacaaac  | ctctgtggca  | tcgtcaaggg  | 1740 |
| cttgccatta  | cctgcacact  | actcctaaat  | caatattcaa  | ttaaactacta | ctctacaaaag | 1800 |
| tgggggtgcaa | tattaaatta  | actaattaac  | cctttcctag  | attttaagtg  | taatttgtaa  | 1860 |
| acccttctt   | tcataacta   | tcataaacc   | ataatcatat  | accaagtttt  | gctttcatt   |      |

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1498600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

Met Lys Pro Gly Lys Thr Tyr Lys Tyr Arg Leu Cys Asn Val Gly Phe  
1 5 10 15  
Lys Ser Thr Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys Leu Val  
20 25 30  
Glu Met Glu Gly Ser His Val Ile Gln Asn Asp Tyr Asp Ser Leu Asp  
35 40 45  
Val His Val Gly Gln Cys Phe Ser Val Leu Val Thr Ala Asn Gln Ala  
50 55 60  
Ala Lys Asp Tyr Tyr Met Val Ala Ser Thr Arg Phe Leu Lys Lys Glu  
65 70 75 80  
Leu Ser Thr Val Gly Val Ile Arg Tyr Glu Gly Ser Asn Val Gln Ala  
85 90 95  
Ser Thr Glu Leu Pro Lys Ala Pro Val Gly Trp Ala Trp Ser Leu Asn  
100 105 110  
Gln Phe Arg Ser Phe Arg Trp Asn Leu Thr Ser Asn Ala Ala Arg Pro  
115 120 125  
Asn Pro Gln Gly Ser Tyr His Tyr Gly Lys Ile Asn Ile Thr Arg Ser  
130 135 140  
Ile Lys Leu Val Asn Ser Lys Ser Val Val Asp Gly Lys Val Arg Phe  
145 150 155 160  
Gly Phe Asn Gly Val Ser His Val Asp Thr Glu Thr Pro Leu Lys Leu  
165 170 175  
Ala Glu Tyr Phe Gln Met Ser Glu Lys Val Phe Lys Tyr Asn Val Ile  
180 185 190  
Lys Asp Glu Pro Ala Ala Lys Ile Thr Ala Leu Thr Val Gln Pro Asn  
195 200 205  
Val Leu Asn Ile Thr Phe Arg Thr Phe Val Glu Ile Ile Phe Glu Asn  
210 215 220  
His Glu Lys Thr Met Gln Ser Phe His Leu Asp Gly Tyr Ser Phe Phe  
225 230 235 240  
Ala Val Ala Ser Glu Pro Gly Arg Trp Thr Pro Glu Lys Arg Glu Asn  
245 250 255  
Tyr Asn Leu Leu Asp Ala Val Ser Arg His Thr Val Gln Val Tyr Pro  
260 265 270  
Lys Ser Trp Ser Ala Ile Leu Leu Thr Phe Asp Asn Ala Gly Met Trp  
275 280 285  
Asn Ile Arg Ser Glu Asn Leu Glu Arg Lys Tyr Leu Gly Glu Gln Leu  
290 295 300  
Tyr Val Ser Val Leu Ser Pro Glu Lys Ser Leu Arg Asp Glu Tyr Asn  
305 310 315 320  
Ile Pro Leu Asn Thr Asn Leu Cys Gly Ile Val Lys Gly Leu Pro Leu  
325 330 335  
Pro Ala His Tyr Ser  
340

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..313

(D) OTHER INFORMATION: / Ceres Seq. ID 1498601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Leu | Val | Glu | Met | Glu | Gly | Ser | His | Val | Ile | Gln | Asn | Asp | Tyr |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Ser | Leu | Asp | Val | His | Val | Gly | Gln | Cys | Phe | Ser | Val | Leu | Val | Thr |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Asn | Gln | Ala | Ala | Lys | Asp | Tyr | Met | Val | Ala | Ser | Thr | Arg | Phe |     |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Leu | Lys | Lys | Glu | Leu | Ser | Thr | Val | Gly | Val | Ile | Arg | Tyr | Glu | Gly | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asn | Val | Gln | Ala | Ser | Thr | Glu | Leu | Pro | Lys | Ala | Pro | Val | Gly | Trp | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Trp | Ser | Leu | Asn | Gln | Phe | Arg | Ser | Phe | Arg | Trp | Asn | Leu | Thr | Ser | Asn |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala | Ala | Arg | Pro | Asn | Pro | Gln | Gly | Ser | Tyr | His | Tyr | Gly | Lys | Ile | Asn |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Thr | Arg | Ser | Ile | Lys | Leu | Val | Asn | Ser | Lys | Ser | Val | Val | Asp | Gly |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Lys | Val | Arg | Phe | Gly | Phe | Asn | Gly | Val | Ser | His | Val | Asp | Thr | Glu | Thr |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |
| Pro | Leu | Lys | Leu | Ala | Glu | Tyr | Phe | Gln | Met | Ser | Glu | Lys | Val | Phe | Lys |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Tyr | Asn | Val | Ile | Lys | Asp | Glu | Pro | Ala | Ala | Lys | Ile | Thr | Ala | Leu | Thr |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Val | Gln | Pro | Asn | Val | Leu | Asn | Ile | Thr | Phe | Arg | Thr | Phe | Val | Glu | Ile |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ile | Phe | Glu | Asn | His | Glu | Lys | Thr | Met | Gln | Ser | Phe | His | Leu | Asp | Gly |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Tyr | Ser | Phe | Phe | Ala | Val | Ala | Ser | Glu | Pro | Gly | Arg | Trp | Thr | Pro | Glu |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Lys | Arg | Glu | Asn | Tyr | Asn | Leu | Leu | Asp | Ala | Val | Ser | Arg | His | Thr | Val |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Gln | Val | Tyr | Pro | Lys | Ser | Trp | Ser | Ala | Ile | Leu | Leu | Thr | Phe | Asp | Asn |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ala | Gly | Met | Trp | Asn | Ile | Arg | Ser | Glu | Asn | Leu | Glu | Arg | Lys | Tyr | Leu |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Gly | Glu | Gln | Leu | Tyr | Val | Ser | Val | Leu | Ser | Pro | Glu | Lys | Ser | Leu | Arg |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |  |
| Asp | Glu | Tyr | Asn | Ile | Pro | Leu | Asn | Thr | Asn | Leu | Cys | Gly | Ile | Val | Lys |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Gly | Leu | Pro | Leu | Pro | Ala | His | Tyr | Ser |     |     |     |     |     |     |     |  |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..308

(D) OTHER INFORMATION: / Ceres Seq. ID 1498602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Gly | Ser | His | Val | Ile | Gln | Asn | Asp | Tyr | Asp | Ser | Leu | Asp | Val |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| His | Val | Gly | Gln | Cys | Phe | Ser | Val | Leu | Val | Thr | Ala | Asn | Gln | Ala | Ala |  |

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| aaaatatcaa  | aacacgagac | agattttgatt | ccattttttat | tactgttact | atcatccaaa | 60  |
| accttggtat  | ttgtagccat | gagtcctgtt  | tcagatctca  | tcaaccttaa | cctctcagac | 120 |
| tccactgaca  | aaatcattgc | tgaatacata  | tgggttggtg  | gttctggaat | ggacatgaga | 180 |
| agcaaagcca  | ggactctacc | tggaccagct  | actgaccctt  | cgcagctacc | aaagtggaa  | 240 |
| tatgatggtt  | caagcacagc | acaagctcct  | ggtgaagaca  | gtgaagtcac | cttatagtta | 300 |
| ataatctttt  | ttctctgac  | tttaaataag  | tttcttctca  | ttgggttttt | tttcgattct | 360 |
| tgtttactaa  | tcttttgtgt | gtttgtatat  | ctttgttttag | ccctcaagcc | atattcaaag | 420 |
| atcctttccg  | tagaggaaac | aacattcttg  | tcatgtgcga  | tgcgtaacct | cccgcgggtg | 480 |
| aaccaatccc  | gactaacaaa | agacacgctg  | cggctaaggt  | ctttagcaac | cctgatgttg | 540 |
| cagctgaagt  | gccatgggat | ggtattgagc  | aagaatacac  | tttactccag | aaagatgtga | 600 |
| ggtggcctgt  | tggttggcct | atttgcggtt  | atcccggccc  | tcagggaccg | tactattgcg | 660 |
| gtatttggagc | agacaaatct | tttggcagag  | atgtttgtga  | ttctcactac | aaggcctgtt | 720 |

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| tatacgctgg | aatcaacatt  | agtggcatca | atggagaagt | catgccgggt | cagtgggagt  | 780  |
| tccaggtcgg | tccagctggt  | ggtatctcgg | ctgctgatga | aatttgggtc | gctcgttaca  | 840  |
| ttttggagag | gatcacagag  | attgctggtg | tagtggtatc | ttttgaccgg | aaaccgattc  | 900  |
| ccggtgactg | gaacgggtgt  | ggtgctcact | gcaactacag | taccaagtca | atgaggggaag | 960  |
| aaggcggtta | cgagatcatc  | aagaaagcaa | tcgataaatt | gggactgaga | cacaaagarc  | 1020 |
| rcatttgctg | ttacsgtgaa  | ggcaatgagc | gtcgtctcac | aggacaccac | gagactgctg  | 1080 |
| acatcaacac | tttcctttgg  | ggtggttgcg | accgtggagc | atcgatccga | gtaggacgtg  | 1140 |
| atacggagaa | agaagggaaa  | ggatactttg | aggacaggag | gccagcttcg | aacatggatc  | 1200 |
| cttacattgt | tactttccatg | attgcagaga | ccaccatcct | ctggaatcct | tgatgatcat  | 1260 |
| cagatcaaga | aaaaatcttg  | aatgtcactc | aaatttgtgt | ttcttgcaag | attcaaagtt  | 1320 |
| tgtgttctct | atcaagcaat  | gtcttaggat | aagtcaaaga | tttgctctgc | ttattctgct  | 1380 |
| ttttatttac | ttcacatcct  | attgaaaaca | tttctgtgta | ttatttatga | ataaacatta  | 1440 |
| tctt       |             |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1498611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Asp | Ala | Tyr | Thr | Pro | Ala | Gly | Glu | Pro | Ile | Pro | Thr | Asn | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | His | Ala | Ala | Ala | Lys | Val | Phe | Ser | Asn | Pro | Asp | Val | Ala | Ala | Glu |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Val | Pro | Trp | Tyr | Gly | Ile | Glu | Gln | Glu | Tyr | Thr | Leu | Leu | Gln | Lys | Asp |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Arg | Trp | Pro | Val | Gly | Trp | Pro | Ile | Gly | Gly | Tyr | Pro | Gly | Pro | Gln |
|     |     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Gly | Pro | Tyr | Tyr | Cys | Gly | Ile | Gly | Ala | Asp | Lys | Ser | Phe | Gly | Arg | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Val | Asp | Ser | His | Tyr | Lys | Ala | Cys | Leu | Tyr | Ala | Gly | Ile | Asn | Ile |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |
| Ser | Gly | Ile | Asn | Gly | Glu | Val | Met | Pro | Gly | Gln | Trp | Glu | Phe | Gln | Val |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |
| Gly | Pro | Ala | Val | Gly | Ile | Ser | Ala | Ala | Asp | Glu | Ile | Trp | Val | Ala | Arg |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Tyr | Ile | Leu | Glu | Arg | Ile | Thr | Glu | Ile | Ala | Gly | Val | Val | Val | Ser | Phe |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asp | Pro | Lys | Pro | Ile | Pro | Gly | Asp | Trp | Asn | Gly | Ala | Gly | Ala | His | Cys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asn | Tyr | Ser | Thr | Lys | Ser | Met | Arg | Glu | Glu | Gly | Gly | Tyr | Glu | Ile | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Lys | Ala | Ile | Asp | Lys | Leu | Gly | Leu | Arg | His | Lys | Xaa | Xaa | Ile | Ala |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |
| Ala | Tyr | Xaa | Glu | Gly | Asn | Glu | Arg | Arg | Leu | Thr | Gly | His | His | Glu | Thr |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Ala | Asp | Ile | Asn | Thr | Phe | Leu | Trp | Gly | Val | Ala | Asn | Arg | Gly | Ala | Ser |
|     |     |     |     | 210 |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Ile | Arg | Val | Gly | Arg | Asp | Thr | Glu | Lys | Glu | Gly | Lys | Gly | Tyr | Phe | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Asp | Arg | Arg | Pro | Ala | Ser | Asn | Met | Asp | Pro | Tyr | Ile | Val | Thr | Ser | Met |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Ala | Glu | Thr | Thr | Ile | Leu | Trp | Asn | Pro |     |     |     |     |     |     |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..163  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498612  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ala Val Gly Ile Ser  
1 5 10 15  
Ala Ala Asp Glu Ile Trp Val Ala Arg Tyr Ile Leu Glu Arg Ile Thr  
20 25 30  
Glu Ile Ala Gly Val Val Val Ser Phe Asp Pro Lys Pro Ile Pro Gly  
35 40 45  
Asp Trp Asn Gly Ala Gly Ala His Cys Asn Tyr Ser Thr Lys Ser Met  
50 55 60  
Arg Glu Glu Gly Gly Tyr Glu Ile Ile Lys Lys Ala Ile Asp Lys Leu  
65 70 75 80  
Gly Leu Arg His Lys Xaa Xaa Ile Ala Ala Tyr Xaa Glu Gly Asn Glu  
85 90 95  
Arg Arg Leu Thr Gly His His Glu Thr Ala Asp Ile Asn Thr Phe Leu  
100 105 110  
Trp Gly Val Ala Asn Arg Gly Ala Ser Ile Arg Val Gly Arg Asp Thr  
115 120 125  
Glu Lys Glu Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ala Ser Asn  
130 135 140  
Met Asp Pro Tyr Ile Val Thr Ser Met Ile Ala Glu Thr Thr Ile Leu  
145 150 155 160  
Trp Asn Pro

- (2) INFORMATION FOR SEQ ID NO:539:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1772 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1772  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| agcacatgac | cgagtcgcg  | tcagaaaaag | gggccaactg | ctccgtagcc  | gccaagaatc | 60   |
| tcgcagatcc | cgattcctct | tgatcatcgt | cttcttctac | caaaattggt  | gcgcgacaat | 120  |
| ggagaaatac | aacagtttat | cagattttct | caaggagttc | tacatcccta  | cgtacgtcct | 180  |
| ctcggcggaa | acagaagagg | aggaggagga | ggagagtcgt | cctacacctg  | cgagccccgt | 240  |
| ccttgctctc | atcaactcca | aaagcggtag | tcagttgggt | ggcgaactca  | ttctcaccta | 300  |
| ccgatctctt | ctcaatcaca | atcaggtctt | tgatctcgac | caggagactc  | cagataaagt | 360  |
| gctccgcaga | atctatctta | acctggagag | gctcaaagat | gatgattccg  | ctcgtcagat | 420  |
| tgaggagaaa | ttaaaaatca | ttgttgagag | aggtgatggc | actgctgggt  | ggctccttgg | 480  |
| agttgtatgt | gaccttaaat | tgtcacatcc | tcctccaatt | gccactgtac  | ctttgggtac | 540  |
| aggaacaac  | cttccctttg | cttttggatg | gggaaagaag | aatccaggaa  | cagataggac | 600  |
| tgcatgtggg | tcgttttttg | aacaagtggt | gaaggcaaaa | gtgatgaaga  | ttgacaattg | 660  |
| gcacatactt | atgaggatga | aaactcccaa | agaaggtggg | tcttgatgat  | ctgttgctcc | 720  |
| tcttgagtta | ccacattctc | tacatgcatt | tcaccgtgtt | tctccaactg  | atgaactaaa | 780  |
| caaggaaggc | tgccacactt | ttcgaggagg | gttctggaat | tacttttagcc | tcggaatgga | 840  |
| tgctcagatt | tcttatgcgt | ttcattctga | gaggaagctt | caccctgaaa  | agtttaagaa | 900  |
| tcagctgggt | aatcagagta | cgtatgtaaa | gcttggttgc | acgcaaggat  | ggttttgtgc | 960  |
| ctctcttttc | caccctgctt | cacggaatat | agctcagctt | gccaaaggta  | agattgcaac | 1020 |

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| tagaaatggc | cagtggcagg  | acctccacat | accacatagc | atcaggtcca | ttgtatgtct  | 1080 |
| gaatctgccc | agcttttcgg  | gaggattaaa | tccttggggc | acaccaaata | ccaggaaaca  | 1140 |
| acgtgataga | ggcttgactc  | caccatttgt | agatgatggc | ctcattgagg | ttgttgggtt  | 1200 |
| tagaaatgct | tggcatggtc  | ttgttctgct | cgctcccaat | ggacatggga | cacgacttgc  | 1260 |
| ccaggcaaat | cgtattcgct  | tcgaatttca | caaaggtgca | accgaccata | cattcatgag  | 1320 |
| gatggatggg | gagccctgga  | aacagccact | gccactggat | gatgaaactg | tgatggtaga  | 1380 |
| gatttcacac | cttggccaag  | tgaacatgct | tgcaactcat | gactgccggg | ccagaagtgt  | 1440 |
| gtttgaccct | tcaacacccc  | gccatcagga | tggtgcagaa | gattatgatg | ataatgaaga  | 1500 |
| cgactcantg | gctgaaggcg  | aagaatttag | aaagtttggt | gctgcgata  | ccttcaagat  | 1560 |
| tcctgatgag | gttgatattt  | ctcaacttag | ttagacaatt | aaccattttc | attgttgatt  | 1620 |
| ctatgcattc | ttcctccgga  | ctccaatttt | tttattcact | ctttcataaa | ggagcaacta  | 1680 |
| gcagcaactg | gttttagattg | gtaaccatct | tttttctttg | cttttgtttg | gttggttcacg | 1740 |
| tttaatggcc | gagataatgt  | atctggattt | at         |            |             |      |

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 530 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..530

(D) OTHER INFORMATION: / Ceres Seq. ID 1498617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | His | Asp | Arg | Val | Arg | Val | Arg | Lys | Arg | Gly | Gln | Leu | Leu | Arg | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gln | Glu | Ser | Arg | Arg | Ser | Arg | Phe | Leu | Ile | Ile | Val | Phe | Phe |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Gln | Asn | Cys | Cys | Ala | Thr | Met | Glu | Lys | Tyr | Asn | Ser | Leu | Ser | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Lys | Glu | Phe | Tyr | Ile | Pro | Thr | Tyr | Val | Leu | Ser | Ala | Glu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Glu | Glu | Glu | Glu | Glu | Glu | Ser | Arg | Pro | Thr | Pro | Ala | Ser | Pro | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Val | Phe | Ile | Asn | Ser | Lys | Ser | Gly | Gly | Gln | Leu | Gly | Gly | Glu | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Leu | Thr | Tyr | Arg | Ser | Leu | Leu | Asn | His | Asn | Gln | Val | Phe | Asp | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Gln | Glu | Thr | Pro | Asp | Lys | Val | Leu | Arg | Arg | Ile | Tyr | Leu | Asn | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Arg | Leu | Lys | Asp | Asp | Asp | Ser | Ala | Arg | Gln | Ile | Gly | Glu | Lys | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ile | Ile | Val | Ala | Gly | Gly | Asp | Gly | Thr | Ala | Gly | Trp | Leu | Leu | Gly |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| Val | Val | Cys | Asp | Leu | Lys | Leu | Ser | His | Pro | Pro | Pro | Ile | Ala | Thr | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Pro | Leu | Gly | Thr | Gly | Asn | Asn | Leu | Pro | Phe | Ala | Phe | Gly | Trp | Gly | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Asn | Pro | Gly | Thr | Asp | Arg | Thr | Ala | Val | Glu | Ser | Phe | Leu | Glu | Gln |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Leu | Lys | Ala | Lys | Val | Met | Lys | Ile | Asp | Asn | Trp | His | Ile | Leu | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Met | Lys | Thr | Pro | Lys | Glu | Gly | Gly | Ser | Cys | Asp | Pro | Val | Ala | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Leu | Glu | Leu | Pro | His | Ser | Leu | His | Ala | Phe | His | Arg | Val | Ser | Pro | Thr |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Asp | Glu | Leu | Asn | Lys | Glu | Gly | Cys | His | Thr | Phe | Arg | Gly | Gly | Phe | Trp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Tyr | Phe | Ser | Leu | Gly | Met | Asp | Ala | Gln | Ile | Ser | Tyr | Ala | Phe | His |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

Ser Glu Arg Lys Leu His Pro Glu Lys Phe Lys Asn Gln Leu Val Asn  
290 295 300  
Gln Ser Thr Tyr Val Lys Leu Gly Cys Thr Gln Gly Trp Phe Cys Ala  
305 310 315 320  
Ser Leu Phe His Pro Ala Ser Arg Asn Ile Ala Gln Leu Ala Lys Val  
325 330 335  
Lys Ile Ala Thr Arg Asn Gly Gln Trp Gln Asp Leu His Ile Pro His  
340 345 350  
Ser Ile Arg Ser Ile Val Cys Leu Asn Leu Pro Ser Phe Ser Gly Gly  
355 360 365  
Leu Asn Pro Trp Gly Thr Pro Asn Pro Arg Lys Gln Arg Asp Arg Gly  
370 375 380  
Leu Thr Pro Pro Phe Val Asp Asp Gly Leu Ile Glu Val Val Gly Phe  
385 390 395 400  
Arg Asn Ala Trp His Gly Leu Val Leu Leu Ala Pro Asn Gly His Gly  
405 410 415  
Thr Arg Leu Ala Gln Ala Asn Arg Ile Arg Phe Glu Phe His Lys Gly  
420 425 430  
Ala Thr Asp His Thr Phe Met Arg Met Asp Gly Glu Pro Trp Lys Gln  
435 440 445  
Pro Leu Pro Leu Asp Asp Glu Thr Val Met Val Glu Ile Ser His Leu  
450 455 460  
Gly Gln Val Asn Met Leu Ala Thr His Asp Cys Arg Ser Arg Ser Val  
465 470 475 480  
Phe Asp Pro Ser Thr Pro Arg His Gln Asp Gly Ala Glu Asp Tyr Asp  
485 490 495  
Asp Asn Glu Asp Ser Xaa Ala Glu Gly Glu Glu Phe Arg Lys Phe  
500 505 510  
Gly Ala Ala Asp Thr Phe Lys Ile Pro Asp Glu Val Asp Ile Ser Gln  
515 520 525  
Leu Ser  
530

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..491

(D) OTHER INFORMATION: / Ceres Seq. ID 1498618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

Met Glu Lys Tyr Asn Ser Leu Ser Asp Phe Leu Lys Glu Phe Tyr Ile  
1 5 10 15  
Pro Thr Tyr Val Leu Ser Ala Glu Thr Glu Glu Glu Glu Glu Glu  
20 25 30  
Ser Arg Pro Thr Pro Ala Ser Pro Val Leu Val Phe Ile Asn Ser Lys  
35 40 45  
Ser Gly Gly Gln Leu Gly Gly Glu Leu Ile Leu Thr Tyr Arg Ser Leu  
50 55 60  
Leu Asn His Asn Gln Val Phe Asp Leu Asp Gln Glu Thr Pro Asp Lys  
65 70 75 80  
Val Leu Arg Arg Ile Tyr Leu Asn Leu Glu Arg Leu Lys Asp Asp Asp  
85 90 95  
Ser Ala Arg Gln Ile Gly Glu Lys Leu Lys Ile Ile Val Ala Gly Gly  
100 105 110  
Asp Gly Thr Ala Gly Trp Leu Leu Gly Val Val Cys Asp Leu Lys Leu  
115 120 125  
Ser His Pro Pro Pro Ile Ala Thr Val Pro Leu Gly Thr Gly Asn Asn

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Leu Pro Phe Ala Phe Gly Trp Gly Lys Lys Asn Pro Gly Thr Asp Arg |     |     |
| 145                                                             | 150 | 155 |
| Thr Ala Val Glu Ser Phe Leu Glu Gln Val Leu Lys Ala Lys Val Met |     | 160 |
|                                                                 | 165 | 170 |
| Lys Ile Asp Asn Trp His Ile Leu Met Arg Met Lys Thr Pro Lys Glu |     | 175 |
|                                                                 | 180 | 185 |
| Gly Gly Ser Cys Asp Pro Val Ala Pro Leu Glu Leu Pro His Ser Leu |     | 190 |
|                                                                 | 195 | 200 |
| His Ala Phe His Arg Val Ser Pro Thr Asp Glu Leu Asn Lys Glu Gly |     | 205 |
|                                                                 | 210 | 215 |
| Cys His Thr Phe Arg Gly Gly Phe Trp Asn Tyr Phe Ser Leu Gly Met |     | 220 |
| 225                                                             | 230 | 235 |
| Asp Ala Gln Ile Ser Tyr Ala Phe His Ser Glu Arg Lys Leu His Pro |     | 240 |
|                                                                 | 245 | 250 |
| Glu Lys Phe Lys Asn Gln Leu Val Asn Gln Ser Thr Tyr Val Lys Leu |     | 255 |
|                                                                 | 260 | 265 |
| Gly Cys Thr Gln Gly Trp Phe Cys Ala Ser Leu Phe His Pro Ala Ser |     | 270 |
|                                                                 | 275 | 280 |
| Arg Asn Ile Ala Gln Leu Ala Lys Val Lys Ile Ala Thr Arg Asn Gly |     | 285 |
|                                                                 | 290 | 295 |
| Gln Trp Gln Asp Leu His Ile Pro His Ser Ile Arg Ser Ile Val Cys |     | 300 |
| 305                                                             | 310 | 315 |
| Leu Asn Leu Pro Ser Phe Ser Gly Gly Leu Asn Pro Trp Gly Thr Pro |     | 320 |
|                                                                 | 325 | 330 |
| Asn Pro Arg Lys Gln Arg Asp Arg Gly Leu Thr Pro Pro Phe Val Asp |     | 335 |
|                                                                 | 340 | 345 |
| Asp Gly Leu Ile Glu Val Val Gly Phe Arg Asn Ala Trp His Gly Leu |     | 350 |
|                                                                 | 355 | 360 |
| Val Leu Leu Ala Pro Asn Gly His Gly Thr Arg Leu Ala Gln Ala Asn |     | 365 |
|                                                                 | 370 | 375 |
| Arg Ile Arg Phe Glu Phe His Lys Gly Ala Thr Asp His Thr Phe Met |     | 380 |
| 385                                                             | 390 | 395 |
| Arg Met Asp Gly Glu Pro Trp Lys Gln Pro Leu Pro Leu Asp Asp Glu |     | 400 |
|                                                                 | 405 | 410 |
| Thr Val Met Val Glu Ile Ser His Leu Gly Gln Val Asn Met Leu Ala |     | 415 |
|                                                                 | 420 | 425 |
| Thr His Asp Cys Arg Ser Arg Ser Val Phe Asp Pro Ser Thr Pro Arg |     | 430 |
|                                                                 | 435 | 440 |
| His Gln Asp Gly Ala Glu Asp Tyr Asp Asp Asn Glu Asp Asp Ser Xaa |     | 445 |
|                                                                 | 450 | 455 |
| Ala Glu Gly Glu Glu Phe Arg Lys Phe Gly Ala Ala Asp Thr Phe Lys |     | 460 |
| 465                                                             | 470 | 475 |
| Ile Pro Asp Glu Val Asp Ile Ser Gln Leu Ser                     |     | 480 |
|                                                                 | 485 | 490 |

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

|                                                                 |
|-----------------------------------------------------------------|
| Met Lys Ile Asp Asn Trp His Ile Leu Met Arg Met Lys Thr Pro Lys |
| 1 5 10 15                                                       |
| Glu Gly Gly Ser Cys Asp Pro Val Ala Pro Leu Glu Leu Pro His Ser |
| 20 25 30                                                        |

Leu His Ala Phe His Arg Val Ser Pro Thr Asp Glu Leu Asn Lys Glu  
35 40 45  
Gly Cys His Thr Phe Arg Gly Gly Phe Trp Asn Tyr Phe Ser Leu Gly  
50 55 60  
Met Asp Ala Gln Ile Ser Tyr Ala Phe His Ser Glu Arg Lys Leu His  
65 70 75 80  
Pro Glu Lys Phe Lys Asn Gln Leu Val Asn Gln Ser Thr Tyr Val Lys  
85 90 95  
Leu Gly Cys Thr Gln Gly Trp Phe Cys Ala Ser Leu Phe His Pro Ala  
100 105 110  
Ser Arg Asn Ile Ala Gln Leu Ala Lys Val Lys Ile Ala Thr Arg Asn  
115 120 125  
Gly Gln Trp Gln Asp Leu His Ile Pro His Ser Ile Arg Ser Ile Val  
130 135 140  
Cys Leu Asn Leu Pro Ser Phe Ser Gly Gly Leu Asn Pro Trp Gly Thr  
145 150 155 160  
Pro Asn Pro Arg Lys Gln Arg Asp Arg Gly Leu Thr Pro Pro Phe Val  
165 170 175  
Asp Asp Gly Leu Ile Glu Val Val Gly Phe Arg Asn Ala Trp His Gly  
180 185 190  
Leu Val Leu Leu Ala Pro Asn Gly His Gly Thr Arg Leu Ala Gln Ala  
195 200 205  
Asn Arg Ile Arg Phe Glu Phe His Lys Gly Ala Thr Asp His Thr Phe  
210 215 220  
Met Arg Met Asp Gly Glu Pro Trp Lys Gln Pro Leu Pro Leu Asp Asp  
225 230 235 240  
Glu Thr Val Met Val Glu Ile Ser His Leu Gly Gln Val Asn Met Leu  
245 250 255  
Ala Thr His Asp Cys Arg Ser Arg Ser Val Phe Asp Pro Ser Thr Pro  
260 265 270  
Arg His Gln Asp Gly Ala Glu Asp Tyr Asp Asp Asn Glu Asp Asp Ser  
275 280 285  
Xaa Ala Glu Gly Glu Glu Phe Arg Lys Phe Gly Ala Ala Asp Thr Phe  
290 295 300  
Lys Ile Pro Asp Glu Val Asp Ile Ser Gln Leu Ser  
305 310 315

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..855
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

|            |              |            |             |            |             |     |
|------------|--------------|------------|-------------|------------|-------------|-----|
| aaacaaaaac | agagcaaagt   | ttttcaaaaa | aaaaaaaaaac | agagccacga | agaaattttac | 60  |
| agaaaattca | aaaccatcga   | taaagatggg | agatgtgatt  | ttgttcattg | atgatacgaa  | 120 |
| atcgaaagtg | agaatcacgc   | gttgcagaat | ttgccatgaa  | gaagaagaag | aaagtttctt  | 180 |
| cgaagttcca | tgtgcttggt   | caggcaccgt | taagttcgca  | cacagaaact | gcatacaacg  | 240 |
| ttggtgtaat | gaaaaaggaa   | acacaacttg | tgaaatctgt  | cttcaggtgt | ataaagatgg  | 300 |
| atatacagca | gtttcaaaac   | aatcgaaatt | gattgaacaa  | gaagtcacaa | tcagagttaa  | 360 |
| tggacgaaga | agaaagaaga   | gtagaagatt | agtgtctata  | gctgaatccg | atattttctca | 420 |
| gtgtaattct | gttgctgata   | gaggagcttc | gtttttgcaga | tcattaactt | ttactctttc  | 480 |
| agtatttttg | ctgatgaaac   | atacattcga | tgtgattttac | ggaaccgaag | aatatccatt  | 540 |
| ctctgtattt | acggtactaa   | cattaaaggc | cattggggata | ctattgccaa | tgtccattat  | 600 |
| aattcgaaca | atctcaacta   | ttcagaaaac | tcttcgctcg  | cgtcacatca | atcctgaatc  | 660 |
| tgaagaagaa | gataggttga   | gctctgacga | cgacgatgac  | ttggaagatg | aagatgaaga  | 720 |
| gcaacaacaa | catttggtgctt | aaaccttcca | attaacgaac  | ttaacgaaat | tttttctttc  | 780 |



tttcttttcta attcttttctt ttttaaaacg aaaagcatct atttgatgct catgggtcatt 840  
tttactcgca agtc

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Lys | Asn | Arg | Ala | Lys | Phe | Phe | Lys | Lys | Lys | Lys | Asn | Arg | Ala | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Lys | Phe | Thr | Glu | Asn | Ser | Lys | Pro | Ser | Ile | Lys | Met | Gly | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Leu | Phe | Ile | Asp | Asp | Thr | Lys | Ser | Lys | Val | Arg | Ile | Thr | Arg | Cys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Ile | Cys | His | Glu | Glu | Glu | Glu | Ser | Phe | Phe | Glu | Val | Pro | Cys |     |
|     | 50  |     |     |     |     | 55  |     |     | 60  |     |     |     |     |     |     |
| Ala | Cys | Ser | Gly | Thr | Val | Lys | Phe | Ala | His | Arg | Asn | Cys | Ile | Gln | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Trp | Cys | Asn | Glu | Lys | Gly | Asn | Thr | Thr | Cys | Glu | Ile | Cys | Leu | Gln | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Tyr | Lys | Asp | Gly | Tyr | Thr | Ala | Val | Ser | Lys | Gln | Ser | Lys | Leu | Ile | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Glu | Val | Thr | Ile | Arg | Val | Asn | Gly | Arg | Arg | Arg | Arg | Arg | Ser | Arg |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Leu | Val | Ser | Ile | Ala | Glu | Ser | Asp | Ile | Ser | Gln | Cys | Asn | Ser | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Asp | Arg | Gly | Ala | Ser | Phe | Cys | Arg | Ser | Leu | Thr | Phe | Thr | Leu | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Phe | Leu | Leu | Met | Lys | His | Thr | Phe | Asp | Val | Ile | Tyr | Gly | Thr | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Glu | Tyr | Pro | Phe | Ser | Val | Phe | Thr | Val | Leu | Thr | Leu | Lys | Ala | Ile | Gly |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Leu | Leu | Pro | Met | Ser | Ile | Ile | Ile | Arg | Thr | Ile | Ser | Thr | Ile | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Thr | Leu | Arg | Arg | Arg | His | Gln | Tyr | Pro | Glu | Ser | Glu | Glu | Glu | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Leu | Ser | Ser | Asp | Asp | Asp | Asp | Leu | Glu | Asp | Glu | Asp | Glu | Glu |     |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Gln | Gln | Gln | His | Leu | Ala |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 245 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..218
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asp | Val | Ile | Leu | Phe | Ile | Asp | Asp | Thr | Lys | Ser | Lys | Val | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Thr | Arg | Cys | Arg | Ile | Cys | His | Glu | Glu | Glu | Glu | Ser | Phe | Phe |     |

|         |                                                         |     |     |     |     |
|---------|---------------------------------------------------------|-----|-----|-----|-----|
|         | 20                                                      |     | 25  |     | 30  |
| Glu Val | Pro Cys Ala Cys Ser Gly Thr Val Lys Phe Ala His Arg Asn |     |     |     |     |
|         | 35                                                      |     | 40  |     | 45  |
| Cys Ile | Gln Arg Trp Cys Asn Glu Lys Gly Asn Thr Cys Glu Ile     |     |     |     |     |
|         | 50                                                      |     | 55  |     | 60  |
| Cys Leu | Gln Val Tyr Lys Asp Gly Tyr Thr Ala Val Ser Lys Gln Ser |     |     |     |     |
| 65      |                                                         | 70  |     | 75  | 80  |
| Lys Leu | Ile Glu Gln Glu Val Thr Ile Arg Val Asn Gly Arg Arg Arg |     |     |     |     |
|         | 85                                                      |     | 90  |     | 95  |
| Arg Arg | Ser Arg Arg Leu Val Ser Ile Ala Glu Ser Asp Ile Ser Gln |     |     |     |     |
|         | 100                                                     |     | 105 |     | 110 |
| Cys Asn | Ser Val Ala Asp Arg Gly Ala Ser Phe Cys Arg Ser Leu Thr |     |     |     |     |
|         | 115                                                     |     | 120 |     | 125 |
| Phe Thr | Leu Ser Val Phe Leu Leu Met Lys His Thr Phe Asp Val Ile |     |     |     |     |
|         | 130                                                     |     | 135 |     | 140 |
| Tyr Gly | Thr Glu Glu Tyr Pro Phe Ser Val Phe Thr Val Leu Thr Leu |     |     |     |     |
| 145     |                                                         | 150 |     | 155 | 160 |
| Lys Ala | Ile Gly Ile Leu Leu Pro Met Ser Ile Ile Ile Arg Thr Ile |     |     |     |     |
|         | 165                                                     |     | 170 |     | 175 |
| Ser Thr | Ile Gln Lys Thr Leu Arg Arg Arg His Gln Tyr Pro Glu Ser |     |     |     |     |
|         | 180                                                     |     | 185 |     | 190 |
| Glu Glu | Glu Asp Arg Leu Ser Ser Asp Asp Asp Asp Leu Glu Asp     |     |     |     |     |
|         | 195                                                     |     | 200 |     | 205 |
| Glu Asp | Glu Glu Gln Gln Gln His Leu Ala                         |     |     |     |     |
|         | 210                                                     |     | 215 |     |     |

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1589 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1589

(D) OTHER INFORMATION: / Ceres Seq. ID 1498631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

|            |             |             |             |            |             |      |
|------------|-------------|-------------|-------------|------------|-------------|------|
| cattgaagtt | aacagtcagc  | atcgttttgc  | ttgcttggtc  | gtttctctcg | aactctctcc  | 60   |
| atggctgttg | cgctccaatt  | cagccgatta  | tgcgttcgac  | cggatacttt | cgtgcgggag  | 120  |
| aatcatctct | ctggatccgg  | atctctccgc  | cgccggaaag  | ctttatcagt | ccggtgctcg  | 180  |
| tctggcgatg | agaacgctcc  | ttcgccatcg  | gtggtgatgg  | actccgattt | cgacgccaaag | 240  |
| gtgttcctga | agaacttgac  | gagaagcgat  | aattacaatc  | gtaaaggggt | cggtcataag  | 300  |
| gaggagacac | tcaagctcat  | gaatcgagag  | tacaccagtg  | atatattgga | gacactgaaa  | 360  |
| acaaatgggt | atacttattc  | ttggggagat  | gttactgtga  | aactcgctaa | agcatatggt  | 420  |
| ttttgctggg | gtgttgagcg  | tgctgttcag  | attgcatatg  | aagcacgaaa | gcagtttcca  | 480  |
| gaggagaggc | tttggtattac | taacgaaaatc | attcataaacc | cgaccgtcaa | taagagggttg | 540  |
| gaagatatgg | atgttaaaat  | tattccggtt  | gaggattcaa  | agaaacagtt | tgatgtagta  | 600  |
| gagaaagatg | atgtggttat  | ccttctctgc  | tttgagctg   | gtgttgacga | gatgtatggt  | 660  |
| cttaatgata | aaaaggtgca  | aattgttgac  | acgacttgtc  | cttgggtgac | aaaggtctgg  | 720  |
| aacacggttg | agaagcacaa  | gaagggggaa  | tacacatcag  | taatccatgg | taaatataat  | 780  |
| catgaagaga | cgattgcaac  | tgcgtctttt  | gcaggaaagt  | acatcattgt | aaagaacatg  | 840  |
| aaagaggcaa | attacgtttg  | tgattacatt  | ctcgggtggc  | aatacgatgg | atctagctcc  | 900  |
| acaaaagagg | agttcatgga  | gaaattcaaa  | tacgcaattt  | cgaagggttt | cgatcccagc  | 960  |
| aatgaccttg | tcaaagttgg  | tattgcaaac  | caaacaacga  | tgctaaagg  | agaaacagag  | 1020 |
| gagataggaa | gattactcga  | gacaacaatg  | atgcgcgaag  | atggagtgga | aaatgtaagc  | 1080 |
| ggacatttca | tcagcttcaa  | cacaatatgc  | gacgctactc  | aagagcgaca | agacgcaatc  | 1140 |
| tatgagctag | tggaagagaa  | gattgacctc  | atgctagtgg  | ttggcggatg | gaattcaagt  | 1200 |
| aacacctctc | accttcagga  | aatctcagag  | gcacggggaa  | tcccatctta | ctggatcgat  | 1260 |
| agtgagaaac | ggataggacc  | tgggaataaa  | atagcctata  | agctccacta | tggagaactg  | 1320 |
| gtcgagkaag | gaaaactttc  | tcccaaagg   | accaataaca  | atcggtgtga | catcaggtgc  | 1380 |
| atcaaccccg | gataaggtcg  | tgggaagatgc | tttggtgaag  | gtgttcgaca | ttaaactgta  | 1440 |

(2) INFORMATION FOR SEO ID NO:547:

(A) LENGTH: 444 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..444  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498632

(xi) SEQUENCE DESCRIPTION: SEO ID NO:547:

| PROTEIN SEQUENCE DESCRIPTION: SEQ ID NO: 13171 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                                            | Ala | Val | Ala | Leu | Gln | Phe | Ser | Arg | Leu | Cys | Val | Arg | Pro | Asp | Thr |  |
| 1                                              |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Phe                                            | Val | Arg | Glu | Asn | His | Leu | Ser | Gly | Ser | Gly | Ser | Leu | Arg | Arg | Arg |  |
|                                                |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys                                            | Ala | Leu | Ser | Val | Arg | Cys | Ser | Ser | Gly | Asp | Glu | Asn | Ala | Pro | Ser |  |
|                                                |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro                                            | Ser | Val | Val | Met | Asp | Ser | Asp | Phe | Asp | Ala | Lys | Val | Phe | Arg | Lys |  |
|                                                |     | 50  |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Asn                                            | Leu | Thr | Arg | Ser | Asp | Asn | Tyr | Asn | Arg | Lys | Gly | Phe | Gly | His | Lys |  |
| 65                                             |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Glu                                            | Glu | Thr | Leu | Lys | Leu | Met | Asn | Arg | Glu | Tyr | Thr | Ser | Asp | Ile | Leu |  |
|                                                |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu                                            | Thr | Leu | Lys | Thr | Asn | Gly | Tyr | Thr | Tyr | Ser | Trp | Gly | Asp | Val | Thr |  |
|                                                |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val                                            | Lys | Leu | Ala | Lys | Ala | Tyr | Gly | Phe | Cys | Trp | Gly | Val | Glu | Arg | Ala |  |
|                                                |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Val                                            | Gln | Ile | Ala | Tyr | Glu | Ala | Arg | Lys | Gln | Phe | Pro | Glu | Glu | Arg | Leu |  |
|                                                |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Trp                                            | Ile | Thr | Asn | Glu | Ile | Ile | His | Asn | Pro | Thr | Val | Asn | Lys | Arg | Leu |  |
| 145                                            |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Glu                                            | Asp | Met | Asp | Val | Lys | Ile | Ile | Pro | Val | Glu | Asp | Ser | Lys | Lys | Gln |  |
|                                                |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Phe                                            | Asp | Val | Val | Glu | Lys | Asp | Asp | Val | Val | Ile | Leu | Pro | Ala | Phe | Gly |  |
|                                                |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Ala                                            | Gly | Val | Asp | Glu | Met | Tyr | Val | Leu | Asn | Asp | Lys | Lys | Val | Gln | Ile |  |
|                                                |     |     | 195 |     |     |     | 200 |     |     |     | 205 |     |     |     |     |  |
| Val                                            | Asp | Thr | Thr | Cys | Pro | Trp | Val | Thr | Lys | Val | Trp | Asn | Thr | Val | Glu |  |
|                                                |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Lys                                            | His | Lys | Lys | Gly | Glu | Tyr | Thr | Ser | Val | Ile | His | Gly | Lys | Tyr | Asn |  |
| 225                                            |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |  |
| His                                            | Glu | Glu | Thr | Ile | Ala | Thr | Ala | Ser | Phe | Ala | Gly | Lys | Tyr | Ile | Ile |  |
|                                                |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Val                                            | Lys | Asn | Met | Lys | Glu | Ala | Asn | Tyr | Val | Cys | Asp | Tyr | Ile | Leu | Gly |  |
|                                                |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |  |
| Gly                                            | Gln | Tyr | Asp | Gly | Ser | Ser | Ser | Thr | Lys | Glu | Glu | Phe | Met | Glu | Lys |  |
|                                                |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Phe                                            | Lys | Tyr | Ala | Ile | Ser | Lys | Gly | Phe | Asp | Pro | Asp | Asn | Asp | Leu | Val |  |
|                                                |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Lys                                            | Val | Gly | Ile | Ala | Asn | Gln | Thr | Thr | Met | Leu | Lys | Gly | Glu | Thr | Glu |  |
| 305                                            |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |  |
| Glu                                            | Ile | Gly | Arg | Leu | Leu | Glu | Thr | Thr | Met | Met | Arg | Lys | Tyr | Gly | Val |  |
|                                                |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Glu                                            | Asn | Val | Ser | Gly | His |     |     |     |     |     |     |     |     |     |     |  |

Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His  
370 375 380  
Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp  
385 390 395 400  
Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His  
405 410 415  
Tyr Gly Glu Leu Val Glu Xaa Gly Lys Leu Ser Pro Lys Gly Thr Asn  
420 425 430  
Asn Asn Arg Cys Asp Ile Arg Cys Ile Asn Pro Gly  
435 440

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1498633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys Asn Leu Thr Arg  
1 5 10 15  
Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys Glu Glu Thr Leu  
20 25 30  
Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu Glu Thr Leu Lys  
35 40 45  
Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr Val Lys Leu Ala  
50 55 60  
Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala Val Gln Ile Ala  
65 70 75 80  
Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu Trp Ile Thr Asn  
85 90 95  
Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu Glu Asp Met Asp  
100 105 110  
Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln Phe Asp Val Val  
115 120 125  
Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly Ala Gly Val Asp  
130 135 140  
Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile Val Asp Thr Thr  
145 150 155 160  
Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu Lys His Lys Lys  
165 170 175  
Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn His Glu Glu Thr  
180 185 190  
Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile Val Lys Asn Met  
195 200 205  
Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly Gly Gln Tyr Asp  
210 215 220  
Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys Phe Lys Tyr Ala  
225 230 235 240  
Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val Lys Val Gly Ile  
245 250 255  
Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu Glu Ile Gly Arg  
260 265 270  
Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val Glu Asn Val Ser  
275 280 285  
Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala Thr Gln Glu Arg  
290 295 300  
Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile Asp Leu Met Leu

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(2) INFORMATION FOR SEQ ID NO:549:

(A) LENGTH: 358 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(A) NAME

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:549:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |     |     |
| Gly | Tyr | Thr | Tyr | Ser | Trp | Gly | Asp | Val | Thr | Val | Lys | Leu | Ala | Lys | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Gly | Phe | Cys | Trp | Gly | Val | Glu | Arg | Ala | Val | Gln | Ile | Ala | Tyr | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ala | Arg | Lys | Gln | Phe | Pro | Glu | Glu | Arg | Leu | Trp | Ile | Thr | Asn | Glu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | His | Asn | Pro | Thr | Val | Asn | Lys | Arg | Leu | Glu | Asp | Met | Asp | Val | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ile | Pro | Val | Glu | Asp | Ser | Lys | Lys | Gln | Phe | Asp | Val | Val | Glu | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Asp | Val | Val | Ile | Leu | Pro | Ala | Phe | Gly | Ala | Gly | Val | Asp | Glu | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Val | Leu | Asn | Asp | Lys | Lys | Val | Gln | Ile | Val | Asp | Thr | Thr | Cys | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Trp | Val | Thr | Lys | Val | Trp | Asn | Thr | Val | Glu | Lys | His | Lys | Lys | Gly | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Tyr | Thr | Ser | Val | Ile | His | Gly | Lys | Tyr | Asn | His | Glu | Glu | Thr | Ile | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Ala | Ser | Phe | Ala | Gly | Lys | Tyr | Ile | Ile | Val | Lys | Asn | Met | Lys | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Asn | Tyr | Val | Cys | Asp | Tyr | Ile | Leu | Gly | Gly | Gln | Tyr | Asp | Gly | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ser | Thr | Lys | Glu | Glu | Phe | Met | Glu | Lys | Phe | Lys | Tyr | Ala | Ile | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Gly | Phe | Asp | Pro | Asp | Asn | Asp | Leu | Val | Lys | Val | Gly | Ile | Ala | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Thr | Thr | Met | Leu | Lys | Gly | Glu | Thr | Glu | Glu | Ile | Gly | Arg | Leu | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Thr | Thr | Met | Met | Arg | Lys | Tyr | Gly | Val | Glu | Asn | Val | Ser | Gly | His |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Ile | Ser | Phe | Asn | Thr | Ile | Cys | Asp | Ala | Thr | Gln | Glu | Arg | Gln | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Ile | Tyr | Glu | Leu | Val | Glu | Glu | Lys | Ile | Asp | Leu | Met | Leu | Val | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Gly | Trp | Asn | Ser | Ser | Asn | Thr | Ser | His | Leu | Gln | Glu | Ile | Ser | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp Ser Glu Lys Arg Ile Gly  
305 310 315 320  
Pro Gly Asn Lys Ile Ala Tyr Lys Leu His Tyr Gly Glu Leu Val Glu  
325 330 335  
Xaa Gly Lys Leu Ser Pro Lys Gly Thr Asn Asn Asn Arg Cys Asp Ile  
340 345 350  
Arg Cys Ile Asn Pro Gly  
355

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

acatcaaagc aattaacaaa tacacaactt gtaacttcaa atagattact ttcaaagaag 60  
agagagagaa agaaagatgg agaagaacat gaagtttcca gtagtagact tgtccaagct 120  
caatggggaa gagagagacc aaacatggc tctaatacat gaagcttggtg agaattgggg 180  
cttctttgag atagtgaacc atggattacc acatgactta atggacaaga tcgagaagat 240  
gacaaaggac cattacaaga catgccaaaga acaaaaagttc aatgacatgc tcaagtccaa 300  
aggtttggat aatcttgaga cagaagtcga agatgtcgat tgggaaagca ctttctacgt 360  
tcgtcacctc cctcaatcca atctcaatga catttcagat gtgtctgatg aatacgacgg 420  
ccatgaaaga ctttggttaag agactggaga atcttgctga ggatttggtg gatctactgt 480  
gtgagaatct aggggttagag aaagggtatt tgaagaaagt gtttcatgga acaaaaaggcc 540  
caacctttgg gacaaagggtg agcaattatc caccatgtcc taaaccagag atgatcaaag 600  
gtcttagggc ccacactgat gcaggaggca tcatcttggt gtttcaagac gacaagggtca 660  
gtggtctcca gcttcttaaa gatggtgact ggattgatgt tcctcctctc aaccactcta 720  
ttgtcatcaa tcttggtgac caacttgagg tgataaccaa cgggaagtat aagagtgtgc 780  
tgcaccgtgt ggtgactcaa caagaaggaa acaggatgtc ggttgcacgc ttttacaacc 840  
cgggaagcga tgcggagatc tcaccagcta cttcgcttgc cgagaaagat tccgagtacc 900  
cgagtttcgt ctttgatgac tacatgaagc tttatgcagg ggtcaagttt cagcccaagg 960  
agccacggtt cgcagcaatg aagaatgctt ctgcagttac agaactgaat cctacagcag 1020  
ccgtagagac tttctaaaaa tggatttgag attcaagtga agcagagaaa gaamsmtgag 1080  
tttggtgtgt gtgttatggc aataagttaa aacttgtatt agtggtgatt aattggtggt 1140  
caattggtgt gttttaaagt gtggggtgtt tatgtttatg gaagatgata ataattataa 1200  
aaatctaaat tct

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

Met Thr Cys Ser Ser Pro Lys Val Trp Ile Ile Leu Arg Gln Lys Ser  
1 5 10 15  
Lys Met Ser Ile Gly Lys Ala Leu Ser Thr Phe Val Thr Ser Leu Asn  
20 25 30  
Pro Ile Ser Met Thr Phe Gln Met Cys Leu Met Asn Thr Thr Ala Met  
35 40 45  
Lys Asp Phe Gly Lys Arg Leu Glu Asn Leu Ala Glu Asp Leu Leu Asp  
50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Cys | Glu | Asn | Leu | Gly | Leu | Glu | Lys | Gly | Tyr | Leu | Lys | Lys | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | His | Gly | Thr | Lys | Gly | Pro | Thr | Phe | Gly | Thr | Lys | Val | Ser | Asn | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Pro | Cys | Pro | Lys | Pro | Glu | Met | Ile | Lys | Gly | Leu | Arg | Ala | His | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Ala | Gly | Gly | Ile | Ile | Leu | Leu | Phe | Gln | Asp | Asp | Lys | Val | Ser | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Gln | Leu | Leu | Lys | Asp | Gly | Asp | Trp | Ile | Asp | Val | Pro | Pro | Leu | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Ser | Ile | Val | Ile | Asn | Leu | Gly | Asp | Gln | Leu | Glu | Val | Ile | Thr | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Lys | Tyr | Lys | Ser | Val | Leu | His | Arg | Val | Val | Thr | Gln | Gln | Glu | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Arg | Met | Ser | Val | Ala | Ser | Phe | Tyr | Asn | Pro | Gly | Ser | Asp | Ala | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Ser | Pro | Ala | Thr | Ser | Leu | Val | Glu | Lys | Asp | Ser | Glu | Tyr | Pro | Ser |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Phe | Val | Phe | Asp | Asp | Tyr | Met | Lys | Leu | Tyr | Ala | Gly | Val | Lys | Phe | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Lys | Glu | Pro | Arg | Phe | Ala | Ala | Met | Lys | Asn | Ala | Ser | Ala | Val | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Leu | Asn | Pro | Thr | Ala | Ala | Val | Glu | Thr | Phe |     |     |     |     |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ile | Gly | Lys | Ala | Leu | Ser | Thr | Phe | Val | Thr | Ser | Leu | Asn | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Ser | Met | Thr | Phe | Gln | Met | Cys | Leu | Met | Asn | Thr | Thr | Ala | Met | Lys |
|     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| Asp | Phe | Gly | Lys | Arg | Leu | Glu | Asn | Leu | Ala | Glu | Asp | Leu | Leu | Asp | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Cys | Glu | Asn | Leu | Gly | Leu | Glu | Lys | Gly | Tyr | Leu | Lys | Lys | Val | Phe |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| His | Gly | Thr | Lys | Gly | Pro | Thr | Phe | Gly | Thr | Lys | Val | Ser | Asn | Tyr | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Cys | Pro | Lys | Pro | Glu | Met | Ile | Lys | Gly | Leu | Arg | Ala | His | Thr | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Gly | Gly | Ile | Ile | Leu | Leu | Phe | Gln | Asp | Asp | Lys | Val | Ser | Gly | Leu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Gln | Leu | Leu | Lys | Asp | Gly | Asp | Trp | Ile | Asp | Val | Pro | Pro | Leu | Asn | His |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ser | Ile | Val | Ile | Asn | Leu | Gly | Asp | Gln | Leu | Glu | Val | Ile | Thr | Asn | Gly |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Lys | Tyr | Lys | Ser | Val | Leu | His | Arg | Val | Val | Thr | Gln | Gln | Glu | Gly | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Met | Ser | Val | Ala | Ser | Phe | Tyr | Asn | Pro | Gly | Ser | Asp | Ala | Glu | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ser | Pro | Ala | Thr | Ser | Leu | Val | Glu | Lys | Asp | Ser | Glu | Tyr | Pro | Ser | Phe |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Val | Phe | Asp | Asp | Tyr | Met | Lys | Leu | Tyr | Ala | Gly | Val | Lys | Phe | Gln | Pro |

195 200 205  
Lys Glu Pro Arg Phe Ala Ala Met Lys Asn Ala Ser Ala Val Thr Glu  
210 215 220  
Leu Asn Pro Thr Ala Ala Val Glu Thr Phe  
225 230

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1498638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

Met Thr Phe Gln Met Cys Leu Met Asn Thr Thr Ala Met Lys Asp Phe  
1 5 10 15  
Gly Lys Arg Leu Glu Asn Leu Ala Glu Asp Leu Leu Asp Leu Leu Cys  
20 25 30  
Glu Asn Leu Gly Leu Glu Lys Gly Tyr Leu Lys Lys Val Phe His Gly  
35 40 45  
Thr Lys Gly Pro Thr Phe Gly Thr Lys Val Ser Asn Tyr Pro Pro Cys  
50 55 60  
Pro Lys Pro Glu Met Ile Lys Gly Leu Arg Ala His Thr Asp Ala Gly  
65 70 75 80  
Gly Ile Ile Leu Leu Phe Gln Asp Asp Lys Val Ser Gly Leu Gln Leu  
85 90 95  
Leu Lys Asp Gly Asp Trp Ile Asp Val Pro Pro Leu Asn His Ser Ile  
100 105 110  
Val Ile Asn Leu Gly Asp Gln Leu Glu Val Ile Thr Asn Gly Lys Tyr  
115 120 125  
Lys Ser Val Leu His Arg Val Val Thr Gln Gln Glu Gly Asn Arg Met  
130 135 140  
Ser Val Ala Ser Phe Tyr Asn Pro Gly Ser Asp Ala Glu Ile Ser Pro  
145 150 155 160  
Ala Thr Ser Leu Val Glu Lys Asp Ser Glu Tyr Pro Ser Phe Val Phe  
165 170 175  
Asp Asp Tyr Met Lys Leu Tyr Ala Gly Val Lys Phe Gln Pro Lys Glu  
180 185 190  
Pro Arg Phe Ala Ala Met Lys Asn Ala Ser Ala Val Thr Glu Leu Asn  
195 200 205  
Pro Thr Ala Ala Val Glu Thr Phe  
210 215

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1065

(D) OTHER INFORMATION: / Ceres Seq. ID 1498639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| acttaaccga | raaagcaaaa | gagaagaaga | agaaggaatc | gaaaaatgaa | gactccgatac | 60  |
| cacgcggttt | cgacatgggt | gaggaggcag | cctccaaagg | tgaaagcttt | ccttgccgctc | 120 |
| gtatctggca | tgccggctct | tggtctctc  | aaactcatcg | ttcacgatca | cgacaatctc  | 180 |
| ttcgttgccg | ccgaagctgt | tcattctatt | ggaatctctg | ttcttatsta | taaactcatg  | 240 |



aaggagaaga cttgtgctgg attgtcattg aaatctcagg agcttacggc gatattttcta 300  
gctgtgagggc tttattgcag ttttgtaatg gaatatgata tacataccat tctggacttg 360  
gctacttttg gaacaaactct ctgggttata tatatgatcc gttttaacct caaagctact 420  
tacatggagg aaaaagacaa cttcgctctc tattatgtgc tggcgccctg tgttgtgcta 480  
gctgtatgga ttcattccatc aacgtcacac aatatattga atagaatatc ctggggattc 540  
tgtgtttacc tcgaagctgt ttcagtactg ccacagttga gagtgatgca gaacacaaaag 600  
attgtcgaac ccttcacggc tcattatgtt tttgcacttg gagtagcaag atttttttagc 660  
tgtgcacact ggggtttaca gatgatggac acgcacggac gactgcttgt agtgctgggt 720  
tatggactat ggccatcgat ggttataatc tcagaaatag tccaagcatt catattggca 780  
gatttctgtt actactacgt taaaagtgtt ttcgggtggcc agcttgttct aaggcttcca 840  
tctgggggtg tgtaagttat aaaggaaaaa agataagaca cattatgacg aaatttggtta 900  
cacgaagata gatctcagct tgggtgtaatc tgagtagcct ctgggttactc tcaagttact 960  
ccctcaggcc aagtcctaata tctattaact gtgttgata tttttgtgtg ggtcatcatc 1020  
atagacagtc ccttggaatg tattgacatg atttttyca ctgcc

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..269
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

Met Lys Thr Pro Ile His Ala Val Ser Thr Trp Val Arg Arg Gln Pro  
1 5 10 15  
Pro Lys Val Lys Ala Phe Leu Ala Val Val Ser Gly Met Ala Ala Leu  
20 25 30  
Val Leu Leu Lys Leu Ile Val His Asp His Asp Asn Leu Phe Val Ala  
35 40 45  
Ala Glu Ala Val His Ser Ile Gly Ile Ser Val Leu Xaa Tyr Lys Leu  
50 55 60  
Met Lys Glu Lys Thr Cys Ala Gly Leu Ser Leu Lys Ser Gln Glu Leu  
65 70 75 80  
Thr Ala Ile Phe Leu Ala Val Arg Leu Tyr Cys Ser Phe Val Met Glu  
85 90 95  
Tyr Asp Ile His Thr Ile Leu Asp Leu Ala Thr Leu Gly Thr Thr Leu  
100 105 110  
Trp Val Ile Tyr Met Ile Arg Phe Asn Leu Lys Ala Thr Tyr Met Glu  
115 120 125  
Glu Lys Asp Asn Phe Ala Leu Tyr Tyr Val Leu Ala Pro Cys Val Val  
130 135 140  
Leu Ala Val Trp Ile His Pro Ser Thr Ser His Asn Ile Leu Asn Arg  
145 150 155 160  
Ile Ser Trp Gly Phe Cys Val Tyr Leu Glu Ala Val Ser Val Leu Pro  
165 170 175  
Gln Leu Arg Val Met Gln Asn Thr Lys Ile Val Glu Pro Phe Thr Ala  
180 185 190  
His Tyr Val Phe Ala Leu Gly Val Ala Arg Phe Phe Ser Cys Ala His  
195 200 205  
Trp Val Leu Gln Met Met Asp Thr His Gly Arg Leu Leu Val Val Leu  
210 215 220  
Gly Tyr Gly Leu Trp Pro Ser Met Val Ile Ile Ser Glu Ile Val Gln  
225 230 235 240  
Ala Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val Lys Ser Val Phe  
245 250 255  
Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val Val  
260 265

(2) INFORMATION FOR SEQ ID NO:556:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 241 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..241  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498641  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

Met Ala Ala Leu Val Leu Leu Lys Leu Ile Val His Asp His Asp Asn  
1                  5                  10                  15  
Leu Phe Val Ala Ala Glu Ala Val His Ser Ile Gly Ile Ser Val Leu  
                  20                  25                  30  
Xaa Tyr Lys Leu Met Lys Glu Lys Thr Cys Ala Gly Leu Ser Leu Lys  
                  35                  40                  45  
Ser Gln Glu Leu Thr Ala Ile Phe Leu Ala Val Arg Leu Tyr Cys Ser  
                  50                  55                  60  
Phe Val Met Glu Tyr Asp Ile His Thr Ile Leu Asp Leu Ala Thr Leu  
65                  70                  75                  80  
Gly Thr Thr Leu Trp Val Ile Tyr Met Ile Arg Phe Asn Leu Lys Ala  
                  85                  90                  95  
Thr Tyr Met Glu Glu Lys Asp Asn Phe Ala Leu Tyr Tyr Val Leu Ala  
                  100                  105                  110  
Pro Cys Val Val Leu Ala Val Trp Ile His Pro Ser Thr Ser His Asn  
                  115                  120                  125  
Ile Leu Asn Arg Ile Ser Trp Gly Phe Cys Val Tyr Leu Glu Ala Val  
                  130                  135                  140  
Ser Val Leu Pro Gln Leu Arg Val Met Gln Asn Thr Lys Ile Val Glu  
145                  150                  155                  160  
Pro Phe Thr Ala His Tyr Val Phe Ala Leu Gly Val Ala Arg Phe Phe  
                  165                  170                  175  
Ser Cys Ala His Trp Val Leu Gln Met Met Asp Thr His Gly Arg Leu  
                  180                  185                  190  
Leu Val Val Leu Gly Tyr Gly Leu Trp Pro Ser Met Val Ile Ile Ser  
                  195                  200                  205  
Glu Ile Val Gln Ala Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val  
210                  215                  220  
Lys Ser Val Phe Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val  
225                  230                  235                  240  
Val

- (2) INFORMATION FOR SEQ ID NO:557:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 205 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..205  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498642  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

Met Lys Glu Lys Thr Cys Ala Gly Leu Ser Leu Lys Ser Gln Glu Leu  
1                  5                  10                  15  
Thr Ala Ile Phe Leu Ala Val Arg Leu Tyr Cys Ser Phe Val Met Glu  
                  20                  25                  30  
Tyr Asp Ile His Thr Ile Leu Asp Leu Ala Thr Leu Gly Thr Thr Leu  
                  35                  40                  45

Trp Val Ile Tyr Met Ile Arg Phe Asn Leu Lys Ala Thr Tyr Met Glu  
50 55 60  
Glu Lys Asp Asn Phe Ala Leu Tyr Tyr Val Leu Ala Pro Cys Val Val  
65 70 75 80  
Leu Ala Val Trp Ile His Pro Ser Thr Ser His Asn Ile Leu Asn Arg  
85 90 95  
Ile Ser Trp Gly Phe Cys Val Tyr Leu Glu Ala Val Ser Val Leu Pro  
100 105 110  
Gln Leu Arg Val Met Gln Asn Thr Lys Ile Val Glu Pro Phe Thr Ala  
115 120 125  
His Tyr Val Phe Ala Leu Gly Val Ala Arg Phe Phe Ser Cys Ala His  
130 135 140  
Trp Val Leu Gln Met Met Asp Thr His Gly Arg Leu Leu Val Val Leu  
145 150 155 160  
Gly Tyr Gly Leu Trp Pro Ser Met Val Ile Ile Ser Glu Ile Val Gln  
165 170 175  
Ala Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val Lys Ser Val Phe  
180 185 190  
Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val Val  
195 200 205

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..772
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| agcgaaaatc ccaaacaaaa aaataaaaaga atggcgctctc tgtgcctttc tctccaccaa | 60  |
| accctaacta atccccctgtc ggctcccaga tgcagaccac tcagcctctc cttccccgga  | 120 |
| tcctcaacct tctcgatccg cccctctagc agacgcgcaa ccgccttgac gaccgcgcc    | 180 |
| tcctacaccc cgacgccggc gactgagcgc gtgatttcga tagcgtcgta cgcgctgccg   | 240 |
| ttcttcaatt ctctgcagta cgggcgggttc ctgttcgcgc agtacccaag gctgggattg  | 300 |
| ctgttcgagc caatcttccc aatcctgaac ctgtacagat cggtgccgta cgcgagcttc   | 360 |
| gtggcattct tcgggctgta cctgggagtg gtgaggaaca cgagtttcag taggtacgtg   | 420 |
| aggttcaacg cgatgcaggc ggtgacgctg gatgtgctcc tggcgggttc ggtgctgctg   | 480 |
| accggaatac tggatccggg tcaaggaggc gggtttgaa tgaaggcgat gatgtggggg    | 540 |
| cacacggggg ttttcgtctt cagctttatg tgttttgtgt atggagtcgt cagctcctta   | 600 |
| ctcggcaaaa ctccatacat tccatttgtc gctgatgccg ccggtagaca actctaattc   | 660 |
| cggccaatat ctacctcaact cagtgttcgg gttttcgatt ctagaatcgg ttattttctgg | 720 |
| tttataagag agaccaaatc aatcagtgtt gtttaattaac cattaccgtt tc          |     |

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..218
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ser Glu Asn Pro Lys Gln Lys Asn Lys Arg Met Ala Ser Leu Cys Leu |  |
| 1 5 10 15                                                       |  |
| Ser Leu His Gln Thr Leu Thr Asn Pro Leu Ser Ala Pro Arg Cys Arg |  |
| 20 25 30                                                        |  |

Pro Leu Ser Leu Ser Phe Pro Gly Ser Ser Thr Phe Ser Ile Arg Pro  
35 40 45  
Ser Ser Arg Arg Ala Thr Ala Leu Thr Thr Arg Ala Ser Tyr Thr Pro  
50 55 60  
Thr Pro Ala Thr Glu Arg Val Ile Ser Ile Ala Ser Tyr Ala Leu Pro  
65 70 75 80  
Phe Phe Asn Ser Leu Gln Tyr Gly Arg Phe Leu Phe Ala Gln Tyr Pro  
85 90 95  
Arg Leu Gly Leu Leu Phe Glu Pro Ile Phe Pro Ile Leu Asn Leu Tyr  
100 105 110  
Arg Ser Val Pro Tyr Ala Ser Phe Val Ala Phe Phe Gly Leu Tyr Leu  
115 120 125  
Gly Val Val Arg Asn Thr Ser Phe Ser Arg Tyr Val Arg Phe Asn Ala  
130 135 140  
Met Gln Ala Val Thr Leu Asp Val Leu Leu Ala Val Pro Val Leu Leu  
145 150 155 160  
Thr Arg Ile Leu Asp Pro Gly Gln Gly Gly Phe Gly Met Lys Ala  
165 170 175  
Met Met Trp Gly His Thr Gly Val Phe Val Phe Ser Phe Met Cys Phe  
180 185 190  
Val Tyr Gly Val Val Ser Ser Leu Gly Lys Thr Pro Tyr Ile Pro  
195 200 205  
Phe Val Ala Asp Ala Ala Gly Arg Gln Leu  
210 215

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1498645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

Met Ala Ser Leu Cys Leu Ser Leu His Gln Thr Leu Thr Asn Pro Leu  
1 5 10 15  
Ser Ala Pro Arg Cys Arg Pro Leu Ser Leu Ser Phe Pro Gly Ser Ser  
20 25 30  
Thr Phe Ser Ile Arg Pro Ser Ser Arg Arg Ala Thr Ala Leu Thr Thr  
35 40 45  
Arg Ala Ser Tyr Thr Pro Thr Pro Ala Thr Glu Arg Val Ile Ser Ile  
50 55 60  
Ala Ser Tyr Ala Leu Pro Phe Phe Asn Ser Leu Gln Tyr Gly Arg Phe  
65 70 75 80  
Leu Phe Ala Gln Tyr Pro Arg Leu Gly Leu Leu Phe Glu Pro Ile Phe  
85 90 95  
Pro Ile Leu Asn Leu Tyr Arg Ser Val Pro Tyr Ala Ser Phe Val Ala  
100 105 110  
Phe Phe Gly Leu Tyr Leu Gly Val Val Arg Asn Thr Ser Phe Ser Arg  
115 120 125  
Tyr Val Arg Phe Asn Ala Met Gln Ala Val Thr Leu Asp Val Leu Leu  
130 135 140  
Ala Val Pro Val Leu Leu Thr Arg Ile Leu Asp Pro Gly Gln Gly Gly  
145 150 155 160  
Gly Phe Gly Met Lys Ala Met Met Trp Gly His Thr Gly Val Phe Val  
165 170 175  
Phe Ser Phe Met Cys Phe Val Tyr Gly Val Val Ser Ser Leu Gly  
180 185 190  
Lys Thr Pro Tyr Ile Pro Phe Val Ala Asp Ala Ala Gly Arg Gln Leu

195

200

205

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1645
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| amcaaaaaaa  | aaaaagaaaa  | aaggagataa  | taatcacaaa  | ctacaaaagt  | agaaagaaga  | 60   |
| aaaaagaaca  | aagtatcagt  | tcttgaatat  | ttgcatcaat  | ggaggaatcc  | aaaacacctc  | 120  |
| acgttgcgat  | cataccaagt  | cgggaatgg   | gtcatctcat  | accactcgtc  | gagtttgcta  | 180  |
| aacgactcgt  | ccatcttcac  | ggcctcaccg  | ttaccttcgt  | catcgccggc  | gaaggtccac  | 240  |
| catcaaaaagc | tcagagaacc  | gtcctcgact  | ctctcccttc  | ttcaatctcc  | tccgtctttc  | 300  |
| tccctcctgt  | tgatctcacc  | gatctctctt  | cgtccactcg  | catcgaatct  | cggatctccc  | 360  |
| tcaccgtgac  | tcgttcaaac  | cggagctcc   | ggaaagtctt  | cgactcgttc  | gtggaggagg  | 420  |
| gtcgtttgcc  | aacggcgctc  | gtcgtcgatc  | tcttcggtac  | ggacgctttc  | gacgtggccg  | 480  |
| tagaatttca  | cgtgccaccg  | tatatcttct  | acccaacaac  | ggccaacgct  | ttgtcgtttt  | 540  |
| ttctccattt  | gcctaaacta  | kacgaaacgg  | tgctcgtgta  | gttcagggaa  | ttaaccgaac  | 600  |
| cgtttatgct  | tcctggatgt  | gtaccgggtg  | ccgggaaaga  | tttccttgac  | ccggcccaag  | 660  |
| accggaaaga  | cgatgcatac  | aaatggcttc  | tccataacac  | caagaggtac  | aaagaagccg  | 720  |
| aagggtattct | tgtgaatacc  | ttctttgagc  | tagagccaaa  | tgctataaag  | gccttgcaag  | 780  |
| aaaccgggtct | tgataaacca  | ccggtttatc  | cggttgacc   | gttggttaac  | attggttaagc | 840  |
| aagaggctaa  | gcaaaccgaa  | gagctctgaat | gtttaaagtg  | gttgataaac  | cagccgctcg  | 900  |
| gttcggtttt  | atatgtgtcc  | tttggtagtg  | gcgggtaccct | cacatgtgag  | cagctcaatg  | 960  |
| agcttgctct  | tggtcttgca  | gatagtgagc  | aacggtttct  | ttgggtcata  | cgaagtccta  | 1020 |
| gtgggatcgc  | taattcgtcg  | tattttgatt  | cacatagcca  | aacagatcca  | ttgacatttt  | 1080 |
| taccaccggg  | atttttagag  | cggactaaaa  | aaagagggtt  | tgtgatccct  | ttttgggctc  | 1140 |
| cacaagccca  | agtcttggcg  | catccatcca  | cgggaggatt  | tttaactcat  | tgtggatgga  | 1200 |
| attcgactct  | agagagtgtg  | gtaagcggta  | ttccacttat  | agcatggcca  | ttatacgtag  | 1260 |
| aacagaagat  | gaatgcgggt  | ttgttgagtg  | aagatattcg  | tgccggcactt | aggccgcgtg  | 1320 |
| ccggggacga  | tgggttagtt  | agaagagaag  | aggtggctag  | agtggtaaaa  | ggattgatgg  | 1380 |
| aagggtgaaga | aggcaaagga  | gtgaggaaca  | agatgaagga  | gttgaaggaa  | gcagcttgta  | 1440 |
| gggtgttgaa  | ggatgatggg  | acttcgacaa  | aagcacttag  | tcttgtggcc  | ttaaagtgga  | 1500 |
| aagcccacaa  | aaaagagtta  | gagcaaaatg  | gcaaccacta  | aatatttgat  | gttctaatat  | 1560 |
| gatttgtata  | atcaacgggtg | ggatttgtgc  | aaatgtgttt  | ctgtatgtat  | atgtatgttc  | 1620 |
| tacttttctt  | tgcttcggtt  | gtctc       |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..480
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Ser | Lys | Thr | Pro | His | Val | Ala | Ile | Ile | Pro | Ser | Pro | Gly |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Met | Gly | His | Leu | Ile | Pro | Leu | Val | Glu | Phe | Ala | Lys | Arg | Leu | Val | His |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Leu | His | Gly | Leu | Thr | Val | Thr | Phe | Val | Ile | Ala | Gly | Glu | Gly | Pro | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Ala | Gln | Arg | Thr | Val | Leu | Asp | Ser | Leu | Pro | Ser | Ser | Ile | Ser |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Val | Phe | Leu | Pro | Pro | Val | Asp | Leu | Thr | Asp | Leu | Ser | Ser | Ser | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Ile | Glu | Ser | Arg | Ile | Ser | Leu | Thr | Val | Thr | Arg | Ser | Asn | Pro | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Arg | Lys | Val | Phe | Asp | Ser | Phe | Val | Glu | Gly | Gly | Arg | Leu | Pro | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Val | Val | Asp | Leu | Phe | Gly | Thr | Asp | Ala | Phe | Asp | Val | Ala | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Phe | His | Val | Pro | Pro | Tyr | Ile | Phe | Tyr | Pro | Thr | Thr | Ala | Asn | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ser | Phe | Phe | Leu | His | Leu | Pro | Lys | Leu | Xaa | Glu | Thr | Val | Ser | Cys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Phe | Arg | Glu | Leu | Thr | Glu | Pro | Leu | Met | Leu | Pro | Gly | Cys | Val | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ala | Gly | Lys | Asp | Phe | Leu | Asp | Pro | Ala | Gln | Asp | Arg | Lys | Asp | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Tyr | Lys | Trp | Leu | Leu | His | Asn | Thr | Lys | Arg | Tyr | Lys | Glu | Ala | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Ile | Leu | Val | Asn | Thr | Phe | Glu | Leu | Glu | Pro | Asn | Ala | Ile | Lys |     |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Ala | Leu | Gln | Glu | Pro | Gly | Leu | Asp | Lys | Pro | Pro | Val | Tyr | Pro | Val | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Leu | Val | Asn | Ile | Gly | Lys | Gln | Glu | Ala | Lys | Gln | Thr | Glu | Glu | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Cys | Leu | Lys | Trp | Leu | Asp | Asn | Gln | Pro | Leu | Gly | Ser | Val | Leu | Tyr |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Val | Ser | Phe | Gly | Ser | Gly | Gly | Thr | Leu | Thr | Cys | Glu | Gln | Leu | Asn | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Ala | Leu | Gly | Leu | Ala | Asp | Ser | Glu | Gln | Arg | Phe | Leu | Trp | Val | Ile |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Ser | Pro | Ser | Gly | Ile | Ala | Asn | Ser | Ser | Tyr | Phe | Asp | Ser | His | Ser |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gln | Thr | Asp | Pro | Leu | Thr | Phe | Leu | Pro | Pro | Gly | Phe | Leu | Glu | Arg | Thr |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Lys | Arg | Gly | Phe | Val | Ile | Pro | Phe | Trp | Ala | Pro | Gln | Ala | Gln | Val |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Ala | His | Pro | Ser | Thr | Gly | Gly | Phe | Leu | Thr | His | Cys | Gly | Trp | Asn |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Thr | Leu | Glu | Ser | Val | Val | Ser | Gly | Ile | Pro | Leu | Ile | Ala | Trp | Pro |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Leu | Tyr | Ala | Glu | Gln | Lys | Met | Asn | Ala | Val | Leu | Leu | Ser | Glu | Asp | Ile |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Arg | Ala | Ala | Leu | Arg | Pro | Arg | Ala | Gly | Asp | Asp | Gly | Leu | Val | Arg | Arg |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Glu | Glu | Val | Ala | Arg | Val | Val | Lys | Gly | Leu | Met | Glu | Gly | Glu | Glu | Gly |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Lys | Gly | Val | Arg | Asn | Lys | Met | Lys | Glu | Leu | Lys | Glu | Ala | Ala | Cys | Arg |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Val | Leu | Lys | Asp | Asp | Gly | Thr | Ser | Thr | Lys | Ala | Leu | Ser | Leu | Val | Ala |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Leu | Lys | Trp | Lys | Ala | His | Lys | Lys | Glu | Leu | Glu | Gln | Asn | Gly | Asn | His |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..464  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498648  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | His | Leu | Ile | Pro | Leu | Val | Glu | Phe | Ala | Lys | Arg | Leu | Val | His |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | His | Gly | Leu | Thr | Val | Thr | Phe | Val | Ile | Ala | Gly | Glu | Gly | Pro | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Lys | Ala | Gln | Arg | Thr | Val | Leu | Asp | Ser | Leu | Pro | Ser | Ser | Ile | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Val | Phe | Leu | Pro | Pro | Val | Asp | Leu | Thr | Asp | Leu | Ser | Ser | Ser | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Ile | Glu | Ser | Arg | Ile | Ser | Leu | Thr | Val | Thr | Arg | Ser | Asn | Pro | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Arg | Lys | Val | Phe | Asp | Ser | Phe | Val | Glu | Gly | Gly | Arg | Leu | Pro | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Leu | Val | Val | Asp | Leu | Phe | Gly | Thr | Asp | Ala | Phe | Asp | Val | Ala | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Glu | Phe | His | Val | Pro | Pro | Tyr | Ile | Phe | Tyr | Pro | Thr | Thr | Ala | Asn | Val |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Phe | Phe | Leu | His | Leu | Pro | Lys | Leu | Xaa | Glu | Thr | Val | Ser | Cys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Phe | Arg | Glu | Leu | Thr | Glu | Pro | Leu | Met | Leu | Pro | Gly | Cys | Val | Pro |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Val | Ala | Gly | Lys | Asp | Phe | Leu | Asp | Pro | Ala | Gln | Asp | Arg | Lys | Asp | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ala | Tyr | Lys | Trp | Leu | Leu | His | Asn | Thr | Lys | Arg | Tyr | Lys | Glu | Ala | Glu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Gly | Ile | Leu | Val | Asn | Thr | Phe | Phe | Glu | Leu | Glu | Pro | Asn | Ala | Ile | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ala | Leu | Gln | Glu | Pro | Gly | Leu | Asp | Lys | Pro | Pro | Val | Tyr | Pro | Val | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Leu | Val | Asn | Ile | Gly | Lys | Gln | Glu | Ala | Lys | Gln | Thr | Glu | Glu | Ser |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Glu | Cys | Leu | Lys | Trp | Leu | Asp | Asn | Gln | Pro | Leu | Gly | Ser | Val | Leu | Tyr |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Val | Ser | Phe | Gly | Ser | Gly | Gly | Thr | Leu | Thr | Cys | Glu | Gln | Leu | Asn | Glu |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Leu | Ala | Leu | Gly | Leu | Ala | Asp | Ser | Glu | Gln | Arg | Phe | Leu | Trp | Val | Ile |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Arg | Ser | Pro | Ser | Gly | Ile | Ala | Asn | Ser | Ser | Tyr | Phe | Asp | Ser | His | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Gln | Thr | Asp | Pro | Leu | Thr | Phe | Leu | Pro | Pro | Gly | Phe | Leu | Glu | Arg | Thr |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Lys | Lys | Arg | Gly | Phe | Val | Ile | Pro | Phe | Trp | Ala | Pro | Gln | Ala | Gln | Val |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Leu | Ala | His | Pro | Ser | Thr | Gly | Gly | Phe | Leu | Thr | His | Cys | Gly | Trp | Asn |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Ser | Thr | Leu | Glu | Ser | Val | Val | Ser | Gly | Ile | Pro | Leu | Ile | Ala | Trp | Pro |
|     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |
| Leu | Tyr | Ala | Glu | Gln | Lys | Met | Asn | Ala | Val | Leu | Leu | Ser | Glu | Asp | Ile |
|     | 370 |     |     |     |     | 375 |     |     |     | 380 |     |     |     |     |     |
| Arg | Ala | Ala | Leu | Arg | Pro | Arg | Ala | Gly | Asp | Asp | Gly | Leu | Val | Arg | Arg |
| 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |     |
| Glu | Glu | Val | Ala | Arg | Val | Val | Lys | Gly | Leu | Met | Glu | Gly | Glu | Glu | Gly |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |
| Lys | Gly | Val | Arg | Asn | Lys | Met | Lys | Glu | Leu | Lys | Glu | Ala | Ala | Cys | Arg |
|     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Lys | Asp | Asp | Gly | Thr | Ser | Thr | Lys | Ala | Leu | Ser | Leu | Val | Ala |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Leu | Lys | Trp | Lys | Ala | His | Lys | Lys | Glu | Leu | Glu | Gln | Asn | Gly | Asn | His |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..311

(D) OTHER INFORMATION: / Ceres Seq. ID 1498649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Pro | Gly | Cys | Val | Pro | Val | Ala | Gly | Lys | Asp | Phe | Leu | Asp | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Gln | Asp | Arg | Lys | Asp | Asp | Ala | Tyr | Lys | Trp | Leu | Leu | His | Asn | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Arg | Tyr | Lys | Glu | Ala | Glu | Gly | Ile | Leu | Val | Asn | Thr | Phe | Phe | Glu |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Glu | Pro | Asn | Ala | Ile | Lys | Ala | Leu | Gln | Glu | Pro | Gly | Leu | Asp | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Pro | Val | Tyr | Pro | Val | Gly | Pro | Leu | Val | Asn | Ile | Gly | Lys | Gln | Glu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Lys | Gln | Thr | Glu | Glu | Ser | Glu | Cys | Leu | Lys | Trp | Leu | Asp | Asn | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Pro | Leu | Gly | Ser | Val | Leu | Tyr | Val | Ser | Phe | Gly | Ser | Gly | Gly | Thr | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Cys | Glu | Gln | Leu | Asn | Glu | Leu | Ala | Leu | Gly | Leu | Ala | Asp | Ser | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Arg | Phe | Leu | Trp | Val | Ile | Arg | Ser | Pro | Ser | Gly | Ile | Ala | Asn | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Tyr | Phe | Asp | Ser | His | Ser | Gln | Thr | Asp | Pro | Leu | Thr | Phe | Leu | Pro |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Pro | Gly | Phe | Leu | Glu | Arg | Thr | Lys | Lys | Arg | Gly | Phe | Val | Ile | Pro | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Trp | Ala | Pro | Gln | Ala | Gln | Val | Leu | Ala | His | Pro | Ser | Thr | Gly | Gly | Phe |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Thr | His | Cys | Gly | Trp | Asn | Ser | Thr | Leu | Glu | Ser | Val | Val | Ser | Gly |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ile | Pro | Leu | Ile | Ala | Trp | Pro | Leu | Tyr | Ala | Glu | Gln | Lys | Met | Asn | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Leu | Leu | Ser | Glu | Asp | Ile | Arg | Ala | Ala | Leu | Arg | Pro | Arg | Ala | Gly |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Asp | Asp | Gly | Leu | Val | Arg | Arg | Glu | Glu | Val | Ala | Arg | Val | Val | Lys | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Met | Glu | Gly | Glu | Glu | Gly | Lys | Gly | Val | Arg | Asn | Lys | Met | Lys | Glu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Lys | Glu | Ala | Ala | Cys | Arg | Val | Leu | Lys | Asp | Asp | Gly | Thr | Ser | Thr |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Lys | Ala | Leu | Ser | Leu | Val | Ala | Leu | Lys | Trp | Lys | Ala | His | Lys | Lys | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Glu | Gln | Asn | Gly | Asn | His |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1499 base pairs



- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1499  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498650  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

```
atctcttgtt ctctccgccc atctctgtct tcttttattt tcccagaaag tttttttttt 60
tttcccgaat tccgttaatc tcattggggt ttccattgat agcaatggcg acggcttttcg 120
ctcccactaa gctcactgcc acggttcctc tgcattggat ccatgagaat cgtctcttgc 180
tcccgatccg attggctcct ccttcttctt tctctggatc caccctgtcc ctctcccttc 240
gcagactcaa tcaactccaa gccaccgcgt gatctcccgt cgtctctgtc caggaagttg 300
tcaaggagaa gcaatccacc aataatacca gcctgttgat aaccaaagag gaaggattgg 360
agttgtatga agatatgata ctaggtagat ctttcgaaga catgtgtgct caaatgtatt 420
accgaggcaa gatgtttggt tttgttcact tgtacaatgg ccaagaggct gtttctactg 480
gctttatcaa gctccttacc aagtctgact ctgtcgttag tacctaccgt gacctgtcc 540
atgccctcag caaagggtgc tctgctcgtg ctgttatgag cgagctcttc ggcaagggtta 600
ctggatgctg cagaggccaa ggtggatcca tgcacatggt ctccaaagaa cacaacatgc 660
ttggtggcct tgcttttatt ggtgaaggca ttctgtgcgc cactggtgct gccttttagct 720
ccaagtacag gaggaagtc ttgaaacagg attgtgatga tgtcactgtc gccttttttcg 780
gagatggaac ttgtaacaac ggacagttct tgcagtgtct caacatggct gctctctata 840
aactgcctat tatctttgtt gtcgagaata acttgtgggc cattgggatg tctcacttga 900
gagccacttc tgaccccagag atttggaaga aaggctcctgc atttgggatg cctggtgttc 960
atgttgacgg tatggatgtc ttgaagggtc ggggaagtcgc taaagaggct gtcactagag 1020
ctagaagagg agaagggtcc accttggttg aatgtgagac ttatagattt agaggacact 1080
ccttggttga tcccgatgag ctccgtgatg ctgctgagaa agccaaatac gcggctagag 1140
acccaatcgc agcattgaag aagtatttga tagagaacaa gcttgcaaag gaagcagagc 1200
taaagtcaat agagaaaaag atagacgagt tgggtggagga agcgggttag tttgcagacg 1260
ctagtccaca gcccggtcgc agtcagttgc tagagaatgt gtttgctgat ccaaaggat 1320
ttggaattgg acctgatgga cggtacagat gtgaggaccc caagtttacc gaaggcacag 1380
ctcaagtctg agaagacaag ttttaaccata agctgtctac tgtctcttcg atgtttctat 1440
atatcttatt aagttaaatg ctacagagaa tcagtttgaa tcatttgcac tttttgctg
```

(2) INFORMATION FOR SEQ ID NO:566:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 462 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..462  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498651  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

```
Leu Leu Phe Ser Pro Pro Ile Ser Ala Leu Phe Tyr Phe Pro Arg Lys
1 5 10 15
Phe Phe Phe Phe Ser Arg Ile Pro Leu Ile Ser Leu Gly Phe Pro Leu
20 25 30
Ile Ala Met Ala Thr Ala Phe Ala Pro Thr Lys Leu Thr Ala Thr Val
35 40 45
Pro Leu His Gly Ser His Glu Asn Arg Leu Leu Leu Pro Ile Arg Leu
50 55 60
Ala Pro Pro Ser Ser Phe Leu Gly Ser Thr Arg Ser Leu Ser Leu Arg
65 70 75 80
Arg Leu Asn His Ser Asn Ala Thr Arg Arg Ser Pro Val Val Ser Val
85 90 95
Gln Glu Val Val Lys Glu Lys Gln Ser Thr Asn Asn Thr Ser Leu Leu
100 105 110
Ile Thr Lys Glu Glu Gly Leu Glu Leu Tyr Glu Asp Met Ile Leu Gly
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Phe | Glu | Asp | Met | Cys | Ala | Gln | Met | Tyr | Tyr | Arg | Gly | Lys | Met |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Gly | Phe | Val | His | Leu | Tyr | Asn | Gly | Gln | Glu | Ala | Val | Ser | Thr | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Ile | Lys | Leu | Leu | Thr | Lys | Ser | Asp | Ser | Val | Val | Ser | Thr | Tyr | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | His | Val | His | Ala | Leu | Ser | Lys | Gly | Val | Ser | Ala | Arg | Ala | Val | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Glu | Leu | Phe | Gly | Lys | Val | Thr | Gly | Cys | Cys | Arg | Gly | Gln | Gly | Gly |
|     |     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Ser | Met | His | Met | Phe | Ser | Lys | Glu | His | Asn | Met | Leu | Gly | Gly | Phe | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Ile | Gly | Glu | Gly | Ile | Pro | Val | Ala | Thr | Gly | Ala | Ala | Phe | Ser | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Tyr | Arg | Arg | Glu | Val | Leu | Lys | Gln | Asp | Cys | Asp | Asp | Val | Thr | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Phe | Phe | Gly | Asp | Gly | Thr | Cys | Asn | Asn | Gly | Gln | Phe | Phe | Glu | Cys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Asn | Met | Ala | Ala | Leu | Tyr | Lys | Leu | Pro | Ile | Ile | Phe | Val | Val | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Asn | Leu | Trp | Ala | Ile | Gly | Met | Ser | His | Leu | Arg | Ala | Thr | Ser | Asp |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | Glu | Ile | Trp | Lys | Lys | Gly | Pro | Ala | Phe | Gly | Met | Pro | Gly | Val | His |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Val | Asp | Gly | Met | Asp | Val | Leu | Lys | Val | Arg | Glu | Val | Ala | Lys | Glu | Ala |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | Thr | Arg | Ala | Arg | Arg | Gly | Glu | Gly | Pro | Thr | Leu | Val | Glu | Cys | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Tyr | Arg | Phe | Arg | Gly | His | Ser | Leu | Ala | Asp | Pro | Asp | Glu | Leu | Arg |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asp | Ala | Ala | Glu | Lys | Ala | Lys | Tyr | Ala | Ala | Arg | Asp | Pro | Ile | Ala | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Leu | Lys | Lys | Tyr | Leu | Ile | Glu | Asn | Lys | Leu | Ala | Lys | Glu | Ala | Glu | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Lys | Ser | Ile | Glu | Lys | Lys | Ile | Asp | Glu | Leu | Val | Glu | Glu | Ala | Val | Glu |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Phe | Ala | Asp | Ala | Ser | Pro | Gln | Pro | Gly | Arg | Ser | Gln | Leu | Leu | Glu | Asn |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Val | Phe | Ala | Asp | Pro | Lys | Gly | Phe | Gly | Ile | Gly | Pro | Asp | Gly | Arg | Tyr |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Arg | Cys | Glu | Asp | Pro | Lys | Phe | Thr | Glu | Gly | Thr | Ala | Gln | Val |     |     |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1498652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Ala | Phe | Ala | Pro | Thr | Lys | Leu | Thr | Ala | Thr | Val | Pro | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Gly | Ser | His | Glu | Asn | Arg | Leu | Leu | Leu | Pro | Ile | Arg | Leu | Ala | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Ser | Phe | Leu | Gly | Ser | Thr | Arg | Ser | Leu | Ser | Leu | Arg | Arg | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | His | Ser | Asn | Ala | Thr | Arg | Arg | Ser | Pro | Val | Val | Ser | Val | Gln | Glu |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Val | Lys | Glu | Lys | Gln | Ser | Thr | Asn | Asn | Thr | Ser | Leu | Leu | Ile | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Glu | Glu | Gly | Leu | Glu | Leu | Tyr | Glu | Asp | Met | Ile | Leu | Gly | Arg | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Glu | Asp | Met | Cys | Ala | Gln | Met | Tyr | Tyr | Arg | Gly | Lys | Met | Phe | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Val | His | Leu | Tyr | Asn | Gly | Gln | Glu | Ala | Val | Ser | Thr | Gly | Phe | Ile |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys | Leu | Leu | Thr | Lys | Ser | Asp | Ser | Val | Val | Ser | Thr | Tyr | Arg | Asp | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | His | Ala | Leu | Ser | Lys | Gly | Val | Ser | Ala | Arg | Ala | Val | Met | Ser | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Phe | Gly | Lys | Val | Thr | Gly | Cys | Cys | Arg | Gly | Gln | Gly | Gly | Ser | Met |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Met | Phe | Ser | Lys | Glu | His | Asn | Met | Leu | Gly | Gly | Phe | Ala | Phe | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Glu | Gly | Ile | Pro | Val | Ala | Thr | Gly | Ala | Ala | Phe | Ser | Ser | Lys | Tyr |
|     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Arg | Arg | Glu | Val | Leu | Lys | Gln | Asp | Cys | Asp | Asp | Val | Thr | Val | Ala | Phe |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Gly | Asp | Gly | Thr | Cys | Asn | Asn | Gly | Gln | Phe | Phe | Glu | Cys | Leu | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Met | Ala | Ala | Leu | Tyr | Lys | Leu | Pro | Ile | Ile | Phe | Val | Val | Glu | Asn | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Trp | Ala | Ile | Gly | Met | Ser | His | Leu | Arg | Ala | Thr | Ser | Asp | Pro | Glu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Ile | Trp | Lys | Lys | Gly | Pro | Ala | Phe | Gly | Met | Pro | Gly | Val | His | Val | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Met | Asp | Val | Leu | Lys | Val | Arg | Glu | Val | Ala | Lys | Glu | Ala | Val | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Ala | Arg | Arg | Gly | Glu | Gly | Pro | Thr | Leu | Val | Glu | Cys | Glu | Thr | Tyr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Phe | Arg | Gly | His | Ser | Leu | Ala | Asp | Pro | Asp | Glu | Leu | Arg | Asp | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ala | Glu | Lys | Ala | Lys | Tyr | Ala | Ala | Arg | Asp | Pro | Ile | Ala | Ala | Leu | Lys |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Lys | Tyr | Leu | Ile | Glu | Asn | Lys | Leu | Ala | Lys | Glu | Ala | Glu | Leu | Lys | Ser |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Glu | Lys | Lys | Ile | Asp | Glu | Leu | Val | Glu | Glu | Ala | Val | Glu | Phe | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asp | Ala | Ser | Pro | Gln | Pro | Gly | Arg | Ser | Gln | Leu | Glu | Asn | Val | Phe |     |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ala | Asp | Pro | Lys | Gly | Phe | Gly | Ile | Gly | Pro | Asp | Gly | Arg | Tyr | Arg | Cys |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Glu | Asp | Pro | Lys | Phe | Thr | Glu | Gly | Thr | Ala | Gln | Val |     |     |     |     |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

Met Ile Leu Gly Arg Ser Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr

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|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Arg Gly Lys Met Phe Gly Phe Val His Leu Tyr Asn Gly Gln Glu Ala |     |     |     |
| 20                                                              | 25  | 30  |     |
| Val Ser Thr Gly Phe Ile Lys Leu Leu Thr Lys Ser Asp Ser Val Val |     |     |     |
| 35                                                              | 40  | 45  |     |
| Ser Thr Tyr Arg Asp His Val His Ala Leu Ser Lys Gly Val Ser Ala |     |     |     |
| 50                                                              | 55  | 60  |     |
| Arg Ala Val Met Ser Glu Leu Phe Gly Lys Val Thr Gly Cys Cys Arg |     |     |     |
| 65                                                              | 70  | 75  | 80  |
| Gly Gln Gly Gly Ser Met His Met Phe Ser Lys Glu His Asn Met Leu |     |     |     |
| 85                                                              | 90  | 95  |     |
| Gly Gly Phe Ala Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala |     |     |     |
| 100                                                             | 105 | 110 |     |
| Ala Phe Ser Ser Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp |     |     |     |
| 115                                                             | 120 | 125 |     |
| Asp Val Thr Val Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln |     |     |     |
| 130                                                             | 135 | 140 |     |
| Phe Phe Glu Cys Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| Phe Val Val Glu Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg |     |     |     |
| 165                                                             | 170 | 175 |     |
| Ala Thr Ser Asp Pro Glu Ile Trp Lys Gly Pro Ala Phe Gly Met     |     |     |     |
| 180                                                             | 185 | 190 |     |
| Pro Gly Val His Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val |     |     |     |
| 195                                                             | 200 | 205 |     |
| Ala Lys Glu Ala Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu |     |     |     |
| 210                                                             | 215 | 220 |     |
| Val Glu Cys Glu Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro |     |     |     |
| 225                                                             | 230 | 235 | 240 |
| Asp Glu Leu Arg Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp |     |     |     |
| 245                                                             | 250 | 255 |     |
| Pro Ile Ala Ala Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys |     |     |     |
| 260                                                             | 265 | 270 |     |
| Glu Ala Glu Leu Lys Ser Ile Glu Lys Lys Ile Asp Glu Leu Val Glu |     |     |     |
| 275                                                             | 280 | 285 |     |
| Glu Ala Val Glu Phe Ala Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln |     |     |     |
| 290                                                             | 295 | 300 |     |
| Leu Leu Glu Asn Val Phe Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro |     |     |     |
| 305                                                             | 310 | 315 | 320 |
| Asp Gly Arg Tyr Arg Cys Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala |     |     |     |
| 325                                                             | 330 | 335 |     |
| Gln Val                                                         |     |     |     |

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1278
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atccttttctc tctgtatctc tgtgtattct tctctcatgg agcctgctca tatcgattgg | 60  |
| aagagaatcg attctogttt tgttgaagac gttttttacg aacacatcag agctcctaaa  | 120 |
| tggttcgatt tcttggtccc taccatttt gactccattg acgacgatgc ttggttctgc   | 180 |
| aaacctgaat gtaatcatcc caagagacct gaggactttt tctcaacgcc gacttcttcc  | 240 |
| aagcatccaa gtctgagggg tacgaatgag actctaacag agcagaatca gaggaggagg  | 300 |
| ggatatgctt tatcaccttc tactccaaac aaccaagaaa gtgaaaatca gaacccgaac  | 360 |

|            |             |             |            |            |             |      |
|------------|-------------|-------------|------------|------------|-------------|------|
| ttagccacac | ctccaagcta  | ccaagcaaaa  | tcatggagag | cagcaattaa | atcaacttct  | 420  |
| gtcaagaaga | tgaataaaga  | agttccaaga  | ctaaagagca | cacaatcagc | tagaaatctg  | 480  |
| ttttcaggga | gagacatatt  | tggtcatatc  | tcagatttbt | gctatgaatt | gaagagatta  | 540  |
| gccacaaggg | ttactgagag  | agaagatact  | gggaaatctg | aagtgaagga | gagtcatcaa  | 600  |
| gtgggtggaa | tagtaaataca | gccttactct  | gttcatgact | tggaattgaa | aaaggaaata  | 660  |
| aagccactgc | ttgaagtaag  | caaagataag  | ctccctgagt | ccacggatgt | taaaggaagc  | 720  |
| acatttaaag | agaaccgtag  | aagaaagaag  | agagtggatg | atgcagagaa | cattcctgtc  | 780  |
| tcacttaatg | tggagactgt  | aaaaaaciaa  | ggagaggagg | gtagaagaaa | gaagagaatg  | 840  |
| gatgatgcag | agaacatccc  | agttcctcta  | aaactggaga | ctataaagaa | caaaggacac  | 900  |
| gaacgattcc | tgcagcaaat  | caggacaaac  | ccaccatctc | ctcaatgctt | ctctgagaac  | 960  |
| cggacagcta | cattgaaacc  | cttgaggacc  | aaacctacgg | aagtgttgaa | gagaaaggaa  | 1020 |
| gatgaagctg | aagaagaaaa  | gaacagaaaag | agtggagaaa | gcaaagaagc | aacaagggga  | 1080 |
| ttggacgttc | tctggttctt  | aaagccttgc  | actttagcca | actagaaaac | cttcacaaaa  | 1140 |
| ttctttctat | attgattcat  | tcttttggtt  | atttcatttt | attcaactgt | aactaacgag  | 1200 |
| atgattatct | tgctcagata  | tataattctg  | ggcaaatttg | attcaatctc | ttactttttac | 1260 |
| acatacaacg | atttgttt    |             |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1498655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Leu | Ser | Leu | Cys | Ile | Ser | Val | Tyr | Ser | Ser | Leu | Met | Glu | Pro | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Ile | Asp | Trp | Lys | Arg | Ile | Asp | Ser | Arg | Phe | Val | Glu | Asp | Val | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Glu | His | Ile | Arg | Ala | Pro | Lys | Trp | Phe | Asp | Phe | Leu | Ala | Pro | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Phe | Asp | Ser | Ile | Asp | Asp | Asp | Ala | Trp | Phe | Cys | Lys | Pro | Glu | Cys |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Asn | His | Pro | Lys | Arg | Pro | Glu | Asp | Phe | Phe | Ser | Thr | Pro | Thr | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | His | Pro | Ser | Leu | Arg | Asp | Thr | Asn | Glu | Thr | Leu | Thr | Glu | Gln | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Arg | Arg | Arg | Gly | Tyr | Ala | Leu | Ser | Pro | Ser | Thr | Pro | Asn | Asn | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ser | Glu | Asn | Gln | Asn | Pro | Asn | Leu | Ala | Thr | Pro | Pro | Ser | Tyr | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Lys | Ser | Trp | Arg | Ala | Ala | Ile | Lys | Ser | Thr | Ser | Val | Lys | Lys | Met |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Asn | Lys | Glu | Val | Pro | Arg | Leu | Lys | Ser | Thr | Gln | Ser | Ala | Arg | Asn | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Phe | Ser | Gly | Arg | Asp | Ile | Phe | Gly | His | Ile | Ser | Asp | Xaa | Cys | Tyr | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Lys | Arg | Leu | Ala | Thr | Arg | Val | Thr | Glu | Arg | Glu | Asp | Thr | Gly | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Glu | Val | Lys | Glu | Ser | His | Gln | Val | Gly | Gly | Ile | Val | Asn | Gln | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Ser | Val | His | Asp | Leu | Glu | Leu | Lys | Lys | Glu | Ile | Lys | Pro | Leu | Leu |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Glu | Val | Ser | Lys | Asp | Lys | Leu | Pro | Glu | Ser | Thr | Asp | Val | Lys | Gly | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Thr | Phe | Lys | Glu | Asn | Arg | Arg | Arg | Lys | Lys | Arg | Val | Asp | Asp | Ala | Glu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Ile | Pro | Val | Ser | Leu | Asn | Val | Glu | Thr | Val | Lys | Asn | Lys | Gly | Glu |

[illegible]

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..362  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |           |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Glu        | Pro        | Ala        | His<br>5   | Ile        | Asp        | Trp        | Lys        | Arg<br>10  | Ile        | Asp        | Ser        | Arg        | Phe<br>15 | Val        |
| Glu        | Asp        | Val        | Phe<br>20  | Tyr        | Glu        | His        | Ile        | Arg<br>25  | Ala        | Pro        | Lys        | Trp        | Phe<br>30  | Asp       | Phe        |
| Leu        | Ala        | Pro<br>35  | Thr        | His        | Phe        | Asp        | Ser<br>40  | Ile        | Asp        | Asp        | Asp        | Ala<br>45  | Trp        | Phe       | Cys        |
| Lys        | Pro        | Glu        | Cys        | Asn        | His        | Pro<br>55  | Lys        | Arg        | Pro        | Glu        | Asp<br>60  | Phe        | Phe        | Ser       | Thr        |
| Pro<br>65  | Thr        | Ser        | Ser        | Lys        | His<br>70  | Pro        | Ser        | Leu        | Arg        | Asp<br>75  | Thr        | Asn        | Glu        | Thr       | Leu<br>80  |
| Thr        | Glu        | Gln        | Asn        | Gln<br>85  | Arg        | Arg        | Arg        | Gly        | Tyr<br>90  | Ala        | Leu        | Ser        | Pro        | Ser       | Thr        |
| Pro        | Asn        | Asn        | Gln<br>100 | Glu        | Ser        | Glu        | Asn        | Gln<br>105 | Asn        | Pro        | Asn        | Leu        | Ala<br>110 | Thr       | Pro        |
| Pro        | Ser        | Tyr<br>115 | Gln        | Ala        | Lys        | Ser        | Trp<br>120 | Arg        | Ala        | Ala        | Ile        | Lys<br>125 | Ser        | Thr       | Ser        |
| Val        | Lys<br>130 | Lys        | Met        | Asn        | Lys        | Glu<br>135 | Val        | Pro        | Arg        | Leu        | Lys<br>140 | Ser        | Thr        | Gln       | Ser        |
| Ala<br>145 | Arg        | Asn        | Leu        | Phe        | Ser<br>150 | Gly        | Arg        | Asp        | Ile        | Phe<br>155 | Gly        | His        | Ile        | Ser       | Asp<br>160 |
| Xaa        | Cys        | Tyr        | Glu        | Leu<br>165 | Lys        | Arg        | Leu        | Ala        | Thr<br>170 | Arg        | Val        | Thr        | Glu        | Arg       | Glu        |
| Asp        | Thr        | Gly        | Lys<br>180 | Ser        | Glu        | Val        | Lys        | Glu<br>185 | Ser        | His        | Gln        | Val        | Gly<br>190 | Gly       | Ile        |
| Val        | Asn        | Gln<br>195 | Pro        | Tyr        | Ser        | Val        | His<br>200 | Asp        | Leu        | Glu        | Leu        | Lys<br>205 | Lys        | Glu       | Ile        |
| Lys        | Pro<br>210 | Leu        | Leu        | Glu        | Val        | Ser<br>215 | Lys        | Asp        | Lys        | Leu        | Pro<br>220 | Glu        | Ser        | Thr       | Asp        |
| Val<br>225 | Lys        | Gly        | Ser        | Thr        | Phe<br>230 | Lys        | Glu        | Asn        | Arg        | Arg<br>235 | Arg        | Lys        | Lys        | Arg       | Val<br>240 |
| Asp        | Asp        | Ala        | Glu        | Asn<br>245 | Ile        | Pro        | Val        | Ser        | Leu<br>250 | Asn        | Val        | Glu        | Thr        | Val       | Lys<br>255 |
| Asn        | Lys        | Gly        | Glu<br>260 | Glu        | Gly        | Arg        | Arg        | Lys<br>265 | Lys        | Arg        | Met        | Asp        | Asp        | Ala       | Glu        |

Asn Ile Pro Val Pro Leu Lys Leu Glu Thr Ile Lys Asn Lys Gly His  
275 280 285  
Glu Arg Phe Leu Gln Gln Ile Arg Thr Asn Pro Pro Ser Pro Gln Cys  
290 295 300  
Phe Ser Glu Asn Arg Thr Ala Thr Leu Lys Pro Leu Arg Thr Lys Pro  
305 310 315 320  
Thr Glu Val Leu Lys Arg Lys Glu Asp Glu Ala Glu Glu Glu Lys Asn  
325 330 335  
Arg Lys Ser Gly Glu Ser Lys Glu Ala Thr Arg Gly Leu Asp Val Leu  
340 345 350  
Trp Phe Leu Lys Pro Cys Thr Leu Ala Asn  
355 360

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1498657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

Met Asn Lys Glu Val Pro Arg Leu Lys Ser Thr Gln Ser Ala Arg Asn  
1 5 10 15  
Leu Phe Ser Gly Arg Asp Ile Phe Gly His Ile Ser Asp Xaa Cys Tyr  
20 25 30  
Glu Leu Lys Arg Leu Ala Thr Arg Val Thr Glu Arg Glu Asp Thr Gly  
35 40 45  
Lys Ser Glu Val Lys Glu Ser His Gln Val Gly Gly Ile Val Asn Gln  
50 55 60  
Pro Tyr Ser Val His Asp Leu Glu Leu Lys Lys Glu Ile Lys Pro Leu  
65 70 75 80  
Leu Glu Val Ser Lys Asp Lys Leu Pro Glu Ser Thr Asp Val Lys Gly  
85 90 95  
Ser Thr Phe Lys Glu Asn Arg Arg Arg Lys Lys Arg Val Asp Asp Ala  
100 105 110  
Glu Asn Ile Pro Val Ser Leu Asn Val Glu Thr Val Lys Asn Lys Gly  
115 120 125  
Glu Glu Gly Arg Arg Lys Lys Arg Met Asp Asp Ala Glu Asn Ile Pro  
130 135 140  
Val Pro Leu Lys Leu Glu Thr Ile Lys Asn Lys Gly His Glu Arg Phe  
145 150 155 160  
Leu Gln Gln Ile Arg Thr Asn Pro Pro Ser Pro Gln Cys Phe Ser Glu  
165 170 175  
Asn Arg Thr Ala Thr Leu Lys Pro Leu Arg Thr Lys Pro Thr Glu Val  
180 185 190  
Leu Lys Arg Lys Glu Asp Glu Ala Glu Glu Glu Lys Asn Arg Lys Ser  
195 200 205  
Gly Glu Ser Lys Glu Ala Thr Arg Gly Leu Asp Val Leu Trp Phe Leu  
210 215 220  
Lys Pro Cys Thr Leu Ala Asn  
225 230

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1135

(D) OTHER INFORMATION: / Ceres Seq. ID 1498658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| acaaactcat | catcataagc  | aacaatggtg  | gtgtcactct | tctcttccag  | aaatgttttc  | 60   |
| tatacgtaa  | gcttatgctt  | atttgcagca  | ttataccagc | cggttatgag  | tagaccggct  | 120  |
| aagtttgaag | atgacttttag | gatcgcatgg  | tccgatactc | atatcactca  | aattgacgga  | 180  |
| ggcatagcca | ttcagctcaa  | attggaccct  | agctcaggat | gtggatttgc  | ttcgaagaag  | 240  |
| caatacttgt | tcggccgtgt  | gagcatgaaa  | atcaaactga | tccccgggtga | ttctgcccggg | 300  |
| actgtcactg | ccttctacat  | gaattcagat  | accgattcgg | tacgagacga  | gcttgatttt  | 360  |
| gagttcttag | gaaatcgaag  | tggacaacct  | tacacagtgc | aaaccaatgt  | gtttgctcat  | 420  |
| ggtaaaggcg | atagagagca  | aagagttaac  | ctttggttcg | acccttctcg  | tgatttccac  | 480  |
| gaatatgcca | tctcatggaa  | ccatctccgt  | attgtcttct | acgtagacaa  | tgtgcccato  | 540  |
| agggtttaca | agaacaatga  | ggcaaggaaa  | gtaccatacc | caagattcca  | accaatgggt  | 600  |
| gtatattcca | cgttatggga  | agccgatgat  | tgggcgacac | gtggaggaat  | agagaaaatc  | 660  |
| aattggtcga | gagcgccatt  | ttatgcttat  | tacaaagatt | ttgatataga  | aggatgtccg  | 720  |
| gttccaggac | ccgcagattg  | tcccgcataat | tcgaagaatt | ggtgggaagg  | cagtgcgtac  | 780  |
| caccagttga | gtccggtgga  | agctcgaagt  | tatagatggg | tccgagtga   | ccatatggtc  | 840  |
| tacgattatt | gcactgacaa  | atctcgtttt  | cctgttccac | ctccagaatg  | ctcggctgga  | 900  |
| atctgatcca | aacattattg  | tcttaaaagc  | aaaacaagtg | cgaagtgggt  | ccataagcaa  | 960  |
| cgttgcaatg | tatgtgaagt  | gattaatgag  | tcttgtggta | tgtgggtgaat | tgctcataat  | 1020 |
| cgatctgatt | gtgggtcaaat | gttcatatat  | atatgtatat | ctttgaattt  | tactttgttt  | 1080 |
| tcatgatgtc | ttatgttttg  | ttgatctatt  | gaagagaacc | atgtttgttt  | gttgc       |      |

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1498659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Val | Ser | Phe | Ser | Ser | Arg | Asn | Val | Phe | Tyr | Thr | Leu | Ser |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Cys | Leu | Phe | Ala | Ala | Leu | Tyr | Gln | Pro | Val | Met | Ser | Arg | Pro |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  | Ala |
| Lys | Phe | Glu | Asp | Asp | Phe | Arg | Ile | Ala | Trp | Ser | Asp | Thr | His | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     | Thr |
| Gln | Ile | Asp | Gly | Gly | Ile | Ala | Ile | Gln | Leu | Lys | Leu | Asp | Pro | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     | Ser |
| Gly | Cys | Gly | Phe | Ala | Ser | Lys | Lys | Gln | Tyr | Leu | Phe | Gly | Arg | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  | Ser |
| Met | Lys | Ile | Lys | Leu | Ile | Pro | Gly | Asp | Ser | Ala | Gly | Thr | Val | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  | Ala |
| Phe | Tyr | Met | Asn | Ser | Asp | Thr | Asp | Ser | Val | Arg | Asp | Glu | Leu | Asp |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 | Phe |
| Glu | Phe | Leu | Gly | Asn | Arg | Ser | Gly | Gln | Pro | Tyr | Thr | Val | Gln | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     | Asn |
| Val | Phe | Ala | His | Gly | Lys | Gly | Asp | Arg | Glu | Gln | Arg | Val | Asn | Leu |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     | Trp |
| Phe | Asp | Pro | Ser | Arg | Asp | Phe | His | Glu | Tyr | Ala | Ile | Ser | Trp | Asn |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | His |
| Leu | Arg | Ile | Val | Phe | Tyr | Val | Asp | Asn | Val | Pro | Ile | Arg | Val | Tyr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 | Lys |
| Asn | Asn | Glu | Ala | Arg | Lys | Val | Pro | Tyr | Pro | Arg | Phe | Gln | Pro | Met |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 | Gly |
| Val | Tyr | Ser | Thr | Leu | Trp | Glu | Ala | Asp | Asp | Trp | Ala | Thr | Arg | Gly |



195 200 205  
Ile Glu Lys Ile Asn Trp Ser Arg Ala Pro Phe Tyr Ala Tyr Tyr Lys  
210 215 220  
Asp Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Ala Asp Cys Pro  
225 230 235 240  
Ala Asn Ser Lys Asn Trp Trp Glu Gly Ser Ala Tyr His Gln Leu Ser  
245 250 255  
Pro Val Glu Ala Arg Ser Tyr Arg Trp Val Arg Val Asn His Met Val  
260 265 270  
Tyr Asp Tyr Cys Thr Asp Lys Ser Arg Phe Pro Val Pro Pro Pro Glu  
275 280 285  
Cys Ser Ala Gly Ile  
290

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1498660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

Met Ser Arg Pro Ala Lys Phe Glu Asp Asp Phe Arg Ile Ala Trp Ser  
1 5 10 15  
Asp Thr His Ile Thr Gln Ile Asp Gly Gly Ile Ala Ile Gln Leu Lys  
20 25 30  
Leu Asp Pro Ser Ser Gly Cys Gly Phe Ala Ser Lys Lys Gln Tyr Leu  
35 40 45  
Phe Gly Arg Val Ser Met Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala  
50 55 60  
Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp Thr Asp Ser Val Arg  
65 70 75 80  
Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg Ser Gly Gln Pro Tyr  
85 90 95  
Thr Val Gln Thr Asn Val Phe Ala His Gly Lys Gly Asp Arg Glu Gln  
100 105 110  
Arg Val Asn Leu Trp Phe Asp Pro Ser Arg Asp Phe His Glu Tyr Ala  
115 120 125  
Ile Ser Trp Asn His Leu Arg Ile Val Phe Tyr Val Asp Asn Val Pro  
130 135 140  
Ile Arg Val Tyr Lys Asn Asn Glu Ala Arg Lys Val Pro Tyr Pro Arg  
145 150 155 160  
Phe Gln Pro Met Gly Val Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp  
165 170 175  
Ala Thr Arg Gly Gly Ile Glu Lys Ile Asn Trp Ser Arg Ala Pro Phe  
180 185 190  
Tyr Ala Tyr Tyr Lys Asp Phe Asp Ile Glu Gly Cys Pro Val Pro Gly  
195 200 205  
Pro Ala Asp Cys Pro Ala Asn Ser Lys Asn Trp Trp Glu Gly Ser Ala  
210 215 220  
Tyr His Gln Leu Ser Pro Val Glu Ala Arg Ser Tyr Arg Trp Val Arg  
225 230 235 240  
Val Asn His Met Val Tyr Asp Tyr Cys Thr Asp Lys Ser Arg Phe Pro  
245 250 255  
Val Pro Pro Pro Glu Cys Ser Ala Gly Ile  
260 265

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..213  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498661  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

Met Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr Ala  
1 5 10 15  
Phe Tyr Met Asn Ser Asp Thr Asp Ser Val Arg Asp Glu Leu Asp Phe  
20 25 30  
Glu Phe Leu Gly Asn Arg Ser Gly Gln Pro Tyr Thr Val Gln Thr Asn  
35 40 45  
Val Phe Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu Trp  
50 55 60  
Phe Asp Pro Ser Arg Asp Phe His Glu Tyr Ala Ile Ser Trp Asn His  
65 70 75 80  
Leu Arg Ile Val Phe Tyr Val Asp Asn Val Pro Ile Arg Val Tyr Lys  
85 90 95  
Asn Asn Glu Ala Arg Lys Val Pro Tyr Pro Arg Phe Gln Pro Met Gly  
100 105 110  
Val Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly  
115 120 125  
Ile Glu Lys Ile Asn Trp Ser Arg Ala Pro Phe Tyr Ala Tyr Tyr Lys  
130 135 140  
Asp Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Ala Asp Cys Pro  
145 150 155 160  
Ala Asn Ser Lys Asn Trp Trp Glu Gly Ser Ala Tyr His Gln Leu Ser  
165 170 175  
Pro Val Glu Ala Arg Ser Tyr Arg Trp Val Arg Val Asn His Met Val  
180 185 190  
Tyr Asp Tyr Cys Thr Asp Lys Ser Arg Phe Pro Val Pro Pro Pro Glu  
195 200 205  
Cys Ser Ala Gly Ile  
210

(2) INFORMATION FOR SEQ ID NO:577:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1519 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1519  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498662  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

aaaaataact taatcacaca caaggagaga agagagaaag agagaaagag agacagagat 60  
aatggcgtac agtgcggtgtt tcctacacca gagcgcattg gcttcatcag ccgcacgatac 120  
atcatcttcc tcctcatccc agcgtcacgt gtcgctctcc aaacctgttc agatcatctg 180  
taaagctcaa cagtctcatg aagacgataa ctccgccgtc tcccgccgtc ttgctctcac 240  
tctcctcgtc ggcgccgctg ctggttggtc caaagtatct cctgctgatg ccgcctacgg 300  
tgaagctgca aacgtgtttg ggaagccaaa gacgaacaca gacttcttgc catacaatgg 360  
agatgggttc aaagtgcagg ttccagcaaa atggaaccca agcaaagaga ttgagtatcc 420  
aggacaagtc cttaggttcg aagacaactt cgatgctact agcaatctca atgtcatggt 480  
cactcctacc gacaagaagt ccatactga ttacggttct cccgaagagt tcctctctca 540  
ggtaattac ctcctaggga aacaagctta cttcggtgag actgcctctg agggaggctt 600  
tgacaacaat gcagtggtgcaa cagcaaacat tctggagtca tcattctcagg aagttggttg 660

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| gaaaccctac | tattacttgt  | ctgtgttgac | aagaacggct | gatggagacg | aaggtgggaa  | 720  |
| gcatcagctg | atcacagcaa  | ccgtgaagga | gggaagcktt | acatctgcaa | agcacaagct  | 780  |
| ggagacaaga | ggtggttcaa  | gggagccagg | aaatttgtcg | agagcgcagc | cacttctttc  | 840  |
| agtgttgctt | gmgrtgaaa   | caacacaacg | taacaatgct | ctgcttgctt | tcttcatttg  | 900  |
| tctcttgtaa | aaaatggaaa  | atgaaactga | gcttttgaga | actatcaaga | tgatgttacc  | 960  |
| ttttcggcat | cacttgtgta  | cctatgatac | cagactcggt | tccaagtttt | cttaaaaaaac | 1020 |
| aactatatct | aatagatatt  | ttctcaaatt | aaaaaaaaaa | aaaaaaaaaa | aaaaaaaaaa  | 1080 |
| aaaaaamcaa | aaaaaaaaaa  | aaaaaagctt | ctcgkgccgt | tttttttttt | tttttttgga  | 1140 |
| gtttttgggt | ggacgggtgga | gattggagaa | gctagaagga | ttgacgggtg | agggccaacg  | 1200 |
| tgcacaggag | tttgtgtgtg  | ggttagctca | gaggattaga | cgccttcaag | agcgtgcaga  | 1260 |
| cgagagagct | aagaagctta  | agaagaccca | tgaggtttgc | tttagttgga | tcttcgataa  | 1320 |
| gcagattagt | gtgtaaaact  | ttgaaaatat | caaacttttc | ctttctccgt | ttcttgtttt  | 1380 |
| tttactctaa | tgaggcctac  | tcatggttgt | gtgagtgggt | cctcaagtat | cattgtccaa  | 1440 |
| taaggagcca | atttatttat  | ggctggctgt | tttattacaa | attatgtgta | tgtgttaata  | 1500 |
| attaaagatt | gaattatct   |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..282
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Tyr | Ser | Ala | Cys | Phe | Leu | His | Gln | Ser | Ala | Leu | Ala | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ala | Arg | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Gln | Arg | His | Val | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Lys | Pro | Val | Gln | Ile | Ile | Cys | Lys | Ala | Gln | Gln | Ser | His | Glu | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Asn | Ser | Ala | Val | Ser | Arg | Arg | Leu | Ala | Leu | Thr | Leu | Leu | Val | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ala | Ala | Val | Gly | Ser | Lys | Val | Ser | Pro | Ala | Asp | Ala | Ala | Tyr | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Ala | Ala | Asn | Val | Phe | Gly | Lys | Pro | Lys | Thr | Asn | Thr | Asp | Phe | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Tyr | Asn | Gly | Asp | Gly | Phe | Lys | Val | Gln | Val | Pro | Ala | Lys | Trp | Asn |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Ser | Lys | Glu | Ile | Glu | Tyr | Pro | Gly | Gln | Val | Leu | Arg | Phe | Glu | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Phe | Asp | Ala | Thr | Ser | Asn | Leu | Asn | Val | Met | Val | Thr | Pro | Thr | Asp |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Lys | Ser | Ile | Thr | Asp | Tyr | Gly | Ser | Pro | Glu | Glu | Phe | Leu | Ser | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Asn | Tyr | Leu | Leu | Gly | Lys | Gln | Ala | Tyr | Phe | Gly | Glu | Thr | Ala | Ser |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Gly | Gly | Phe | Asp | Asn | Asn | Ala | Val | Ala | Thr | Ala | Asn | Ile | Leu | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ser | Ser | Gln | Glu | Val | Gly | Gly | Lys | Pro | Tyr | Tyr | Tyr | Leu | Ser | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Thr | Arg | Thr | Ala | Asp | Gly | Asp | Glu | Gly | Gly | Lys | His | Gln | Leu | Ile |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Ala | Thr | Val | Lys | Glu | Gly | Ser | Xaa | Thr | Ser | Ala | Lys | His | Lys | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Glu | Thr | Arg | Gly | Gly | Ser | Arg | Glu | Pro | Gly | Asn | Leu | Ser | Arg | Ala | Gln |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Leu | Leu | Ser | Val | Leu | Leu | Xaa | Xaa | Lys | Ala | Thr | Gln | Arg | Asn | Asn |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |

Ala Leu Leu Ala Phe Phe Ile Cys Leu Leu  
275 280

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1498664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Thr | Pro | Thr | Asp | Lys | Lys | Ser | Ile | Thr | Asp | Tyr | Gly | Ser | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Glu | Phe | Leu | Ser | Gln | Val | Asn | Tyr | Leu | Leu | Gly | Lys | Gln | Ala | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Phe | Gly | Glu | Thr | Ala | Ser | Glu | Gly | Gly | Phe | Asp | Asn | Asn | Ala | Val | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr | Ala | Asn | Ile | Leu | Glu | Ser | Ser | Ser | Gln | Glu | Val | Gly | Gly | Lys | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Tyr | Tyr | Tyr | Leu | Ser | Val | Leu | Thr | Arg | Thr | Ala | Asp | Gly | Asp | Glu | Gly |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Gly | Lys | His | Gln | Leu | Ile | Thr | Ala | Thr | Val | Lys | Glu | Gly | Ser | Xaa | Thr |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Ala | Lys | His | Lys | Leu | Glu | Thr | Arg | Gly | Gly | Ser | Arg | Glu | Pro | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Leu | Ser | Arg | Ala | Gln | Pro | Leu | Leu | Ser | Val | Leu | Leu | Xaa | Xaa | Lys |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ala | Thr | Gln | Arg | Asn | Asn | Ala | Leu | Leu | Ala | Phe | Phe | Ile | Cys | Leu | Leu |
| 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476

(D) OTHER INFORMATION: / Ceres Seq. ID 1498665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| tctctctctc | tctctctctc  | tggtctttta | tttagagaga | aaaaataagc | attcttcctt | 60  |
| ctctggtttc | gagcgggaaa  | ttctggagat | ggctatacaa | gcgcagttga | attacaacgc | 120 |
| tccgaatgcg | aatcaaatacg | gttttggttg | gtccgagttt | tctttgatca | acaacaatgg | 180 |
| cgttattgga | atcgcatcat  | caacaacaac | agtctccttc | tcaaagcttt | ttagctgctc | 240 |
| agatggagaa | acagaagcaa  | gagatcgatc | agttcatcaa | aatacagaac | gagaggttga | 300 |
| gatattgtgt | gcaagaacag  | aggaagcgag | aaatggagat | gattttaagg | aaaatggaga | 360 |
| gtaaagcttt | gcttttgatg  | agtcagaagg | aagaagaaat | gtcgaaagca | ttgaacaaga | 420 |
| acatggaact | cgaagatctg  | ttgagaaaaa | tggaaatgga | gaatcagacg | tggcag     |     |

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1498666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Leu | Ser | Leu | Phe | Phe | Asn | Leu | Glu | Arg | Lys | Asn | Lys |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Ser | Ser | Phe | Ser | Val | Phe | Glu | Arg | Glu | Ile | Leu | Glu | Met |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  | Ala |
| Gln | Ala | Gln | Leu | Asn | Tyr | Asn | Ala | Pro | Asn | Ala | Asn | Gln | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  | Gly |
| Gly | Gly | Ser | Glu | Phe | Ser | Leu | Ile | Asn | Asn | Asn | Gly | Val | Ile |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     | Gly |
| Ala | Ser | Ser | Thr | Thr | Thr | Val | Ser | Phe | Ser | Lys | Leu | Phe | Ser |
|     |     |     |     |     |     | 70  |     |     |     | 75  |     |     | Cys |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     | 80  |
| Asp | Gly | Glu | Thr | Glu | Ala | Arg | Asp | Arg | Ser | Val | His | Gln | Asn |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |
| Arg | Glu | Val | Glu | Ile | Cys | Val | Ala | Arg | Thr | Glu | Glu | Ala | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |
| Asp | Asp | Phe | Lys | Glu | Asn | Gly | Glu |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1498667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ile | Gln | Ala | Gln | Leu | Asn | Tyr | Asn | Ala | Pro | Asn | Ala | Asn | Gln |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Gly | Phe | Gly | Gly | Ser | Glu | Phe | Ser | Leu | Ile | Asn | Asn | Asn | Gly | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ile | Gly | Ile | Ala | Ser | Ser | Thr | Thr | Thr | Val | Ser | Phe | Ser | Lys | Leu | Phe |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ser | Cys | Ser | Asp | Gly | Glu | Thr | Glu | Ala | Arg | Asp | Arg | Ser | Val | His | Gln |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Asn | Thr | Glu | Arg | Glu | Val | Glu | Ile | Cys | Val | Ala | Arg | Thr | Glu | Glu | Ala |
|     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Arg | Asn | Gly | Asp | Asp | Phe | Lys | Glu | Asn | Gly | Glu |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1498668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Leu | Glu | Ser | His | His | Gln | Gln | Gln | Ser | Pro | Ser | Gln |     |
| 1   |     |     |     |     | 5   |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Phe | Leu | Ala | Ala | Gln | Met | Glu | Lys | Gln | Lys | Gln | Glu | Ile | Asp | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |

Phe Ile Lys Ile Gln Asn Glu Arg Leu Arg Tyr Val Leu Gln Glu Gln  
35 40 45  
Arg Lys Arg Glu Met Glu Met Ile Leu Arg Lys Met Glu Ser Lys Ala  
50 55 60  
Leu Leu Leu Met Ser Gln Lys Glu Glu Glu Met Ser Lys Ala Leu Asn  
65 70 75 80  
Lys Asn Met Glu Leu Glu Asp Leu Leu Arg Lys Met Glu Met Glu Asn  
85 90 95  
Gln Thr Trp Gln  
100

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..777
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

attggaacaa aatattttct tagaaaaaaa attatgggat tttgcttctc caaatttggc 60  
aaatcacaaa cacatgagat cccaatctct tcctcttccg attcaagccc tcctcatcac 120  
taccaacctc tccctaaacc aactgtttct caaggtaaaa ccagtaatcc cacctccaat 180  
cctcagccca aacccaaacc cgctcctcct cctcctccgt caacatcctc cggttcacaa 240  
atcgggtccaa tcctaaaccg accaatgatc gatctctcag ctctctacga cctccacaaa 300  
gaactcggcc gtggccaatt cggaatcact tacaaatgca cggacaaatc caacggtcga 360  
gaatacgccct gcaaatccat ctcaaaacgt aaactcatac gtcgcaaaga catcgaagac 420  
gtgagacgtg aggtcatgat cttgcaacac cttactggtc aaccaaacat agtcgagttt 480  
cgaggcgctg atgaagacaa agacaatctt catttggtta tggagctctg ttctggagga 540  
gattatgttg gtggtggcca tcaactgatga gtggtgaggc tcatgctcat gcattcgtaa 600  
cgttgttata ttattttaatt aaatggaaaa tgataaatta attattgcaa taaaatgata 660  
cattagcaat tgtgtatgtc gttattttta ttttgagtcg cattgtatgc tgattccata 720  
tgttcggctt tggtcggttt caagtgtggt taataaaatg gttattttac ttttggc

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

Ile Gly Thr Lys Tyr Phe Leu Arg Lys Lys Ile Met Gly Phe Cys Phe  
1 5 10 15  
Ser Lys Phe Gly Lys Ser Gln Thr His Glu Ile Pro Ile Ser Ser Ser  
20 25 30  
Ser Asp Ser Ser Pro Pro His His Tyr Gln Pro Leu Pro Lys Pro Thr  
35 40 45  
Val Ser Gln Gly Gln Thr Ser Asn Pro Thr Ser Asn Pro Gln Pro Lys  
50 55 60  
Pro Lys Pro Ala Pro Pro Pro Pro Pro Ser Thr Ser Ser Gly Ser Gln  
65 70 75 80  
Ile Gly Pro Ile Leu Asn Arg Pro Met Ile Asp Leu Ser Ala Leu Tyr  
85 90 95  
Asp Leu His Lys Glu Leu Gly Arg Gly Gln Phe Gly Ile Thr Tyr Lys  
100 105 110

Cys Thr Asp Lys Ser Asn Gly Arg Glu Tyr Ala Cys Lys Ser Ile Ser  
115 120 125  
Lys Arg Lys Leu Ile Arg Arg Lys Asp Ile Glu Asp Val Arg Arg Glu  
130 135 140  
Val Met Ile Leu Gln His Leu Thr Gly Gln Pro Asn Ile Val Glu Phe  
145 150 155 160  
Arg Gly Ala Tyr Glu Asp Lys Asp Asn Leu His Leu Val Met Glu Leu  
165 170 175  
Cys Ser Gly Gly Asp Tyr Val Gly Gly His His  
180 185

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1498673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Met Gly Phe Cys Phe Ser Lys Phe Gly Lys Ser Gln Thr His Glu Ile  
1 5 10 15  
Pro Ile Ser Ser Ser Ser Asp Ser Ser Pro Pro His His Tyr Gln Pro  
20 25 30  
Leu Pro Lys Pro Thr Val Ser Gln Gly Gln Thr Ser Asn Pro Thr Ser  
35 40 45  
Asn Pro Gln Pro Lys Pro Lys Pro Ala Pro Pro Pro Pro Pro Ser Thr  
50 55 60  
Ser Ser Gly Ser Gln Ile Gly Pro Ile Leu Asn Arg Pro Met Ile Asp  
65 70 75 80  
Leu Ser Ala Leu Tyr Asp Leu His Lys Glu Leu Gly Arg Gly Gln Phe  
85 90 95  
Gly Ile Thr Tyr Lys Cys Thr Asp Lys Ser Asn Gly Arg Glu Tyr Ala  
100 105 110  
Cys Lys Ser Ile Ser Lys Arg Lys Leu Ile Arg Arg Lys Asp Ile Glu  
115 120 125  
Asp Val Arg Arg Glu Val Met Ile Leu Gln His Leu Thr Gly Gln Pro  
130 135 140  
Asn Ile Val Glu Phe Arg Gly Ala Tyr Glu Asp Lys Asp Asn Leu His  
145 150 155 160  
Leu Val Met Glu Leu Cys Ser Gly Gly Asp Tyr Val Gly Gly Gly His  
165 170 175  
His

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1498674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

Met Ile Asp Leu Ser Ala Leu Tyr Asp Leu His Lys Glu Leu Gly Arg  
1 5 10 15  
Gly Gln Phe Gly Ile Thr Tyr Lys Cys Thr Asp Lys Ser Asn Gly Arg

20 25 30  
Glu Tyr Ala Cys Lys Ser Ile Ser Lys Arg Lys Leu Ile Arg Arg Lys  
35 40 45  
Asp Ile Glu Asp Val Arg Arg Glu Val Met Ile Leu Gln His Leu Thr  
50 55 60  
Gly Gln Pro Asn Ile Val Glu Phe Arg Gly Ala Tyr Glu Asp Lys Asp  
65 70 75 80  
Asn Leu His Leu Val Met Glu Leu Cys Ser Gly Gly Asp Tyr Val Gly  
85 90 95  
Gly Gly His His  
100

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..489  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| aatacaagtg | atttccatta | tttctcgtct  | acgtatacaa | ttgatcttcc  | cccattctcca | 60  |
| attcagattt | ggacagaggt | atTTTTtgat  | ccgattctta | cgaatcctga  | atcttcctcg  | 120 |
| tagattaatc | gatcgatcgg | ttcttaattc  | gcggaaaatt | gtttcagtaa  | cctgtgatcg  | 180 |
| tgtcggttgg | ggtagaagag | atcgaaagtgg | gagcaaaatc | atgatgaatc  | ggctattcgg  | 240 |
| gaaacccaag | caggaggcta | atgctctcca  | aactttagac | aagcttaacg  | agacgcttgg  | 300 |
| agatgctaga | gaaaaaggag | aaagtactct  | tgaagaaagc | tgggtgcagag | gttgagaagg  | 360 |
| caaaagaata | ctcccgggct | aagaacaaac  | gagcggctat | acagtstttg  | aaaaggaaga  | 420 |
| ggtyatatga | gggacaagtc | gaacagcttg  | ggaatttctt | ttgccttctc  | acctctatca  | 480 |
| tcattctatc |            |             |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..117  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

Ile Gln Val Ile Ser Ile Ile Ser Arg Leu Arg Ile Gln Leu Ile Phe  
1 5 10 15  
Pro His Leu Gln Phe Arg Phe Gly Gln Arg Tyr Phe Leu Ile Arg Phe  
20 25 30  
Leu Arg Ile Leu Asn Leu Pro Arg Arg Leu Ile Asp Arg Ser Val Leu  
35 40 45  
Asn Ser Arg Lys Ile Val Ser Val Thr Cys Asp Arg Val Gly Trp Gly  
50 55 60  
Arg Arg Asp Arg Ser Gly Ser Lys Ile Met Met Asn Arg Leu Phe Gly  
65 70 75 80  
Lys Pro Lys Gln Glu Ala Asn Ala Leu Gln Thr Leu Asp Lys Leu Asn  
85 90 95  
Glu Thr Leu Gly Asp Ala Arg Glu Lys Gly Glu Ser Thr Leu Glu Glu  
100 105 110  
Ser Trp Cys Arg Gly  
115

(2) INFORMATION FOR SEQ ID NO:590:

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(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 62 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..62  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498681  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:  
Met Leu Glu Lys Lys Glu Lys Val Leu Leu Lys Lys Ala Gly Ala Glu  
1                    5                    10                    15  
Val Glu Lys Ala Lys Glu Tyr Ser Arg Ala Lys Asn Lys Arg Ala Ala  
                    20                    25                    30  
Ile Gln Xaa Leu Lys Arg Lys Arg Xaa Tyr Glu Gly Gln Val Glu Gln  
                    35                    40                    45  
Leu Gly Asn Phe Phe Cys Leu Leu Thr Ser Ile Ile Ile Tyr  
50                    55                    60

(2) INFORMATION FOR SEQ ID NO:591:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 2409 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..2409  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1498682  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:  
aaaaaaaaaga tttctagtag aaagagagaa gggcgtgaat tcctgagcga gagattcttc 60  
gccggagtaa tctctttgcg tgatcttacc ggctgcttaa ttcgtcttcg cctgattcgt 120  
tggtttcaaa attcgtctct ctctttcaat cggagggttaa ttgtttttct gtttggggggt 180  
caaagcgaag atggtgaacg ctatggtgga gagagcgacg agcgangatg ctgatcgggc 240  
ctgattgggc tatgaacctc gagatctgtg atatgctcaa tagcgatcca ggcgaasaaa 300  
agatgtttgt aaaggcatta aaaaacggat tggtagcagg aatccaaaag ctcagcttct 360  
tgcttaact ctgcttgaga caatagtga gaactgtggt gacatgggtc atatgcatgt 420  
ggctgagaaa ggtgttattc atgagatggt ccggaatagt aagaagaagc cggacttcca 480  
tgtcaaagag aagattctgg tccttatcga tacatggcaa gaggcctttg gtggccctag 540  
ggcaagatat ccacaatact atgcaggata ccaggaattg ttgcgtgctg gtgctgtttt 600  
ccctcagaga tcagagagat cagctcctgt gttcacacct cctcaaacac agcctttgac 660  
atcttaccct ccaaattctt gtaacgctgg acctggtaat gatgtgcctg aaccttcagc 720  
agagccagaa tttccgactc taagtgtgtc ggagattcaa aatgcaaaaag gtatcatgga 780  
tgtgcttgcg gagatgctga gtgcattaga gcccggaaac aaggaggatc tcaaacaaga 840  
ggttatggtc gatctggtgg agcagtgtcg tacatacaaa caaagagtgg tgcacctcgt 900  
caactcgact tcggacgagt ctttgttatg tcaaggctctg gctttgaatg atgacttgca 960  
gcgtgtctta accaattatg aagcaattgc ttctggatta cctggaactt cttctcagat 1020  
cgagaagccc aagtccgaga caggaaaatc ccttggtgat gttgatggtc cacttattga 1080  
tacaggggac agcagtaatc aggcgaacgg agctacatcg agctctggta acggggttct 1140  
aaatcagttg gccctccctg caccacctgt aactaatggt tcagccaatt ccaaaataga 1200  
cctcctcagt ggcgatgata ttgcccttgt tcctgttggg accttctca gccagcaagt 1260  
ccggttgcat cagatcaaaa tgcaactcgc cttatcgaca tgttctcaga taataactat 1320  
aatccaagtc ctgcaactgc accaagtggc aatccagctc agaataattoc tttgaatcct 1380  
caagggcacc aacaacaaaa tagtcaagct ggagaagctg gattacaaca atccaatgga 1440  
tttgcgctc aagtgggtta ttgcagttt gagcagccat catacgggca aggagtctct 1500  
tctccctgga gcagtcagcc tgcacagcaa ccagtccagc catcttatga aggtgccccaa 1560  
gacagtacgg catttccacc tcccccatgg gaagctcagc tccaagacta tagtccctct 1620  
gcggagtcag gaagtccgtt ttctcctgga atgcatccaa ctcagactgc cttcacacat 1680  
gctcaaccag ttaacaacaa caatccatat cctcaaattc cccaaaccgg gccaccagtc 1740  
aacaataaca gtccatatgc tcaaatgccc caaacaggtc aagcagttgc caacatcagt 1800

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| ccatatacctc | aaattccaca | aaacggcgtg | tacatgccar | actttcaacc | aaatcaggct  | 1860 |
| cttgggtcag  | gctatcaacc | acagcaacaa | cagcagcagc | agatgatgat | ggctcagtac  | 1920 |
| tatgcccac   | agcaacagct | acagcaacaa | caacagcaac | aggcgtatgg | aaaccagatg  | 1980 |
| ggaggatacg  | gatatggcta | ntamtcaaca | gcaacaagga | agcagcccat | atctggacca  | 2040 |
| gcaaagtac   | ggtttatcca | tgagagacca | gacatcgcat | caggtagcat | catcatcatc  | 2100 |
| taccacatct  | tatctgcctc | caatgaaacc | taagaataaa | ccagaggaca | agctatttgg  | 2160 |
| ggatcttgtg  | gacatctcca | aattcaagcc | tacaaaaccg | acttccggaa | gagctggtag  | 2220 |
| catgtgaaaa  | ttcctccatc | cattcatcat | ttaccagtat | tcattctctc | tatcctcctc  | 2280 |
| agctaactct  | ctttcttctc | tttgtaagc  | ttttttcatc | attgatttta | ttaccctctt  | 2340 |
| gggagataca  | tagatataca | tatgtgttat | gttcttcctt | ataatttacc | gttgggttatg | 2400 |
| ggtttggtc   |            |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1498683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | His | Met | His | Val | Ala | Glu | Lys | Gly | Val | Ile | His | Glu | Met | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ile | Val | Lys | Lys | Pro | Asp | Phe | His | Val | Lys | Glu | Lys | Ile | Leu |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Val | Leu | Ile | Asp | Thr | Trp | Gln | Glu | Ala | Phe | Gly | Gly | Pro | Arg | Ala | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Tyr | Pro | Gln | Tyr | Tyr | Ala | Gly | Tyr | Gln | Glu | Leu | Leu | Arg | Ala | Gly | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Phe | Pro | Gln | Arg | Ser | Glu | Arg | Ser | Ala | Pro | Val | Phe | Thr | Pro | Pro |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Thr | Gln | Pro | Leu | Thr | Ser | Tyr | Pro | Pro | Asn | Leu | Arg | Asn | Ala | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Gly | Asn | Asp | Val | Pro | Glu | Pro | Ser | Ala | Glu | Pro | Glu | Phe | Pro | Thr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ser | Leu | Ser | Glu | Ile | Gln | Asn | Ala | Lys | Gly | Ile | Met | Asp | Val | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Glu | Met | Leu | Ser | Ala | Leu | Glu | Pro | Gly | Asn | Lys | Glu | Asp | Leu | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Glu | Val | Met | Val | Asp | Leu | Val | Glu | Gln | Cys | Arg | Thr | Tyr | Lys | Gln |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | Val | Val | His | Leu | Val | Asn | Ser | Thr | Ser | Asp | Glu | Ser | Leu | Leu | Cys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Gly | Leu | Ala | Leu | Asn | Asp | Asp | Leu | Gln | Arg | Val | Leu | Thr | Asn | Tyr |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Ala | Ile | Ala | Ser | Gly | Leu | Pro | Gly | Thr | Ser | Ser | Gln | Ile | Glu | Lys |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Lys | Ser | Glu | Thr | Gly | Lys | Ser | Leu | Val | Asp | Val | Asp | Gly | Pro | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Asp | Thr | Gly | Asp | Ser | Ser | Asn | Gln | Ala | Asn | Gly | Ala | Thr | Ser | Ser |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Gly | Asn | Gly | Val | Leu | Asn | Gln | Leu | Ala | Leu | Pro | Ala | Pro | Pro | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Asn | Gly | Ser | Ala | Asn | Ser | Lys | Ile | Asp | Leu | Leu | Ser | Gly | Asp | Asp |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Ala | Leu | Val | Pro | Val | Gly | Thr | Phe | Leu | Ser | Gln | Gln | Val | Arg | Leu |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| His | Gln | Ile | Lys | Met | His | Ser | Pro | Leu | Ser | Thr | Cys | Ser | Gln | Ile | Ile |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

Leu Ile Ile Gln Val Leu Gln Leu His Gln Val Ala Ile Gln Leu Arg  
305 310 315 320  
Ile Phe Leu

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 1498684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

Met His Val Ala Glu Lys Gly Val Ile His Glu Met Val Arg Ile Val  
1 5 10 15  
Lys Lys Lys Pro Asp Phe His Val Lys Glu Lys Ile Leu Val Leu Ile  
20 25 30  
Asp Thr Trp Gln Glu Ala Phe Gly Gly Pro Arg Ala Arg Tyr Pro Gln  
35 40 45  
Tyr Tyr Ala Gly Tyr Gln Glu Leu Leu Arg Ala Gly Ala Val Phe Pro  
50 55 60  
Gln Arg Ser Glu Arg Ser Ala Pro Val Phe Thr Pro Pro Gln Thr Gln  
65 70 75 80  
Pro Leu Thr Ser Tyr Pro Pro Asn Leu Arg Asn Ala Gly Pro Gly Asn  
85 90 95  
Asp Val Pro Glu Pro Ser Ala Glu Pro Glu Phe Pro Thr Leu Ser Leu  
100 105 110  
Ser Glu Ile Gln Asn Ala Lys Gly Ile Met Asp Val Leu Ala Glu Met  
115 120 125  
Leu Ser Ala Leu Glu Pro Gly Asn Lys Glu Asp Leu Lys Gln Glu Val  
130 135 140  
Met Val Asp Leu Val Glu Gln Cys Arg Thr Tyr Lys Gln Arg Val Val  
145 150 155 160  
His Leu Val Asn Ser Thr Ser Asp Glu Ser Leu Leu Cys Gln Gly Leu  
165 170 175  
Ala Leu Asn Asp Asp Leu Gln Arg Val Leu Thr Asn Tyr Glu Ala Ile  
180 185 190  
Ala Ser Gly Leu Pro Gly Thr Ser Ser Gln Ile Glu Lys Pro Lys Ser  
195 200 205  
Glu Thr Gly Lys Ser Leu Val Asp Val Asp Gly Pro Leu Ile Asp Thr  
210 215 220  
Gly Asp Ser Ser Asn Gln Ala Asn Gly Ala Thr Ser Ser Ser Gly Asn  
225 230 235 240  
Gly Val Leu Asn Gln Leu Ala Leu Pro Ala Pro Pro Val Thr Asn Gly  
245 250 255  
Ser Ala Asn Ser Lys Ile Asp Leu Leu Ser Gly Asp Asp Leu Ala Leu  
260 265 270  
Val Pro Val Gly Thr Phe Leu Ser Gln Gln Val Arg Leu His Gln Ile  
275 280 285  
Lys Met His Ser Pro Leu Ser Thr Cys Ser Gln Ile Leu Ile Ile  
290 295 300  
Gln Val Leu Gln Leu His Gln Val Ala Ile Gln Leu Arg Ile Phe Leu  
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..309  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498685  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Arg | Ile | Val | Lys | Lys | Lys | Pro | Asp | Phe | His | Val | Lys | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Leu | Val | Leu | Ile | Asp | Thr | Trp | Gln | Glu | Ala | Phe | Gly | Gly | Pro | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Arg | Tyr | Pro | Gln | Tyr | Tyr | Ala | Gly | Tyr | Gln | Glu | Leu | Leu | Arg | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ala | Val | Phe | Pro | Gln | Arg | Ser | Glu | Arg | Ser | Ala | Pro | Val | Phe | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Pro | Gln | Thr | Gln | Pro | Leu | Thr | Ser | Tyr | Pro | Pro | Asn | Leu | Arg | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Gly | Pro | Gly | Asn | Asp | Val | Pro | Glu | Pro | Ser | Ala | Glu | Pro | Glu | Phe |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Pro | Thr | Leu | Ser | Leu | Ser | Glu | Ile | Gln | Asn | Ala | Lys | Gly | Ile | Met | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Leu | Ala | Glu | Met | Leu | Ser | Ala | Leu | Glu | Pro | Gly | Asn | Lys | Glu | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Lys | Gln | Glu | Val | Met | Val | Asp | Leu | Val | Glu | Gln | Cys | Arg | Thr | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Gln | Arg | Val | Val | His | Leu | Val | Asn | Ser | Thr | Ser | Asp | Glu | Ser | Leu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Cys | Gln | Gly | Leu | Ala | Leu | Asn | Asp | Asp | Leu | Gln | Arg | Val | Leu | Thr |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asn | Tyr | Glu | Ala | Ile | Ala | Ser | Gly | Leu | Pro | Gly | Thr | Ser | Ser | Gln | Ile |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Glu | Lys | Pro | Lys | Ser | Glu | Thr | Gly | Lys | Ser | Leu | Val | Asp | Val | Asp | Gly |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Leu | Ile | Asp | Thr | Gly | Asp | Ser | Ser | Asn | Gln | Ala | Asn | Gly | Ala | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Ser | Ser | Gly | Asn | Gly | Val | Leu | Asn | Gln | Leu | Ala | Leu | Pro | Ala | Pro |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Pro | Val | Thr | Asn | Gly | Ser | Ala | Asn | Ser | Lys | Ile | Asp | Leu | Leu | Ser | Gly |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Asp | Asp | Leu | Ala | Leu | Val | Pro | Val | Gly | Thr | Phe | Leu | Ser | Gln | Gln | Val |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Arg | Leu | His | Gln | Ile | Lys | Met | His | Ser | Pro | Leu | Ser | Thr | Cys | Ser | Gln |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ile | Ile | Leu | Ile | Ile | Gln | Val | Leu | Gln | Leu | His | Gln | Val | Ala | Ile | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Arg | Ile | Phe | Leu |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 860 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..860  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498686  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| aaacccaaaa  | aaaaaaactt | aagaaaat   | gaaatcctca | gaattgcaga  | gcaaagaaca | 60  |
| accatggcga  | atcctattca | agagattctg | gagaaccaag | ttctaacggt  | ggctaaagct | 120 |
| atggaagata  | agatagacaa | cgagatcgcc | tctttagaaa | agcttgacga  | ggacgatcta | 180 |
| gaggttttga  | gagagagaag | gttaaagcaa | atgaagaaaa | tggcagagaa  | gaagaaacgt | 240 |
| tggattagtc  | ttggacatgg | tgaatactct | gagatccatt | ctgagaaaaga | cttcttctcc | 300 |
| gtcgttaaag  | ccagcgaacg | cgtcgtctgc | catttctacc | gcgagaattg  | gccatgtaaa | 360 |
| gtgatggata  | mscacatgag | tatattggca | aagcaacaca | ttgagacacg  | ttttgtgaag | 420 |
| atccaagctg  | agaaaagtc  | gttcttggct | gagaggctca | agattgttgt  | tctacctact | 480 |
| cttgcaactta | ttaagaacac | taaagtcgat | gattatgtgg | ttgggttcaa  | tgagcttgga | 540 |
| gggaaagatg  | atttcagcac | tgaggatttg | gaagagagaa | tagctagagc  | gcaagtgatt | 600 |
| cattacgatg  | gagagtcac  | gtcgtctaaa | ccaaagtcga | caacacaagt  | tagaaggaa  | 660 |
| gtgaggcaga  | gtgctcgttc | agattcagac | tccgaataga | ctctcggtt   | tttcagcaaa | 720 |
| cgtttgttg   | tatgttcac  | atcttcactc | tatcttcagc | ccttttttgg  | tgtgagttg  | 780 |
| tattgtgcga  | attcagttgt | gatgtgtaat | acaaagtagg | agatgatctt  | atatgcata  | 840 |
| ttgatgagtt  | tttaacctg  |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Lys | Lys | Lys | Asn | Leu | Arg | Lys | Phe | Glu | Ile | Leu | Arg | Ile | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Gln | Arg | Thr | Thr | Met | Ala | Asn | Pro | Ile | Gln | Glu | Ile | Leu | Glu | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Val | Leu | Thr | Val | Ala | Lys | Ala | Met | Glu | Asp | Lys | Ile | Asp | Asn | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ala | Ser | Leu | Glu | Lys | Leu | Asp | Glu | Asp | Asp | Leu | Glu | Val | Leu | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Arg | Arg | Leu | Lys | Gln | Met | Lys | Lys | Met | Ala | Glu | Lys | Lys | Lys | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Trp | Ile | Ser | Leu | Gly | His | Gly | Glu | Tyr | Ser | Glu | Ile | His | Ser | Glu | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Phe | Phe | Ser | Val | Val | Lys | Ala | Ser | Glu | Arg | Val | Val | Cys | His | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Arg | Glu | Asn | Trp | Pro | Cys | Lys | Val | Met | Asp | Xaa | His | Met | Ser | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ala | Lys | Gln | His | Ile | Glu | Thr | Arg | Phe | Val | Lys | Ile | Gln | Ala | Glu |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Lys | Ser | Pro | Phe | Leu | Ala | Glu | Arg | Leu | Lys | Ile | Val | Val | Leu | Pro | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Ala | Leu | Ile | Lys | Asn | Thr | Lys | Val | Asp | Tyr | Val | Val | Gly | Phe |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asn | Glu | Leu | Gly | Gly | Lys | Asp | Asp | Phe | Ser | Thr | Glu | Asp | Leu | Glu | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ile | Ala | Arg | Ala | Gln | Val | Ile | His | Tyr | Asp | Gly | Glu | Ser | Ser | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Lys | Pro | Lys | Ser | Thr | Thr | Gln | Val | Arg | Arg | Asn | Val | Arg | Gln | Ser |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Ala | Arg | Ser | Asp | Ser | Asp | Ser | Glu |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..211  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498688  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

Met Ala Asn Pro Ile Gln Glu Ile Leu Glu Asn Gln Val Leu Thr Val  
1 5 10 15  
Ala Lys Ala Met Glu Asp Lys Ile Asp Asn Glu Ile Ala Ser Leu Glu  
20 25 30  
Lys Leu Asp Glu Asp Asp Leu Glu Val Leu Arg Glu Arg Arg Leu Lys  
35 40 45  
Gln Met Lys Lys Met Ala Glu Lys Lys Lys Arg Trp Ile Ser Leu Gly  
50 55 60  
His Gly Glu Tyr Ser Glu Ile His Ser Glu Lys Asp Phe Phe Ser Val  
65 70 75 80  
Val Lys Ala Ser Glu Arg Val Val Cys His Phe Tyr Arg Glu Asn Trp  
85 90 95  
Pro Cys Lys Val Met Asp Xaa His Met Ser Ile Leu Ala Lys Gln His  
100 105 110  
Ile Glu Thr Arg Phe Val Lys Ile Gln Ala Glu Lys Ser Pro Phe Leu  
115 120 125  
Ala Glu Arg Leu Lys Ile Val Val Leu Pro Thr Leu Ala Leu Ile Lys  
130 135 140  
Asn Thr Lys Val Asp Asp Tyr Val Val Gly Phe Asn Glu Leu Gly Gly  
145 150 155 160  
Lys Asp Asp Phe Ser Thr Glu Asp Leu Glu Glu Arg Ile Ala Arg Ala  
165 170 175  
Gln Val Ile His Tyr Asp Gly Glu Ser Ser Ser Leu Lys Pro Lys Ser  
180 185 190  
Thr Thr Gln Val Arg Arg Asn Val Arg Gln Ser Ala Arg Ser Asp Ser  
195 200 205  
Asp Ser Glu  
210

(2) INFORMATION FOR SEQ ID NO:598:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 192 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..192  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498689  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

Met Glu Asp Lys Ile Asp Asn Glu Ile Ala Ser Leu Glu Lys Leu Asp  
1 5 10 15  
Glu Asp Asp Leu Glu Val Leu Arg Glu Arg Arg Leu Lys Gln Met Lys  
20 25 30  
Lys Met Ala Glu Lys Lys Lys Arg Trp Ile Ser Leu Gly His Gly Glu  
35 40 45  
Tyr Ser Glu Ile His Ser Glu Lys Asp Phe Phe Ser Val Val Lys Ala  
50 55 60  
Ser Glu Arg Val Val Cys His Phe Tyr Arg Glu Asn Trp Pro Cys Lys  
65 70 75 80  
Val Met Asp Xaa His Met Ser Ile Leu Ala Lys Gln His Ile Glu Thr  
85 90 95  
Arg Phe Val Lys Ile Gln Ala Glu Lys Ser Pro Phe Leu Ala Glu Arg

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 100 |     | 105 |     | 110 |     |     |     |     |     |     |     |     |     |     |
| Leu | Lys | Ile | Val | Val | Leu | Pro | Thr | Leu | Ala | Leu | Ile | Lys | Asn | Thr | Lys |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Asp | Asp | Tyr | Val | Val | Gly | Phe | Asn | Glu | Leu | Gly | Gly | Lys | Asp | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Ser | Thr | Glu | Asp | Leu | Glu | Glu | Arg | Ile | Ala | Arg | Ala | Gln | Val | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| His | Tyr | Asp | Gly | Glu | Ser | Ser | Ser | Leu | Lys | Pro | Lys | Ser | Thr | Thr | Gln |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Val | Arg | Arg | Asn | Val | Arg | Gln | Ser | Ala | Arg | Ser | Asp | Ser | Asp | Ser | Glu |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1418
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| aacttagcct  | tgttcttctt  | cttcatcgcg  | atatctccgg  | tgtcttcttc  | gtctccatca | 60   |
| gaagaagaag  | ctctctgtat  | ccatccatat  | cgaaaaacca  | gagatcggag  | gaaggagaga | 120  |
| gagataccaa  | tctctgttgc  | tttggtttta  | agggtttaga  | ggagatgtca  | aaccacccga | 180  |
| agatcacatc  | ggcgcatcag  | aatgtggagg  | agaagctaag  | ggaacttcag  | gagaggttct | 240  |
| gtcatcttca  | agctgctagg  | aaagaagggc  | ggcatggtga  | ccttgcgctt  | ttagaagccc | 300  |
| aaatctctca  | gaatattcgg  | gagtggaag   | ctgaactcac  | tgctccttct  | cctgaatctt | 360  |
| ctctgttggg  | tgaaggtatt  | agccaattcc  | ttgaggagtt  | tgctcctctg  | ttgaaattag | 420  |
| acgaggagga  | tgatgcaact  | agtacgctaa  | aagaacatgc  | tggagcaaaag | cctgatcctg | 480  |
| agggtttttc  | tcaaagcttg  | tgccctcctg  | aatggacatc  | tgagaatttt  | agtcaaagtc | 540  |
| ctttcaacgg  | aaatttctcc  | tgcggttttg  | aggatgctct  | taatagcaca  | gaaacacatg | 600  |
| gccagcaact  | ccattatgga  | tatgaagggt  | ttgatccaag  | cataaaactcc | gctcctgatt | 660  |
| tccatgacca  | aaaactcagc  | agcaacttgg  | atataacttc  | tcagtatgat  | tatatcttct | 720  |
| ccgaagtgcg  | tcaggaacta  | gataacagcc  | cttccactaa  | gcttgattct  | tctgaagaga | 780  |
| ttgacaaact  | tgctgaattt  | tctactccat  | caagtgtccg  | tgtgcctcca  | tctgcttttc | 840  |
| tgggacctaa  | gtgtgcaact  | tgggattgca  | caaggcctgc  | tcagggtctc  | gagtggtacc | 900  |
| tggattactg  | cagtaactac  | catgggactc  | tagctctgaa  | tgaagattcg  | cctggcacag | 960  |
| cacctgtatt  | gaggccaggg  | ggcatcagtt  | tgaagataaa  | tctattgatt  | gatgctcttc | 1020 |
| gtgcaaagac  | tcagggttaag | aatgtttggga | tcccagtgtg  | tgaaggagct  | gttaacacaa | 1080 |
| aatgcccattg | gaacgcagca  | gagctatttc  | atcttgaact  | ggttgaaggc  | gaaacaatta | 1140 |
| gagagtggct  | cttctttgac  | aaacctagaa  | gagcatatga  | tagcggaaac  | cgaaagcaaa | 1200 |
| gatcaacttc  | agattacagt  | ggaagagggt  | ggcatgaatc  | aagaaaacaa  | ctgatgaagg | 1260 |
| aacaagaagg  | ccagaagaga  | tcttactata  | tggatccaca  | acctccaggt  | ccctttgagt | 1320 |
| ggcatctctt  | tgaataccaa  | atcaatgaat  | ctgacgcgatg | tgcgttatat  | cgcctagaac | 1380 |
| ttaaagttagg | aaatggaaaag | aagagtccta  | agggaaaag   |             |            |      |

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..472
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

Leu Ser Leu Val Leu Leu Leu His Arg Asp Ile Ser Gly Val Phe Phe  
1 5 10 15  
Val Ser Ile Arg Arg Arg Ser Ser Leu Tyr Pro Ser Ile Ser Lys Asn  
20 25 30  
Gln Arg Ser Glu Glu Gly Glu Arg Asp Thr Asn Leu Cys Cys Phe Gly  
35 40 45  
Phe Lys Gly Leu Glu Glu Met Ser Asn His Pro Lys Ile Thr Ser Ala  
50 55 60  
His Gln Asn Val Glu Glu Lys Leu Arg Glu Leu Gln Glu Arg Phe Cys  
65 70 75 80  
His Leu Gln Ala Ala Arg Lys Glu Gly Arg His Gly Asp Leu Ala Leu  
85 90 95  
Leu Glu Ala Gln Ile Ser Gln Asn Ile Arg Glu Trp Gln Ala Glu Leu  
100 105 110  
Thr Ala Pro Ser Pro Glu Ser Ser Leu Leu Gly Glu Gly Ile Ser Gln  
115 120 125  
Phe Leu Glu Glu Phe Ala Pro Leu Leu Lys Leu Asp Glu Glu Asp Asp  
130 135 140  
Ala Thr Ser Thr Leu Lys Glu His Ala Gly Ala Lys Pro Asp Pro Glu  
145 150 155 160  
Gly Phe Ser Gln Ser Leu Cys Pro Pro Glu Trp Thr Ser Glu Asn Phe  
165 170 175  
Ser Gln Ser Pro Phe Asn Gly Asn Phe Ser Cys Gly Phe Glu Asp Ala  
180 185 190  
Leu Asn Ser Thr Glu Thr His Gly Gln Gln Leu His Tyr Gly Tyr Glu  
195 200 205  
Gly Phe Asp Pro Ser Ile Asn Ser Ala Pro Asp Phe His Asp Gln Lys  
210 215 220  
Leu Ser Ser Asn Leu Asp Ile Thr Ser Gln Tyr Asp Tyr Ile Phe Ser  
225 230 235 240  
Glu Val Arg Gln Glu Leu Asp Asn Ser Pro Ser Thr Lys Leu Asp Ser  
245 250 255  
Ser Glu Glu Ile Asp Asn Phe Ala Glu Phe Ser Thr Pro Ser Ser Val  
260 265 270  
Arg Val Pro Pro Ser Ala Phe Leu Gly Pro Lys Cys Ala Leu Trp Asp  
275 280 285  
Cys Thr Arg Pro Ala Gln Gly Ser Glu Trp Tyr Leu Asp Tyr Cys Ser  
290 295 300  
Asn Tyr His Gly Thr Leu Ala Leu Asn Glu Asp Ser Pro Gly Thr Ala  
305 310 315 320  
Pro Val Leu Arg Pro Gly Gly Ile Ser Leu Lys Asp Asn Leu Leu Ile  
325 330 335  
Asp Ala Leu Arg Ala Lys Thr Gln Gly Lys Asn Val Gly Ile Pro Val  
340 345 350  
Cys Glu Gly Ala Val Asn Thr Lys Cys Pro Trp Asn Ala Ala Glu Leu  
355 360 365  
Phe His Leu Glu Leu Val Glu Gly Glu Thr Ile Arg Glu Trp Leu Phe  
370 375 380  
Phe Asp Lys Pro Arg Arg Ala Tyr Asp Ser Gly Asn Arg Lys Gln Arg  
385 390 395 400  
Ser Leu Pro Asp Tyr Ser Gly Arg Gly Trp His Glu Ser Arg Lys Gln  
405 410 415  
Leu Met Lys Glu Gln Glu Gly Gln Lys Arg Ser Tyr Tyr Met Asp Pro  
420 425 430  
Gln Pro Pro Gly Pro Phe Glu Trp His Leu Phe Glu Tyr Gln Ile Asn  
435 440 445  
Glu Ser Asp Ala Cys Ala Leu Tyr Arg Leu Glu Leu Lys Val Gly Asn  
450 455 460  
Gly Lys Lys Ser Pro Lys Gly Lys  
465 470  
(2) INFORMATION FOR SEQ ID NO:601:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 418 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..418  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498692  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Asn | His | Pro | Lys | Ile | Thr | Ser | Ala | His | Gln | Asn | Val | Glu | Glu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Lys | Leu | Arg | Glu | Leu | Gln | Glu | Arg | Phe | Cys | His | Leu | Gln | Ala | Ala | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Glu | Gly | Arg | His | Gly | Asp | Leu | Ala | Leu | Leu | Glu | Ala | Gln | Ile | Ser |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Gln | Asn | Ile | Arg | Glu | Trp | Gln | Ala | Glu | Leu | Thr | Ala | Pro | Ser | Pro | Glu |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Ser | Ser | Leu | Leu | Gly | Glu | Gly | Ile | Ser | Gln | Phe | Leu | Glu | Glu | Phe | Ala |  |
| 65  |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |  |
| Pro | Leu | Leu | Lys | Leu | Asp | Glu | Glu | Asp | Asp | Ala | Thr | Ser | Thr | Leu | Lys |  |
|     |     |     | 85  |     |     |     |     |     |     | 90  |     |     |     |     | 95  |  |
| Glu | His | Ala | Gly | Ala | Lys | Pro | Asp | Pro | Glu | Gly | Phe | Ser | Gln | Ser | Leu |  |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |  |
| Cys | Pro | Pro | Glu | Trp | Thr | Ser | Glu | Asn | Phe | Ser | Gln | Ser | Pro | Phe | Asn |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Gly | Asn | Phe | Ser | Cys | Gly | Phe | Glu | Asp | Ala | Leu | Asn | Ser | Thr | Glu | Thr |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |  |
| His | Gly | Gln | Gln | Leu | His | Tyr | Gly | Tyr | Glu | Gly | Phe | Asp | Pro | Ser | Ile |  |
| 145 |     |     |     |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |  |
| Asn | Ser | Ala | Pro | Asp | Phe | His | Asp | Gln | Lys | Leu | Ser | Ser | Asn | Leu | Asp |  |
|     |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |  |
| Ile | Thr | Ser | Gln | Tyr | Asp | Tyr | Ile | Phe | Ser | Glu | Val | Arg | Gln | Glu | Leu |  |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |  |
| Asp | Asn | Ser | Pro | Ser | Thr | Lys | Leu | Asp | Ser | Ser | Glu | Glu | Ile | Asp | Asn |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |  |
| Phe | Ala | Glu | Phe | Ser | Thr | Pro | Ser | Ser | Val | Arg | Val | Pro | Pro | Ser | Ala |  |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |  |
| Phe | Leu | Gly | Pro | Lys | Cys | Ala | Leu | Trp | Asp | Cys | Thr | Arg | Pro | Ala | Gln |  |
| 225 |     |     |     |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |  |
| Gly | Ser | Glu | Trp | Tyr | Leu | Asp | Tyr | Cys | Ser | Asn | Tyr | His | Gly | Thr | Leu |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ala | Leu | Asn | Glu | Asp | Ser | Pro | Gly | Thr | Ala | Pro | Val | Leu | Arg | Pro | Gly |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |  |
| Gly | Ile | Ser | Leu | Lys | Asp | Asn | Leu | Leu | Ile | Asp | Ala | Leu | Arg | Ala | Lys |  |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |  |
| Thr | Gln | Gly | Lys | Asn | Val | Gly | Ile | Pro | Val | Cys | Glu | Gly | Ala | Val | Asn |  |
|     |     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |  |
| Thr | Lys | Cys | Pro | Trp | Asn | Ala | Ala | Glu | Leu | Phe | His | Leu | Glu | Leu | Val |  |
| 305 |     |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |  |
| Glu | Gly | Glu | Thr | Ile | Arg | Glu | Trp | Leu | Phe | Phe | Asp | Lys | Pro | Arg | Arg |  |
|     |     |     | 325 |     |     |     |     |     |     | 330 |     |     |     |     | 335 |  |
| Ala | Tyr | Asp | Ser | Gly | Asn | Arg | Lys | Gln | Arg | Ser | Leu | Pro | Asp | Tyr | Ser |  |
|     |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |  |
| Gly | Arg | Gly | Trp | His | Glu | Ser | Arg | Lys | Gln | Leu | Met | Lys | Glu | Gln | Glu |  |
|     |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |  |
| Gly | Gln | Lys | Arg | Ser | Tyr | Tyr | Met | Asp | Pro | Gln | Pro | Pro | Gly | Pro | Phe |  |
|     |     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |  |
| Glu | Trp | His | Leu | Phe | Glu | Tyr | Gln | Ile | Asn | Glu | Ser | Asp | Ala | Cys | Ala |  |
| 385 |     |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |  |

Leu Tyr Arg Leu Glu Leu Lys Val Gly Asn Gly Lys Lys Ser Pro Lys  
405 410 415  
Gly Lys

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1896

(D) OTHER INFORMATION: / Ceres Seq. ID 1498703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| aaaaactcgc  | cgccgtggag  | agagaagaga | gaatggagga  | tatcgaggat  | ttgttgggccg | 60   |
| gaggagtcgg  | tggtgcacca  | ccgggattcc | gattaccctt  | gaatgcagtc  | gggattaatc  | 120  |
| cgaagacgaa  | taagagcaaa  | cgtattagct | cgaaaccgga  | tcaaattact  | gcttcgaatc  | 180  |
| gtgactcgct  | tgctccacca  | tcgatgaaga | ttccaggaac  | tcagacgata  | tacatcaaga  | 240  |
| cgtttggtatg | ttctcataat  | cagagtata  | gtgagtatat  | ggctgggtcag | ctttctgcat  | 300  |
| ttggctatgc  | gttgacagaa  | gtcccggagg | aagctgattt  | atggctcatt  | aacacctgta  | 360  |
| ctgtgaagtc  | ccctagccag  | tctgcgatgt | ctactttgat  | aacgaggggt  | agaagtggga  | 420  |
| aaaagcctct  | tgtgattgca  | ggatgtgttc | ctcagggcag  | tcgtgatctt  | aaagaactgg  | 480  |
| aaggcgtag   | tgtagttgga  | gtccaacaga | ttgatcgtgt  | tggtgagatt  | gttgaagaaa  | 540  |
| ctcttaaggg  | tcatgaagta  | cggttgctga | ctcgggaagac | tttgccctgcg | cttgatctcc  | 600  |
| caaaggtgcg  | gaggaacaat  | tttatcgaaa | ttctcccat   | taatgttggc  | tggttggtg   | 660  |
| cctgtactta  | ctgcaagacc  | aagcatgcc  | gtggtcattt  | aggaagttac  | acagttgata  | 720  |
| gtcttggtga  | gcggttgaga  | actgtaatct | ctgaaggagt  | caaggagatt  | tggttaagca  | 780  |
| gcgaggacac  | tgagcatat   | ggtcgtgaca | taggagttaa  | tcttccaata  | ctgcttaatg  | 840  |
| ctatcgttaa  | ggaacttct   | tctgatcaaa | gcacaatgct  | aaggattggg  | atgactaatc  | 900  |
| ctccctttat  | tttagagcat  | ttgaaagaaa | tagcggcagt  | gttacgtcac  | ccatgtgtct  | 960  |
| acacctttct  | tcatgtccct  | gtgcaatctg | gtagcgattc  | tggtgtgacg  | gccatgaaca  | 1020 |
| gggaatatac  | agcaagtgcg  | ttcaggactg | tggtagacac  | cttaacagag  | cttggtgccg  | 1080 |
| gaatgcaaat  | tgctactgat  | ataatatgct | gttttcctgg  | tgaaaccgat  | gaagattttt  | 1140 |
| ctcagacagt  | tgaactcatc  | aaggattaca | agtttcctca  | agttcatatt  | tctcagtttt  | 1200 |
| accccgagacc | agggaccccca | gcagcaaaga | tgaagaaggt  | acaaagtaaa  | atagtgaagc  | 1260 |
| aacgaagccg  | tgaattgact  | tctgtctttg | aggcttttgc  | accttacacc  | ggaatggagt  | 1320 |
| gcagagaaga  | gaggatatgg  | ataactgaag | tagctactga  | tggaattcat  | ttggttgac   | 1380 |
| atacgaaggg  | atatgtacag  | gtcttagtta | ctggaccaga  | aagtatgctt  | gggacttcag  | 1440 |
| ctatggcgag  | gataacatct  | gtggggagat | ggtcagattt  | tggggaagtg  | attgagacat  | 1500 |
| ttagctctgc  | aaatagagaa  | acaaaatccc | gagaggaaaac | aaagctgcct  | tggtcgtcga  | 1560 |
| atgtagcac   | ttgtgagact  | tgcacttgct | ctgctgagag  | ctgtggagaa  | gagagatcag  | 1620 |
| gagaggcgtg  | taacatttct  | ggaaatatct | caggacaaga  | tgataacaag  | ggaaagtcaa  | 1680 |
| agaaagaaga  | gaaggaggta  | caagagggtc | tcgtaccggg  | aagcagcgta  | gcaaattggg  | 1740 |
| gtttcattga  | taaggcactt  | gtctgtggag | tggtcgtgaag | ctctgtcacc  | attcttgttt  | 1800 |
| tggttgattag | cattgcatgt  | agagttttgc | tgcggtaatg  | aatcagtggt  | tccgactaat  | 1860 |
| gtagtctttc  | gaataatttt  | cgtcttttac | ttgtct      |             |             |      |

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..611

(D) OTHER INFORMATION: / Ceres Seq. ID 1498704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

Lys Leu Ala Ala Val Glu Arg Glu Glu Arg Met Glu Asp Ile Glu Asp

|                                                                 |   |     |     |
|-----------------------------------------------------------------|---|-----|-----|
| 1                                                               | 5 | 10  | 15  |
| Leu Leu Ala Gly Gly Val Gly Gly Ala Pro Pro Gly Phe Arg Leu Pro |   |     |     |
| 20                                                              |   | 25  | 30  |
| Leu Asn Ala Val Gly Ile Asn Pro Lys Thr Asn Lys Ser Lys Arg Ile |   |     |     |
| 35                                                              |   | 40  | 45  |
| Ser Ser Lys Pro Asp Gln Ile Thr Ala Ser Asn Arg Asp Ser Leu Ala |   |     |     |
| 50                                                              |   | 55  | 60  |
| Pro Pro Ser Met Lys Ile Pro Gly Thr Gln Thr Ile Tyr Ile Lys Thr |   |     |     |
| 65                                                              |   | 70  | 75  |
| Phe Gly Cys Ser His Asn Gln Ser Asp Ser Glu Tyr Met Ala Gly Gln |   |     |     |
| 85                                                              |   | 90  | 95  |
| Leu Ser Ala Phe Gly Tyr Ala Leu Thr Glu Val Pro Glu Glu Ala Asp |   |     |     |
| 100                                                             |   | 105 | 110 |
| Leu Trp Leu Ile Asn Thr Cys Thr Val Lys Ser Pro Ser Gln Ser Ala |   |     |     |
| 115                                                             |   | 120 | 125 |
| Met Ser Thr Leu Ile Thr Arg Gly Arg Ser Gly Lys Lys Pro Leu Val |   |     |     |
| 130                                                             |   | 135 | 140 |
| Ile Ala Gly Cys Val Pro Gln Gly Ser Arg Asp Leu Lys Glu Leu Glu |   |     |     |
| 145                                                             |   | 150 | 155 |
| Gly Val Ser Val Val Gly Val Gln Gln Ile Asp Arg Val Val Glu Ile |   |     |     |
| 165                                                             |   | 170 | 175 |
| Val Glu Glu Thr Leu Lys Gly His Glu Val Arg Leu Leu Thr Arg Lys |   |     |     |
| 180                                                             |   | 185 | 190 |
| Thr Leu Pro Ala Leu Asp Leu Pro Lys Val Arg Arg Asn Asn Phe Ile |   |     |     |
| 195                                                             |   | 200 | 205 |
| Glu Ile Leu Pro Ile Asn Val Gly Cys Leu Gly Ala Cys Thr Tyr Cys |   |     |     |
| 210                                                             |   | 215 | 220 |
| Lys Thr Lys His Ala Arg Gly His Leu Gly Ser Tyr Thr Val Asp Ser |   |     |     |
| 225                                                             |   | 230 | 235 |
| Leu Val Glu Arg Val Arg Thr Val Ile Ser Glu Gly Val Lys Glu Ile |   |     |     |
| 245                                                             |   | 250 | 255 |
| Trp Leu Ser Ser Glu Asp Thr Gly Ala Tyr Gly Arg Asp Ile Gly Val |   |     |     |
| 260                                                             |   | 265 | 270 |
| Asn Leu Pro Ile Leu Leu Asn Ala Ile Val Lys Glu Leu Pro Ser Asp |   |     |     |
| 275                                                             |   | 280 | 285 |
| Gln Ser Thr Met Leu Arg Ile Gly Met Thr Asn Pro Pro Phe Ile Leu |   |     |     |
| 290                                                             |   | 295 | 300 |
| Glu His Leu Lys Glu Ile Ala Ala Val Leu Arg His Pro Cys Val Tyr |   |     |     |
| 305                                                             |   | 310 | 315 |
| Thr Phe Leu His Val Pro Val Gln Ser Gly Ser Asp Ser Val Leu Thr |   |     |     |
| 325                                                             |   | 330 | 335 |
| Ala Met Asn Arg Glu Tyr Thr Ala Ser Glu Phe Arg Thr Val Val Asp |   |     |     |
| 340                                                             |   | 345 | 350 |
| Thr Leu Thr Glu Leu Val Pro Gly Met Gln Ile Ala Thr Asp Ile Ile |   |     |     |
| 355                                                             |   | 360 | 365 |
| Cys Gly Phe Pro Gly Glu Thr Asp Glu Asp Phe Ser Gln Thr Val Glu |   |     |     |
| 370                                                             |   | 375 | 380 |
| Leu Ile Lys Asp Tyr Lys Phe Pro Gln Val His Ile Ser Gln Phe Tyr |   |     |     |
| 385                                                             |   | 390 | 395 |
| Pro Arg Pro Gly Thr Pro Ala Ala Lys Met Lys Lys Val Gln Ser Lys |   |     |     |
| 405                                                             |   | 410 | 415 |
| Ile Val Lys Gln Arg Ser Arg Glu Leu Thr Ser Val Phe Glu Ala Phe |   |     |     |
| 420                                                             |   | 425 | 430 |
| Ala Pro Tyr Thr Gly Met Glu Cys Arg Glu Glu Arg Ile Trp Ile Thr |   |     |     |
| 435                                                             |   | 440 | 445 |
| Glu Val Ala Thr Asp Gly Ile His Leu Val Gly His Thr Lys Gly Tyr |   |     |     |
| 450                                                             |   | 455 | 460 |
| Val Gln Val Leu Val Thr Gly Pro Glu Ser Met Leu Gly Thr Ser Ala |   |     |     |
| 465                                                             |   | 470 | 475 |
| Met Ala Arg Ile Thr Ser Val Gly Arg Trp Ser Val Phe Gly Glu Val |   |     |     |
| 485                                                             |   | 490 | 495 |

2025 RELEASE UNDER E.O. 14176

[illegible]

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 601 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..601

(D) OTHER INFORMATION: / Ceres Seq. ID 1498705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

|            |            |            |           |            |            |            |            |           |            |            |            |            |            |           |            |
|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Glu        | Asp        | Ile       | Glu<br>5   | Asp        | Leu        | Leu        | Ala       | Gly<br>10  | Gly        | Val        | Gly        | Gly        | Ala<br>15 | Pro        |
| Pro        | Gly        | Phe        | Arg<br>20 | Leu        | Pro        | Leu        | Asn        | Ala<br>25 | Val        | Gly        | Ile        | Asn        | Pro<br>30  | Lys       | Thr        |
| Asn        | Lys        | Ser<br>35  | Lys       | Arg        | Ile        | Ser        | Ser<br>40  | Lys       | Pro        | Asp        | Gln        | Ile<br>45  | Thr        | Ala       | Ser        |
| Asn        | Arg<br>50  | Asp        | Ser       | Leu        | Ala<br>55  | Pro        | Pro        | Ser       | Met        | Lys<br>60  | Ile        | Pro        | Gly        | Thr       | Gln        |
| Thr<br>65  | Ile        | Tyr        | Ile       | Lys<br>70  | Thr        | Phe        | Gly        | Cys       | Ser<br>75  | His        | Asn        | Gln        | Ser        | Asp       | Ser<br>80  |
| Glu        | Tyr        | Met        | Ala       | Gly<br>85  | Gln        | Leu        | Ser        | Ala       | Phe<br>90  | Gly        | Tyr        | Ala        | Leu        | Thr       | Glu        |
| Val        | Pro        | Glu<br>100 | Glu       | Ala        | Asp        | Leu        | Trp<br>105 | Leu       | Ile        | Asn        | Thr        | Cys<br>110 | Thr        | Val       | Lys        |
| Ser        | Pro        | Ser<br>115 | Gln       | Ser        | Ala        | Met        | Ser<br>120 | Thr       | Leu        | Ile        | Thr        | Arg<br>125 | Gly        | Arg       | Ser        |
| Gly        | Lys<br>130 | Lys        | Pro       | Leu        | Val        | Ile<br>135 | Ala        | Gly       | Cys        | Val<br>140 | Pro        | Gln        | Gly        | Ser       | Arg        |
| Asp<br>145 | Leu        | Lys        | Glu       | Leu<br>150 | Glu        | Gly        | Val        | Ser       | Val<br>155 | Val        | Gly        | Val        | Gln        | Gln       | Ile<br>160 |
| Asp        | Arg        | Val        | Val       | Glu<br>165 | Ile        | Val        | Glu        | Glu       | Thr<br>170 | Leu        | Lys        | Gly        | His<br>175 | Glu       | Val        |
| Arg        | Leu        | Leu<br>180 | Thr       | Arg        | Lys        | Thr        | Leu<br>185 | Pro       | Ala        | Leu        | Asp        | Leu<br>190 | Pro        | Lys       | Val        |
| Arg        | Arg        | Asn<br>195 | Asn       | Phe        | Ile        | Glu        | Ile<br>200 | Leu       | Pro        | Ile        | Asn<br>205 | Val        | Gly        | Cys       | Leu        |
| Gly        | Ala<br>210 | Cys        | Thr       | Tyr        | Cys<br>215 | Lys        | Thr        | Lys       | His        | Ala<br>220 | Arg        | Gly        | His        | Leu       | Gly        |
| Ser<br>225 | Tyr        | Thr        | Val       | Asp<br>230 | Ser        | Leu        | Val        | Glu       | Arg<br>235 | Val        | Arg        | Thr        | Val        | Ile       | Ser<br>240 |
| Glu        | Gly        | Val        | Lys       | Glu<br>245 | Ile        | Trp        | Leu        | Ser       | Ser<br>250 | Glu        | Asp        | Thr        | Gly        | Ala       | Tyr        |
| Gly        | Arg        | Asp        | Ile       | Gly        | Val        | Asn        | Leu        | Pro       | Ile        | Leu        | Leu        | Asn        | Ala        | Ile       | Val        |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Glu | Leu | Pro | Ser | Asp | Gln | Ser | Thr | Met | Leu | Arg | Ile | Gly | Met | Thr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Pro | Pro | Phe | Ile | Leu | Glu | His | Leu | Lys | Glu | Ile | Ala | Ala | Val | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | His | Pro | Cys | Val | Tyr | Thr | Phe | Leu | His | Val | Pro | Val | Gln | Ser | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Asp | Ser | Val | Leu | Thr | Ala | Met | Asn | Arg | Glu | Tyr | Thr | Ala | Ser | Glu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Phe | Arg | Thr | Val | Val | Asp | Thr | Leu | Thr | Glu | Leu | Val | Pro | Gly | Met | Gln |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ile | Ala | Thr | Asp | Ile | Ile | Cys | Gly | Phe | Pro | Gly | Glu | Thr | Asp | Glu | Asp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Phe | Ser | Gln | Thr | Val | Glu | Leu | Ile | Lys | Asp | Tyr | Lys | Phe | Pro | Gln | Val |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| His | Ile | Ser | Gln | Phe | Tyr | Pro | Arg | Pro | Gly | Thr | Pro | Ala | Ala | Lys | Met |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Lys | Lys | Val | Gln | Ser | Lys | Ile | Val | Lys | Gln | Arg | Ser | Arg | Glu | Leu | Thr |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ser | Val | Phe | Glu | Ala | Phe | Ala | Pro | Tyr | Thr | Gly | Met | Glu | Cys | Arg | Glu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Glu | Arg | Ile | Trp | Ile | Thr | Glu | Val | Ala | Thr | Asp | Gly | Ile | His | Leu | Val |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Gly | His | Thr | Lys | Gly | Tyr | Val | Gln | Val | Leu | Val | Thr | Gly | Pro | Glu | Ser |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Met | Leu | Gly | Thr | Ser | Ala | Met | Ala | Arg | Ile | Thr | Ser | Val | Gly | Arg | Trp |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ser | Val | Phe | Gly | Glu | Val | Ile | Glu | Thr | Phe | Ser | Ser | Ala | Asn | Arg | Glu |
|     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Thr | Lys | Ser | Arg | Glu | Glu | Thr | Lys | Leu | Pro | Cys | Ser | Ser | Asn | Val | Ser |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Thr | Cys | Glu | Thr | Cys | Thr | Cys | Ser | Ala | Glu | Ser | Cys | Gly | Glu | Glu | Arg |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Ser | Gly | Glu | Ala | Cys | Asn | Ile | Ser | Gly | Asn | Ile | Ser | Gly | Gln | Asp | Asp |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Asn | Lys | Gly | Lys | Ser | Lys | Lys | Glu | Glu | Lys | Glu | Val | Gln | Glu | Val | Val |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Val | Pro | Gly | Ser | Ser | Val | Ala | Asn | Trp | Gly | Phe | Ile | Asp | Lys | Ala | Leu |
|     |     |     | 565 |     |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Val | Cys | Gly | Val | Phe | Val | Ser | Ser | Val | Thr | Ile | Leu | Val | Leu | Leu | Ile |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Ser | Ile | Ala | Cys | Arg | Val | Leu | Leu | Arg |     |     |     |     |     |     |     |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..544
(D) OTHER INFORMATION
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1498706
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

Met	Lys	Ile	Pro	Gly	Thr	Gln	Thr	Ile	Tyr	Ile	Lys	Thr	Phe	Gly	Cys
1				5					10					15	
Ser	His	Asn	Gln	Ser	Asp	Ser	Glu	Tyr	Met	Ala	Gly	Gln	Leu	Ser	Ala
			20					25					30		
Phe	Gly	Tyr	Ala	Leu	Thr	Glu	Val	Pro	Glu	Glu	Ala	Asp	Leu	Trp	Leu
		35					40					45			

Ile	Asn	Thr	Cys	Thr	Val	Lys	Ser	Pro	Ser	Gln	Ser	Ala	Met	Ser	Thr
50						55					60				
Leu	Ile	Thr	Arg	Gly	Arg	Ser	Gly	Lys	Lys	Pro	Leu	Val	Ile	Ala	Gly
65					70					75					80
Cys	Val	Pro	Gln	Gly	Ser	Arg	Asp	Leu	Lys	Glu	Leu	Glu	Gly	Val	Ser
				85					90					95	
Val	Val	Gly	Val	Gln	Gln	Ile	Asp	Arg	Val	Val	Glu	Ile	Val	Glu	Glu
				100				105					110		
Thr	Leu	Lys	Gly	His	Glu	Val	Arg	Leu	Leu	Thr	Arg	Lys	Thr	Leu	Pro
							120					125			
Ala	Leu	Asp	Leu	Pro	Lys	Val	Arg	Arg	Asn	Asn	Phe	Ile	Glu	Ile	Leu
	130					135					140				
Pro	Ile	Asn	Val	Gly	Cys	Leu	Gly	Ala	Cys	Thr	Tyr	Cys	Lys	Thr	Lys
145					150					155					160
His	Ala	Arg	Gly	His	Leu	Gly	Ser	Tyr	Thr	Val	Asp	Ser	Leu	Val	Glu
				165					170					175	
Arg	Val	Arg	Thr	Val	Ile	Ser	Glu	Gly	Val	Lys	Glu	Ile	Trp	Leu	Ser
				180				185					190		
Ser	Glu	Asp	Thr	Gly	Ala	Tyr	Gly	Arg	Asp	Ile	Gly	Val	Asn	Leu	Pro
		195					200					205			
Ile	Leu	Leu	Asn	Ala	Ile	Val	Lys	Glu	Leu	Pro	Ser	Asp	Gln	Ser	Thr
	210					215					220				
Met	Leu	Arg	Ile	Gly	Met	Thr	Asn	Pro	Pro	Phe	Ile	Leu	Glu	His	Leu
225					230					235					240
Lys	Glu	Ile	Ala	Ala	Val	Leu	Arg	His	Pro	Cys	Val	Tyr	Thr	Phe	Leu
				245					250					255	
His	Val	Pro	Val	Gln	Ser	Gly	Ser	Asp	Ser	Val	Leu	Thr	Ala	Met	Asn
				260				265					270		
Arg	Glu	Tyr	Thr	Ala	Ser	Glu	Phe	Arg	Thr	Val	Val	Asp	Thr	Leu	Thr
		275					280					285			
Glu	Leu	Val	Pro	Gly	Met	Gln	Ile	Ala	Thr	Asp	Ile	Ile	Cys	Gly	Phe
	290					295					300				
Pro	Gly	Glu	Thr	Asp	Glu	Asp	Phe	Ser	Gln	Thr	Val	Glu	Leu	Ile	Lys
305					310					315					320
Asp	Tyr	Lys	Phe	Pro	Gln	Val	His	Ile	Ser	Gln	Phe	Tyr	Pro	Arg	Pro
				325					330					335	
Gly	Thr	Pro	Ala	Ala	Lys	Met	Lys	Lys	Val	Gln	Ser	Lys	Ile	Val	Lys
				340				345					350		
Gln	Arg	Ser	Arg	Glu	Leu	Thr	Ser	Val	Phe	Glu	Ala	Phe	Ala	Pro	Tyr
		355					360					365			
Thr	Gly	Met	Glu	Cys	Arg	Glu	Glu	Arg	Ile	Trp	Ile	Thr	Glu	Val	Ala
	370					375					380				
Thr	Asp	Gly	Ile	His	Leu	Val	Gly	His	Thr	Lys	Gly	Tyr	Val	Gln	Val
385					390					395					400
Leu	Val	Thr	Gly	Pro	Glu	Ser	Met	Leu							

530

535

540

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

```
ctctttcctt aagtgtcaaa ctcttgaaaa aactactttg aaggaaaaaa tgtctaagaa      60
gaagaaaggc agcaacaact ttaagcttct ctgtttcttc ctgttttttg gtggtttggt      120
tcagacagat gcttcttttg gagtaggagg cggcggttga gtaggaatcg gcggcggcgg      180
cgggtggcggg ggcggtggtg tttgggttgg cggtggtata aacaacggtt gaaatcgtaa      240
tgctgttcca ggatcatcag ctccaaacag ggtagcttac aatgctcttc aagtttgtaa      300
atcagccatg agagaggatc catcaaatgt tctcaaaaca tgggttggat cagatgtttg      360
ttcttacaaa ggtgtgttct gttctggtca atctataacc tctatagatc ttaacctgc      420
aatcttcaaa ggcacacttg tcaaagacct agctttactc tcagacctca atattctcca      480
tctcaacagt aacagattct cagggcacaa cccagattct ttcaaactct tagcttctct      540
tcaagaactt gatctaagca acaataaact ctacaggtcct ttccctttag tcacactcta      600
cataccaaat ctggtttacc tcgatctccg gtttaatagt ttaaccggtt tcatccctga      660
agagcttttc aacaaacggt tagacgcgat tctcctcaat aacaatcaat tcgtcggaga      720
aatcccaaga aacctcgga attctccggc ttcggttatt aatctcgcga ataacagatt      780
ttccggcgaa attccgacga gttttggtct gacgggatcg aggggttaagg aagttttgct      840
tttgaataac cagttaaccg gttgtatacc ggaatctggt ggtatgttct ctgaaattga      900
agtctttgac gttagctaca atgcattgat ggtcatggt ccagatacga tctcttgctt      960
gtcggcgatt gaaattttga atcttgcctc caataaattc tctggggagg ttcctgattt     1020
ggtttggttcg ttgaggaatc ttattaatct cactgttgcg ttcaatttct tctctgggtt     1080
tagctctgaa tgttcttcca ggtttagttt cgggttgat ttcggtggga attgtattcc     1140
cgggaggaat tcgcagcggc cgcagccgga ttgttccggt tattccggcg gagctatgag     1200
ctgttttagg attccgacgc agcctttggc ttgtgctgcg ataagtgttg gattgagaga     1260
gagtaataat caatactaca cttcatctcc tccatgaaag tttctaaagt tagaagcttt     1320
tttttattaa tgggtgatgc tgaatgatct atcttttttg taacttatta attagttgat     1380
tagtgaccaa attaaacggt aattcctctt ctgtgtaatc caatcggtgc taatgttgtt     1440
ttgt
```

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..329
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

```
Met Arg Glu Asp Pro Ser Asn Val Leu Lys Thr Trp Val Gly Ser Asp
1          5          10          15
Val Cys Ser Tyr Lys Gly Val Phe Cys Ser Gly Gln Ser Ile Thr Ser
20          25          30
Ile Asp Leu Asn His Ala Asn Leu Lys Gly Thr Leu Val Lys Asp Leu
35          40          45
Ala Leu Leu Ser Asp Leu Asn Ile Leu His Leu Asn Ser Asn Arg Phe
50          55          60
Ser Gly Gln Ile Pro Asp Ser Phe Lys Ser Leu Ala Ser Leu Gln Glu
```

65					70					75					80
Leu	Asp	Leu	Ser	Asn 85	Asn	Lys	Leu	Ser	Gly 90	Pro	Phe	Pro	Leu	Val 95	Thr
Leu	Tyr	Ile	Pro 100	Asn	Leu	Val	Tyr	Leu 105	Asp	Leu	Arg	Phe	Asn 110	Ser	Leu
Thr	Gly	Phe 115	Ile	Pro	Glu	Glu	Leu 120	Phe	Asn	Lys	Arg	Leu 125	Asp	Ala	Ile
Leu	Leu	Asn	Asn	Asn 130	Gln	Phe	Val 135	Gly	Glu	Ile	Pro	Arg 140	Asn	Leu	Gly
Asn 145	Ser	Pro	Ala	Ser	Val 150	Ile	Asn	Leu	Ala	Asn 155	Asn	Arg	Phe	Ser	Gly 160
Glu	Ile	Pro	Thr	Ser 165	Phe	Gly	Leu	Thr	Gly 170	Ser	Arg	Val	Lys 175	Glu	Val
Leu	Leu	Leu	Asn 180	Asn	Gln	Leu	Thr	Gly 185	Cys	Ile	Pro	Glu	Ser 190	Val	Gly
Met	Phe	Ser 195	Glu	Ile	Glu	Val	Phe 200	Asp	Val	Ser	Tyr	Asn 205	Ala	Leu	Met
Gly	His 210	Val	Pro	Asp	Thr 215	Ile	Ser	Cys	Leu	Ser	Ala 220	Ile	Glu	Ile	Leu
Asn 225	Leu	Ala	His	Asn 230	Lys	Phe	Ser	Gly	Glu	Val 235	Pro	Asp	Leu	Val	Cys 240
Ser	Leu	Arg	Asn 245	Leu	Ile	Asn	Leu	Thr	Val 250	Ala	Phe	Asn	Phe 255	Phe	Ser
Gly	Phe	Ser	Ser 260	Glu	Cys	Ser	Ser	Arg 265	Val	Ser	Phe	Gly	Phe 270	Asp	Phe
Val	Gly	Asn 275	Cys	Ile	Pro	Gly	Arg 280	Asn	Ser	Gln	Arg	Pro 285	Gln	Pro	Asp
Cys	Ser 290	Gly	Tyr	Ser	Gly 295	Gly	Ala	Met	Ser	Cys	Phe 300	Arg	Ile	Pro	Thr
Gln 305	Pro	Leu	Ala	Cys 310	Ala	Ala	Ile	Ser	Val	Gly 315	Leu	Arg	Glu	Ser	Asn 320
Asn	Gln	Tyr	Tyr	Thr 325	Ser	Ser	Pro	Pro							

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1981 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1981
(D) OTHER INFORMATION: / Ceres Seq. ID 1498735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

atcgtttcacg	caaaaacttca	cgatttcagat	ctgtgtgtgtg	cagaatttga	atcgaagcat	60
aggatcaatc	cggtaagcag	ccgtaacttg	caatcgatcg	ccgatctgga	tccgttaaag	120
gatccctcgc	agtccttgaa	gatatcggcg	tcctccgcc	ccgggaacag	gatccgttac	180
cgttcacctt	ccgctttctg	gctattggag	tctggactag	ccaccggatt	atcccggtaac	240
cattctccta	cttcgcagc	tcatcaggga	cttgtgtcta	tcgacggagg	aaaaatgacg	300
cggaagcgag	cgatcggacg	gcacgaatcc	cttgctgaca	aggctccatcg	acatcgtggt	360
cttctacttg	tgatttctgat	ccccattgtg	ttgatagctc	ttgtgcttct	gttaatgccg	420
gggacgtcga	cgtcgcgtct	tgtcacgcag	tacacgatga	aaaaccacga	gggaggttcc	480
aattcagagg	gtccgaagaa	ttacgctgtg	atcttttgatg	ctggaagattc	tggaagccgt	540
gtcgtcggtt	actgttttga	tcagaatttg	gatcttgttc	ctttggagaa	tgagctcgag	600
ctcttctttac	agctaaaacc	gggtttaagt	gcatatccta	atgatcctcg	gcaatcagca	660
aactcttttag	taactcttct	ggacaaaagca	gaagcttccg	ttccccgtga	gttgcggtcca	720
aagactcctg	tcagagttgg	ggcaactgca	ggtttgagag	ctttgggtca	ccaagcctct	780
gaaaacattt	tgcaagcggg	agtcctctca	aggtagaagt	aggctgaaga	ctgaggcaaa	840
tgcagtgaact	gttctggatg	gtactcagga	aggatcttat	cagtgggtga	caattaaata	900
cttgcctaagg	actttgggaa	agccgtactc	ggacacagtt	ggagtggttg	atcttgaggg	960

ggggtcggtt	caaatggcat	atgctatacc	agaggaagat	gctgcaactg	cacaaaaacc	1020
agtagaaggc	gaggattctt	atgtcagaga	aatgtatttg	aagggacgaa	agtatttcct	1080
ctatgttcat	agctacctac	attacgggtt	actggctgct	cgggctgaga	ttttgaaagt	1140
ttctgaggac	tctaacaacc	cctgtatcgc	gactggatat	gctggtacct	acaaatatgg	1200
aggaaaagcg	tttaaagctg	cagcttctcc	atccggtgca	agtctagatg	agtgccggcg	1260
agtagctatt	aacgcactca	aagtcaataa	ttcattgtgc	acacacatga	aatgcacttt	1320
tggtggagta	tggaatgggtg	gaggcgggtg	tggccagaag	aaaatgtttg	ttgcatcatt	1380
tttcttcgat	cgagccgcag	aggctgggtt	tggtgaccca	aaccaacctg	tggctgaggt	1440
tcgaccactt	gactttgaga	aagcggccaa	caaagcttgt	aacatgagaa	tggagaagg	1500
gaaatcgaag	ttcccacgtg	tggaggaaga	taatcttcct	tacttgtgct	tggatcttgt	1560
ttaccaatat	actcttctcg	tcgatggatt	cggattgaag	ccatcacaga	caataacgtt	1620
agtgaagaag	gtgaaatacg	gagattacgc	cgtggaagct	gcgtggccac	taggaagcgc	1680
catagaagca	gtatcctcac	catgaggaag	gcaattttgg	gtatttgcac	taaacctctt	1740
attcttttag	tttctcccaa	aatcacccca	agcttttttt	gccttacctc	aaattttttt	1800
tatcgtcaac	atcttcctta	catcaatttt	tgttacaata	atcatctaga	gaaaagagtt	1860
tcaattctta	atataacctat	aatttttatt	ttcttgtaat	ctaaactgct	taccgcatac	1920
gtaacctctg	tttctttctt	ataaaatatt	ttccttgcg	ttttttttct	tttgacgact	1980

g

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1498736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

Ile	Val	His	Ala	Lys	Leu	His	Asp	Ser	Asp	Leu	Cys	Val	Ala	Glu	Phe
1				5					10					15	
Glu	Ser	Lys	His	Arg	Ile	Asn	Pro	Val	Ser	Ser	Arg	Asn	Leu	Gln	Ser
			20					25					30		
Ile	Ala	Asp	Leu	Asp	Pro	Leu	Lys	Asp	Pro	Ser	Gln	Ser	Leu	Lys	Ile
		35				40					45				
Ser	Ala	Ser	Ser	Ala	Thr	Gly	Asn	Arg	Ile	Arg	Tyr	Arg	Ser	Pro	Ser
	50					55					60				
Ala	Ser	Glu	Leu	Leu	Glu	Ser	Gly	Leu	Ala	Thr	Gly	Leu	Ser	Gly	Asn
65					70					75				80	
His	Ser	Pro	Thr	Ser	Asp	Ser	His	Gln	Gly	Leu	Val	Ser	Ile	Asp	Gly
			85					90						95	
Gly	Lys	Met	Thr	Ala	Lys	Arg	Ala	Ile	Gly	Arg	His	Glu	Ser	Leu	Ala
			100					105						110	
Asp	Lys	Val	His	Arg	His	Arg	Gly	Leu	Leu	Leu	Val	Ile	Ser	Ile	Pro
		115					120					125			
Ile	Val	Leu	Ile	Ala	Leu	Val	Leu	Leu	Leu	Met	Pro	Gly	Thr	Ser	Thr
	130				135						140				
Ser	Val	Ser	Val	Ile	Glu	Tyr	Thr	Met	Lys	Asn	His	Glu	Gly	Gly	Ser
145					150					155				160	
Asn	Ser	Arg	Gly	Pro	Lys	Asn	Tyr	Ala	Val	Ile	Phe	Asp	Ala	Gly	Ser
			165					170						175	
Ser	Gly	Ser	Arg	Val	His	Val	Tyr	Cys	Phe	Asp	Gln	Asn	Leu	Asp	Leu
			180					185					190		
Val	Pro	Leu	Glu	Asn	Glu	Leu	Glu	Leu	Phe	Leu	Gln	Leu	Lys	Pro	Gly
		195					200					205			
Leu	Ser	Ala	Tyr	Pro	Asn	Asp	Pro	Arg	Gln	Ser	Ala	Asn	Ser	Leu	Val
	210				215						220				
Thr	Leu	Leu	Asp	Lys	Ala	Glu	Ala	Ser	Val	Pro	Arg	Glu	Leu	Arg	Pro
225				230						235				240	
Lys	Thr	Pro	Val	Arg	Val	Gly	Ala	Thr	Ala	Gly	Leu	Arg	Ala	Leu	Gly

245 250 255
His Gln Ala Ser Glu Asn Ile Leu Gln Ala Gly Ala Pro Gln Arg
260 265 270

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1498737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

Met Ala Tyr Ala Ile Pro Glu Glu Asp Ala Ala Thr Ala Pro Lys Pro
1 5 10 15
Val Glu Gly Glu Asp Ser Tyr Val Arg Glu Met Tyr Leu Lys Gly Arg
20 25 30
Lys Tyr Phe Leu Tyr Val His Ser Tyr Leu His Tyr Gly Leu Leu Ala
35 40 45
Ala Arg Ala Glu Ile Leu Lys Val Ser Glu Asp Ser Asn Asn Pro Cys
50 55 60
Ile Ala Thr Gly Tyr Ala Gly Thr Tyr Lys Tyr Gly Gly Lys Ala Phe
65 70 75 80
Lys Ala Ala Ala Ser Pro Ser Gly Ala Ser Leu Asp Glu Cys Arg Arg
85 90 95
Val Ala Ile Asn Ala Leu Lys Val Asn Asn Ser Leu Cys Thr His Met
100 105 110
Lys Cys Thr Phe Gly Gly Val Trp Asn Gly Gly Gly Gly Gly Gly Gln
115 120 125
Lys Lys Met Phe Val Ala Ser Phe Phe Phe Asp Arg Ala Ala Glu Ala
130 135 140
Gly Phe Val Asp Pro Asn Gln Pro Val Ala Glu Val Arg Pro Leu Asp
145 150 155 160
Phe Glu Lys Ala Ala Asn Lys Ala Cys Asn Met Arg Met Glu Glu Gly
165 170 175
Lys Ser Lys Phe Pro Arg Val Glu Glu Asp Asn Leu Pro Tyr Leu Cys
180 185 190
Leu Asp Leu Val Tyr Gln Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu
195 200 205
Lys Pro Ser Gln Thr Ile Thr Leu Val Lys Lys Val Lys Tyr Gly Asp
210 215 220
Tyr Ala Val Glu Ala Ala Trp Pro Leu Gly Ser Ala Ile Glu Ala Val
225 230 235 240
Ser Ser Pro

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1498738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Met Tyr Leu Lys Gly Arg Lys Tyr Phe Leu Tyr Val His Ser Tyr Leu
1 5 10 15

His Tyr Gly Leu Leu Ala Ala Arg Ala Glu Ile Leu Lys Val Ser Glu
20 25 30
Asp Ser Asn Asn Pro Cys Ile Ala Thr Gly Tyr Ala Gly Thr Tyr Lys
35 40 45
Tyr Gly Gly Lys Ala Phe Lys Ala Ala Ala Ser Pro Ser Gly Ala Ser
50 55 60
Leu Asp Glu Cys Arg Arg Val Ala Ile Asn Ala Leu Lys Val Asn Asn
65 70 75 80
Ser Leu Cys Thr His Met Lys Cys Thr Phe Gly Gly Val Trp Asn Gly
85 90 95
Gly Gly Gly Gly Gly Gln Lys Lys Met Phe Val Ala Ser Phe Phe
100 105 110
Asp Arg Ala Ala Glu Ala Gly Phe Val Asp Pro Asn Gln Pro Val Ala
115 120 125
Glu Val Arg Pro Leu Asp Phe Glu Lys Ala Ala Asn Lys Ala Cys Asn
130 135 140
Met Arg Met Glu Glu Gly Lys Ser Lys Phe Pro Arg Val Glu Glu Asp
145 150 155 160
Asn Leu Pro Tyr Leu Cys Leu Asp Leu Val Tyr Gln Tyr Thr Leu Leu
165 170 175
Val Asp Gly Phe Gly Leu Lys Pro Ser Gln Thr Ile Thr Leu Val Lys
180 185 190
Lys Val Lys Tyr Gly Asp Tyr Ala Val Glu Ala Ala Trp Pro Leu Gly
195 200 205
Ser Ala Ile Glu Ala Val Ser Ser Pro
210 215

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1418
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

ttctctccgg	atTTTTctag	gttttcaatt	tttgttttac	cttcaaaggt	tgttcccttg	60
tgatataaaa	atatagtttt	caccttcttt	caatctctgc	ggtttctaaa	tagaacattg	120
gagagatttg	tttctgcatc	tgtaaatttt	gatttctttg	accatctctc	tgtttttgrt	180
ggcaacacac	gtattccaat	ccaaatcgac	aatatacgcg	tctctgatgg	atatgttttg	240
gattcagtga	gaaacagaga	ttgattttgg	ttttctttaa	tcattggtgga	gccttatgag	300
acacgtaaca	acggtgaagc	atcccagatg	atcagatatc	agagttataa	ccatcacaat	360
tccagactac	catcttcatt	atcatcgcca	ttgcttgatt	tgagagtgtt	ctatgtcaga	420
atcagtaatt	tcaaggtgga	tcattcgaca	cctgagggtc	tcaccattac	tcatttcctt	480
ttggatccag	attcacttct	ggagattaat	ggtgttagaa	tgagcatgta	ctctgaagga	540
gtttcttctc	agcttagggc	tgatcgtgtt	gataagaaat	ctgaagttgc	tactttttatc	600
agcacggata	atatcagggt	atctggtagt	gtgaagtttg	aggtttatga	taaagatgag	660
ctgggttttg	ctggaacgct	tgagatgtct	ggtagtaatg	gtttcactgg	tgaatctaag	720
catagcgtga	agcgggtgga	catgaattgt	gaagctgaga	tcactgcagg	gtctgggttc	780
ttgaaggaga	aacatatttg	tggttcggag	ttatcttctc	cattgccaac	tattgaagtc	840
tatgtcactg	gctgcttttc	tggaaactct	atcatcctaa	cgaagactct	acagcttggt	900
ttcagaaga	agcaggttag	agtgactgca	ttagattcga	ttcccagata	tgaactgat	960
gagcctcata	aaggaaactc	atctgagctt	gattatcagg	ttactgaata	tggaaagttat	1020
aaacaagaat	atgaaggaga	acacagcgac	atgtactgga	atagagagta	cgcagatggg	1080
gaagatgggtg	agatgtcgtg	gttcaacgct	ggtgtgaggg	ttggtgtggg	aattgggtctt	1140
ggtgtctgtg	taggtctttg	cattgggggt	ggccttcttg	tgcgtaacct	tcaatcgacc	1200
accagaaaact	tcagaaggag	gattatctag	tttcaattcaa	attgcctcaa	gcttcactcta	1260
ctctctccct	ctaactccaa	tccggttgca	atcaactttg	actgcagaac	tctaagctat	1320
atagtctaag	ctaatactgc	tgtgtagtat	aattttttgtt	ttatgtactt	tttaattctt	1380

ttgtgccttc aaattttgaa agaaatcatt ttcccttg

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..315

(D) OTHER INFORMATION: / Ceres Seq. ID 1498740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

Met	Val	Glu	Pro	Tyr	Glu	Thr	Arg	Asn	Asn	Gly	Glu	Ala	Ser	Gln	Met
1				5					10					15	
Ile	Arg	Tyr	Gln	Ser	Tyr	Asn	His	His	Asn	Ser	Arg	Leu	Pro	Ser	Ser
			20					25					30		
Leu	Ser	Ser	Pro	Leu	Leu	Asp	Leu	Arg	Val	Phe	Tyr	Val	Arg	Ile	Ser
			35				40					45			
Asn	Phe	Lys	Val	Asp	His	Ser	Thr	Pro	Glu	Val	Leu	Thr	Ile	Thr	His
	50					55					60				
Ile	Pro	Leu	Asp	Pro	Asp	Ser	Leu	Leu	Glu	Ile	Asn	Gly	Val	Arg	Met
65					70				75						80
Ser	Met	Tyr	Ser	Glu	Gly	Val	Ser	Ser	Gln	Leu	Arg	Arg	Asp	Arg	Val
				85					90					95	
Asp	Lys	Lys	Ser	Glu	Val	Ala	Thr	Phe	Ile	Ser	Thr	Asp	Asn	Ile	Arg
			100					105					110		
Leu	Ser	Gly	Ser	Val	Lys	Phe	Glu	Val	Tyr	Asp	Lys	Asp	Glu	Leu	Val
		115					120					125			
Leu	Ser	Gly	Thr	Leu	Glu	Met	Ser	Gly	Ser	Asn	Gly	Phe	Thr	Gly	Glu
		130				135					140				
Ser	Lys	His	Ser	Val	Lys	Arg	Trp	Asn	Met	Asn	Cys	Glu	Ala	Glu	Ile
145					150					155					160
Thr	Ala	Gly	Ser	Gly	Phe	Leu	Lys	Glu	Lys	His	Ile	Gly	Gly	Ser	Glu
				165				170						175	
Leu	Ser	Ser	Pro	Leu	Pro	Thr	Ile	Glu	Val	Tyr	Val	Thr	Gly	Cys	Phe
			180					185					190		
Ser	Gly	Thr	Pro	Ile	Ile	Leu	Thr	Lys	Thr	Leu	Gln	Leu	Gly	Phe	Arg
		195					200					205			
Lys	Lys	His	Gly	Arg	Val	Thr	Ala	Leu	Asp	Ser	Ile	Pro	Glu	Tyr	Glu
		210				215					220				
Thr	Asp	Glu	Pro	His	Lys	Gly	Asn	Ser	Ser	Glu	Leu	Asp	Tyr	Gln	Val
225					230					235					240
Thr	Glu	Tyr	Gly	Ser	Tyr	Lys	Gln	Glu	Tyr	Glu	Gly	Glu	His	Ser	Asp
				245				250						255	
Met	Tyr	Trp	Asn	Arg	Glu	Tyr	Ala	Asp	Gly	Glu	Asp	Gly	Glu	Met	Ser
			260					265					270		
Trp	Phe	Asn	Ala	Gly	Val	Arg	Val	Gly	Val	Gly	Ile	Gly	Leu	Gly	Val
		275					280					285			
Cys	Val	Gly	Leu	Gly	Ile	Gly	Val	Gly	Leu	Leu	Val	Arg	Thr	Tyr	Gln
		290				295					300				
Ser	Thr	Thr	Arg	Asn	Phe	Arg	Arg	Arg	Ile	Ile					
305					310				315						

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..300

(D) OTHER INFORMATION: / Ceres Seq. ID 1498741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

Met	Ile	Arg	Tyr	Gln	Ser	Tyr	Asn	His	His	Asn	Ser	Arg	Leu	Pro	Ser
1				5					10					15	
Ser	Leu	Ser	Ser	Pro	Leu	Leu	Asp	Leu	Arg	Val	Phe	Tyr	Val	Arg	Ile
			20					25					30		
Ser	Asn	Phe	Lys	Val	Asp	His	Ser	Thr	Pro	Glu	Val	Leu	Thr	Ile	Thr
		35					40					45			
His	Ile	Pro	Leu	Asp	Pro	Asp	Ser	Leu	Leu	Glu	Ile	Asn	Gly	Val	Arg
	50					55					60				
Met	Ser	Met	Tyr	Ser	Glu	Gly	Val	Ser	Ser	Gln	Leu	Arg	Arg	Asp	Arg
65					70					75				80	
Val	Asp	Lys	Lys	Ser	Glu	Val	Ala	Thr	Phe	Ile	Ser	Thr	Asp	Asn	Ile
			85						90					95	
Arg	Leu	Ser	Gly	Ser	Val	Lys	Phe	Glu	Val	Tyr	Asp	Lys	Asp	Glu	Leu
			100					105					110		
Val	Leu	Ser	Gly	Thr	Leu	Glu	Met	Ser	Gly	Ser	Asn	Gly	Phe	Thr	Gly
			115				120					125			
Glu	Ser	Lys	His	Ser	Val	Lys	Arg	Trp	Asn	Met	Asn	Cys	Glu	Ala	Glu
			130				135				140				
Ile	Thr	Ala	Gly	Ser	Gly	Phe	Leu	Lys	Glu	Lys	His	Ile	Gly	Gly	Ser
145					150					155					160
Glu	Leu	Ser	Ser	Pro	Leu	Pro	Thr	Ile	Glu	Val	Tyr	Val	Thr	Gly	Cys
				165					170					175	
Phe	Ser	Gly	Thr	Pro	Ile	Ile	Leu	Thr	Lys	Thr	Leu	Gln	Leu	Gly	Phe
			180					185					190		
Arg	Lys	Lys	His	Gly	Arg	Val	Thr	Ala	Leu	Asp	Ser	Ile	Pro	Glu	Tyr
			195				200					205			
Glu	Thr	Asp	Glu	Pro	His	Lys	Gly	Asn	Ser	Ser	Glu	Leu	Asp	Tyr	Gln
			210				215				220				
Val	Thr	Glu	Tyr	Gly	Ser	Tyr	Lys	Gln	Glu	Tyr	Glu	Gly	Glu	His	Ser
225					230					235					240
Asp	Met	Tyr	Trp	Asn	Arg	Glu	Tyr	Ala	Asp	Gly	Glu	Asp	Gly	Glu	Met
				245					250					255	
Ser	Trp	Phe	Asn	Ala	Gly	Val	Arg	Val	Gly	Val	Gly	Ile	Gly	Leu	Gly
			260					265					270		
Val	Cys	Val	Gly	Leu	Gly	Ile	Gly	Val	Gly	Leu	Leu	Val	Arg	Thr	Tyr
			275				280					285			
Gln	Ser	Thr	Thr	Arg	Asn	Phe	Arg	Arg	Arg	Ile	Ile				
			290			295					300				

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1498742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

Met	Ser	Met	Tyr	Ser	Glu	Gly	Val	Ser	Ser	Gln	Leu	Arg	Arg	Asp	Arg
1				5						10				15	
Val	Asp	Lys	Lys	Ser	Glu	Val	Ala	Thr	Phe	Ile	Ser	Thr	Asp	Asn	Ile
			20					25					30		
Arg	Leu	Ser	Gly	Ser	Val	Lys	Phe	Glu	Val	Tyr	Asp	Lys	Asp	Glu	Leu
		35					40					45			
Val	Leu	Ser	Gly	Thr	Leu	Glu	Met	Ser	Gly	Ser	Asn	Gly	Phe	Thr	Gly

50						55						60					
Glu	Ser	Lys	His	Ser	Val	Lys	Arg	Trp	Asn	Met	Asn	Cys	Glu	Ala	Glu		
65					70					75					80		
Ile	Thr	Ala	Gly	Ser	Gly	Phe	Leu	Lys	Glu	Lys	His	Ile	Gly	Gly	Ser		
				85					90					95			
Glu	Leu	Ser	Ser	Pro	Leu	Pro	Thr	Ile	Glu	Val	Tyr	Val	Thr	Gly	Cys		
			100					105					110				
Phe	Ser	Gly	Thr	Pro	Ile	Ile	Leu	Thr	Lys	Thr	Leu	Gln	Leu	Gly	Phe		
		115					120					125					
Arg	Lys	Lys	His	Gly	Arg	Val	Thr	Ala	Leu	Asp	Ser	Ile	Pro	Glu	Tyr		
	130					135					140						
Glu	Thr	Asp	Glu	Pro	His	Lys	Gly	Asn	Ser	Ser	Glu	Leu	Asp	Tyr	Gln		
145				150					155						160		
Val	Thr	Glu	Tyr	Gly	Ser	Tyr	Lys	Gln	Glu	Tyr	Glu	Gly	Glu	His	Ser		
				165				170						175			
Asp	Met	Tyr	Trp	Asn	Arg	Glu	Tyr	Ala	Asp	Gly	Glu	Asp	Gly	Glu	Met		
		180						185					190				
Ser	Trp	Phe	Asn	Ala	Gly	Val	Arg	Val	Gly	Val	Gly	Ile	Gly	Leu	Gly		
		195					200					205					
Val	Cys	Val	Gly	Leu	Gly	Ile	Gly	Val	Gly	Leu	Leu	Val	Arg	Thr	Tyr		
	210					215					220						
Gln	Ser	Thr	Thr	Arg	Asn	Phe	Arg	Arg	Arg	Ile	Ile						
225					230					235							

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1608
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

aatcggagat	tttctctcct	tctcttttca	gccgccaatc	gccgccgcaa	tcttcttcat	60
cggcctccgt	tctacatcga	cgggtgtttgc	cgtaacttct	gtcaaactct	cagaatttgc	120
ttaagtatac	cacctaaactc	gagacgctat	gaccgttttc	tcagttcagt	ccactatctt	180
cagtcgagcc	tccgtagctc	ttctctcgag	caatggcttc	aaacgatttt	cattcgtttc	240
ttcgttttct	tctccgccg	cttactctcc	acctaaaatg	aggaagcgtc	gctacccaat	300
cgtctctgct	gttgatattg	gtggcgctgc	aatcgctaga	aatgatgtgg	tgagagagga	360
tgatccaaca	aataatgtac	cagattcgat	tttctctaaa	ctaggaatsc	agctacacag	420
aagagataag	catccgattg	gtatcttaaa	aaacgctatc	tacgattact	ttgattccaa	480
ttactcaaac	aagtttgaga	agttcgaaga	cctttcccca	attgttacca	caaagcaaaa	540
ctttgatgat	gtgctagtcc	ctgctgatca	tgtaagcaga	agtcttaatg	acacgtacta	600
tgtagactca	caaactgttt	tgagatgtca	tacgagtgtc	caccaagctg	agctgttgag	660
gaaaggatcat	agtcgtttcc	ttgtaaccgg	ggatgtttac	cgaagagatt	ctattgactc	720
tactcattat	ccggttttcc	atcagatgga	aggtttttgt	gttttctctc	ctgaggactg	780
gaacgggtct	ggcaaggatt	ccactttgta	tgctgctgag	gatttgaaaga	aatgtcttga	840
gggattggca	cgccacttat	ttggttcggt	ggagatgaga	tgggttgata	catatttccc	900
atttaccat	ccatcttttg	agcttgagat	atattttaag	gaagactggg	tggagggttt	960
gggctgtggg	gtgaccgagc	aagtaattct	gaaacaaagt	ggataagaaa	ataatgttgc	1020
ttgggccttc	ggacttggac	ttgagagact	tgctatgggt	ttgtttgaca	tacctgatat	1080
acgatttttc	tggtcatccg	atgaacgatt	cacgtcccag	tttgaaaaag	gagaacttgg	1140
agtgaatttc	aagccatatt	caaagtatcc	tccttggttac	aaggacatca	gtttctggat	1200
aagtgatttg	ttcacagaga	ataatttttg	tgaagtgtgt	agaggaattg	ctggggatct	1260
tgttgaagag	gtgaagttaa	ttgaccaatt	caccaataag	aagaaaaggg	tgacgagtca	1320
ttgttacaga	atcgtgttcc	gttccatgga	gcggtctctt	acggacgagg	aggtcaatga	1380
tctgcagagt	aaagtgcgtg	atgaggtgca	gaagaagcta	aatgtcgaat	taaggtgaga	1440
attttgaaaa	gagtagcggt	gttgacagaca	gtgatgaata	ttgaagggtt	ggcattgtta	1500
ttcctacata	aacttttatt	acttctggca	gaattgcatt	accctcaaaa	aaatatatgt	1560

acattgggttt cgttattcta aaggaatgaa aaataaggtg tccgtttt

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..285

(D) OTHER INFORMATION: / Ceres Seq. ID 1498744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

Met	Thr	Val	Phe	Ser	Val	Gln	Ser	Thr	Ile	Phe	Ser	Arg	Ala	Ser	Val
1				5					10					15	
Ala	Leu	Leu	Ser	Ser	Asn	Gly	Phe	Lys	Arg	Phe	Ser	Phe	Val	Ser	Ser
			20					25					30		
Phe	Ser	Ser	Ser	Ala	Ala	Tyr	Ser	Pro	Pro	Lys	Met	Arg	Lys	Arg	Arg
		35				40					45				
Tyr	Pro	Ile	Val	Ser	Ala	Val	Asp	Ile	Gly	Gly	Val	Ala	Ile	Ala	Arg
	50					55					60				
Asn	Asp	Val	Val	Arg	Glu	Asp	Asp	Pro	Thr	Asn	Asn	Val	Pro	Asp	Ser
65					70					75				80	
Ile	Phe	Ser	Lys	Leu	Gly	Xaa	Gln	Leu	His	Arg	Arg	Asp	Lys	His	Pro
			85					90					95		
Ile	Gly	Ile	Leu	Lys	Asn	Ala	Ile	Tyr	Asp	Tyr	Phe	Asp	Ser	Asn	Tyr
			100					105					110		
Ser	Asn	Lys	Phe	Glu	Lys	Phe	Glu	Asp	Leu	Ser	Pro	Ile	Val	Thr	Thr
		115					120					125			
Lys	Gln	Asn	Phe	Asp	Asp	Val	Leu	Val	Pro	Ala	Asp	His	Val	Ser	Arg
	130					135					140				
Ser	Leu	Asn	Asp	Thr	Tyr	Val	Asp	Ser	Gln	Thr	Val	Leu	Arg	Cys	
145				150					155					160	
His	Thr	Ser	Ala	His	Gln	Ala	Glu	Leu	Leu	Arg	Lys	Gly	His	Ser	Arg
			165					170					175		
Phe	Leu	Val	Thr	Gly	Asp	Val	Tyr	Arg	Arg	Asp	Ser	Ile	Asp	Ser	Thr
		180						185					190		
His	Tyr	Pro	Val	Phe	His	Gln	Met	Glu	Gly	Phe	Cys	Val	Phe	Ser	Pro
		195					200					205			
Glu	Asp	Trp	Asn	Gly	Ser	Gly	Lys	Asp	Ser	Thr	Leu	Tyr	Ala	Ala	Glu
	210					215					220				
Asp	Leu	Lys	Lys	Cys	Leu	Glu	Gly	Leu	Ala	Arg	His	Leu	Phe	Gly	Ser
225				230						235				240	
Val	Glu	Met	Arg	Trp	Val	Asp	Thr	Tyr	Phe	Pro	Phe	Thr	Asn	Pro	Ser
			245						250				255		
Phe	Glu	Leu	Glu	Ile	Tyr	Phe	Lys	Glu	Asp	Trp	Leu	Glu	Val	Leu	Gly
		260						265					270		
Cys	Gly	Val	Thr	Glu	Gln	Val	Ile	Leu	Lys	Gln	Ser	Gly			
	275					280						285			

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1498745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

Met	Arg	Lys	Arg	Arg	Tyr	Pro	Ile	Val	Ser	Ala	Val	Asp	Ile	Gly	Gly
1				5					10					15	
Val	Ala	Ile	Ala	Arg	Asn	Asp	Val	Val	Arg	Glu	Asp	Asp	Pro	Thr	Asn
			20					25					30		
Asn	Val	Pro	Asp	Ser	Ile	Phe	Ser	Lys	Leu	Gly	Xaa	Gln	Leu	His	Arg
		35					40					45			
Arg	Asp	Lys	His	Pro	Ile	Gly	Ile	Leu	Lys	Asn	Ala	Ile	Tyr	Asp	Tyr
	50					55					60				
Phe	Asp	Ser	Asn	Tyr	Ser	Asn	Lys	Phe	Glu	Lys	Phe	Glu	Asp	Leu	Ser
65					70				75					80	
Pro	Ile	Val	Thr	Thr	Lys	Gln	Asn	Phe	Asp	Asp	Val	Leu	Val	Pro	Ala
				85					90					95	
Asp	His	Val	Ser	Arg	Ser	Leu	Asn	Asp	Thr	Tyr	Tyr	Val	Asp	Ser	Gln
			100					105					110		
Thr	Val	Leu	Arg	Cys	His	Thr	Ser	Ala	His	Gln	Ala	Glu	Leu	Leu	Arg
		115					120					125			
Lys	Gly	His	Ser	Arg	Phe	Leu	Val	Thr	Gly	Asp	Val	Tyr	Arg	Arg	Asp
	130					135					140				
Ser	Ile	Asp	Ser	Thr	His	Tyr	Pro	Val	Phe	His	Gln	Met	Glu	Gly	Phe
145					150					155				160	
Cys	Val	Phe	Ser	Pro	Glu	Asp	Trp	Asn	Gly	Ser	Gly	Lys	Asp	Ser	Thr
				165				170						175	
Leu	Tyr	Ala	Ala	Glu	Asp	Leu	Lys	Lys	Cys	Leu	Glu	Gly	Leu	Ala	Arg
			180					185					190		
His	Leu	Phe	Gly	Ser	Val	Glu	Met	Arg	Trp	Val	Asp	Thr	Tyr	Phe	Pro
		195					200					205			
Phe	Thr	Asn	Pro	Ser	Phe	Glu	Leu	Glu	Ile	Tyr	Phe	Lys	Glu	Asp	Trp
	210					215					220				
Leu	Glu	Val	Leu	Gly	Cys	Gly	Val	Thr	Glu	Gln	Val	Ile	Leu	Lys	Gln
225					230					235					240
Ser	Gly														

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

accagaagaa	gagccacaca	ctcacaaatt	aaaaagagag	agagagagag	agagacagag	60
agagagagag	attctgcgga	ggagcttctt	cttcgtaggg	tggtcatcgt	tattaacggt	120
atcgccccta	cgtcagctcc	atctccagaa	acatgggtgc	aggtggaaga	atgccgggttc	180
ctacttcttc	caagaaatcg	gaaaccgcga	ccacaaagcg	tgtgccgtgc	gagaaaccgc	240
ctttctcggt	gggagatctg	aagaaagcaa	tccgcgcgca	ttgtttcaaa	cgctcaatcc	300
ctcgctcttt	ctcctacctt	atcagtgaca	tcattatagc	ctcatgcttc	tactacgtcg	360
ccaccaatta	cttctctctc	ctccctcagc	ctctctctta	cttggttgg	ccactctatt	420
gggcctgtca	aggctgtgtc	ctaactggta	tctgggtcat	agcccacgaa	tgcggtoacc	480
acgcattcga	cgactaccaa	tggttggtat	acacagttgg	tcttatcttc	cattccttcc	540
tctctgctcc	ttacttctcc	tggaagtata	gtcatcgccg	tcaccattcc	aacactggat	600
ccctcgaaag	agatgaagta	tttgtcccaa	agcagaaatc	agcaatcaag	tggtacggga	660
aatacctcaa	caaccctctt	ggacgcacat	tgatgttaac	cgtccagttt	gtcctcgggt	720
ggcccttgta	cttagccttt	aacgtctctg	gcagaccgta	tgacgggttc	gcttgccatt	780
tcttccccaa	cgctcccatc	tacaatgacc	gagaacgcct	ccagatatata	ctctctgatg	840
cgggtattct	agccgtctgt	tttggtcttt	accgttacgc	tgctgcacaa	gggatggcct	900
cgatgatctg	cctctacgga	gtaccgcttc	tgatagtga	tgcgttcctc	gtcttgatca	960
cttacttgca	gcacactcat	ccctcggttc	ctcactacga	ttcatcagag	tgggactggc	1020

tcaggggagc	tttggctacc	gtagacagag	actacggaat	cttgaacaag	gtgttccaca	1080
acattacaga	cacacacgtg	gctcatcacc	tggtctcgac	aatgccgcat	tataacgcaa	1140
tggaagctac	aaaggcgata	aagccaattc	tgggagacta	ttaccagttc	gatggaacac	1200
cgtggatatgt	ggcgatgtat	agggaggcaa	aggagtgtat	ctatgtagaa	ccggacaggg	1260
aaggtgacaa	gaaaggtgtg	tactgggtaca	acaataagtt	atgaggatga	tggtgaagaa	1320
attgtcgact	tttctcttgt	ctgtttgtct	tttgtaaag	aagctatgct	tcgttttaat	1380
aatcttattg	tccattttgt	tgtgttatga	cattttggct	gctcattatg	ttatgtggga	1440
agttagtgtt	c					

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..383

(D) OTHER INFORMATION: / Ceres Seq. ID 1498747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

Met	Gly	Ala	Gly	Gly	Arg	Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser
1			5					10					15		
Glu	Thr	Asp	Thr	Thr	Lys	Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser
			20					25					30		
Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser
			35				40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Ser	Asp	Ile	Ile	Ile	Ala	Ser
			50				55				60				
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro
65					70				75					80	
Leu	Ser	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val
			85					90					95		
Leu	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe
			100					105					110		
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser
			115				120					125			
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His
			130				135				140				
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145					150					155				160	
Gln	Lys	Ser	Ala	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu
			165					170					175		
Gly	Arg	Ile	Met	Met	Leu	Thr	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro	Leu
			180					185					190		
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Cys
			195				200					205			
His	Phe	Phe	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	Gln
			210				215				220				
Ile	Tyr	Leu	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu	Tyr
225					230					235				240	
Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Met	Ala	Ser	Met	Ile	Cys	Leu	Tyr	Gly
			245					250					255		
Val	Pro	Leu	Leu	Ile	Val	Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr	Tyr	Leu
			260					265					270		
Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp
			275					280				285			
Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	Leu
			290				295				300				
Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	Leu
305					310					315				320	
Phe	Ser	Thr	Met	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile

				325				330					335		
Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Trp	Tyr
			340					345					350		
Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro	Asp
		355					360					365			
Arg	Glu	Gly	Asp	Lys	Lys	Gly	Val	Tyr	Trp	Tyr	Asn	Asn	Lys	Leu	
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..377
(D) OTHER INFORMATION: / Ceres Seq. ID 1498748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

Met 1	Pro	Val	Pro	Thr 5	Ser	Ser	Lys	Lys	Ser 10	Glu	Thr	Asp	Thr	Thr 15	Lys
Arg	Val	Pro	Cys 20	Glu	Lys	Pro	Pro	Phe 25	Ser	Val	Gly	Asp	Leu 30	Lys	Lys
Ala	Ile	Pro 35	Pro	His	Cys	Phe	Lys 40	Arg	Ser	Ile	Pro	Arg 45	Ser	Phe	Ser
Tyr	Leu	Ile	Ser	Asp	Ile	Ile	Ile 55	Ala	Ser	Cys	Phe 60	Tyr	Tyr	Val	Ala
Thr 65	Asn	Tyr	Phe	Ser	Leu 70	Leu	Pro	Gln	Pro	Leu 75	Ser	Tyr	Leu	Ala	Trp 80
Pro	Leu	Tyr	Trp	Ala 85	Cys	Gln	Gly	Cys	Val 90	Leu	Thr	Gly	Ile	Trp 95	Val
Ile	Ala	His	Glu 100	Cys	Gly	His	His	Ala 105	Phe	Ser	Asp	Tyr	Gln 110	Trp	Leu
Asp	Asp	Thr 115	Val	Gly	Leu	Ile	Phe 120	His	Ser	Phe	Leu	Leu 125	Val	Pro	Tyr
Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg 135	Arg	His	His	Ser 140	Asn	Thr	Gly	Ser
Leu 145	Glu	Arg	Asp	Glu 150	Val	Phe	Val	Pro	Lys	Gln 155	Lys	Ser	Ala	Ile	Lys 160
Trp	Tyr	Gly	Lys	Tyr 165	Leu	Asn	Asn	Pro	Leu 170	Gly	Arg	Ile	Met	Met	Leu
Thr	Val	Gln	Phe 180	Val	Leu	Gly	Trp 185	Pro	Leu	Tyr	Leu	Ala 190	Phe	Asn	Val
Ser	Gly	Arg 195	Pro	Tyr	Asp	Gly	Phe 200	Ala	Cys	His	Phe	Phe 205	Pro	Asn	Ala
Pro	Ile 210	Tyr	Asn	Asp	Arg	Glu 215	Arg	Leu	Gln	Ile	Tyr 220	Leu	Ser	Asp	Ala
Gly 225	Ile	Leu	Ala	Val 230	Cys	Phe	Gly	Leu	Tyr	Arg 235	Tyr	Ala	Ala	Ala	Gln 240
Gly	Met	Ala	Ser	Met 245	Ile	Cys	Leu	Tyr	Gly 250	Val	Pro	Leu	Leu	Ile	Val
Asn	Ala	Phe 260	Leu	Val	Leu	Ile	Thr 265	Tyr	Leu	Gln	His	Thr 270	His	Pro	Ser
Leu	Pro	His 275	Tyr	Asp	Ser	Ser	Glu 280	Trp	Asp	Trp	Leu	Arg 285	Gly	Ala	Leu
Ala	Thr 290	Val	Asp	Arg	Asp	Tyr 295	Gly	Ile	Leu	Asn	Lys 300	Val	Phe	His	Asn
Ile 305	Thr	Asp	Thr	His 310	Val	Ala	His	His	Leu	Phe 315	Ser	Thr	Met	Pro	His 320
Tyr	Asn	Ala	Met	Glu 325	Ala	Thr	Lys	Ala	Ile 330	Lys	Pro	Ile	Leu	Gly	Asp

Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu
340 345 350
Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly Asp Lys Lys
355 360 365
Gly Val Tyr Trp Tyr Asn Asn Lys Leu
370 375

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1498749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala
1 5 10 15
Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe
20 25 30
Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu
35 40 45
Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala
50 55 60
Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu
65 70 75 80
Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr
85 90 95
His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg
100 105 110
Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val
115 120 125
Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr
130 135 140
Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile
145 150 155 160
Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met
165 170 175
Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly
180 185 190
Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu
195 200

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1813

(D) OTHER INFORMATION: / Ceres Seq. ID 1498750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

ctccttttaga gagagcgtgc catttttatt tttctctttc ttctctcatt tttattttct	60
tttctttttt ttcacctttt tttttccttt ttttttcttt cttcttcttc ttacttgatt	120
ttgaacccta gcttaagggg aattttctcg ggaaacaaaa gagatatttt tatcgcagtg	180
agaaagaaac acaaaaaatg cagaatcaaa ggcttattaa gcagcaacaa caacaacaac	240
aacagcaaca tcaacaagct atgattcaac aagctatgat gcaacaacat ccttctcttt	300

atcatcctgg tggatatggct cctcctcaga tggagccttt accaagtgga aaccttcctc 360
ctgggttttga tccaactact tgccgtagtg tgtatgctgg aaacattcat acgcagggtca 420
cagagattct tcttcaagag atttttgcaa gtactgggtcc tattgaaagc tgtaaactca 480
tcagaaagga taagtcataca tatggatttg ttcactactt tgatcgaaga tgtgctagta 540
tggctataat gactcttaac ggaaggcata tatttggaca gcctatgaaa gttaatggg 600
cgtatgcaac tgggtcaaagg gaagatacat caagtcattt caacattttt gttggagatc 660
ttagtccaga ggttactgat gcagcattgt ttgatagctt ttctgctttt aacagctgct 720
cggacgcaag agtaatgtgg gaccagaaaa ctggacgctc aagaggcttt ggttttgttt 780
ccttccgtaa tcagcaggat gctcaaactg ccattaatga gatgaatggt aaatgggtaa 840
gtagcagaca gatcagatgc aactgggcga caaaaggtgc tacttttggc gaggacaaac 900
atagctctga tgaaaaaagt gttgtagaac ttactaacgg atcttcagag gatggtagag 960
agctgtcaaa tgaagatgcc cctgaaaaca atcctcaatt tacaactgtc tatgtaggaa 1020
atctctctcc agaaataact cagcttgatc tacaccgtct attctatacc cttgggtgctg 1080
gagtgatcga agagggtccgt gtccagcgag acaaaggggt tggttttgtg agatataaca 1140
ctcatgacga ggctgctctt gctattcaga tgggcaacgc tcagcctttc ctcttttagca 1200
gacagataag gtgttctctg ggaacaaaac caactccatc aggcacagcc tcaaaccac 1260
ttccccacc agccccggca tcagtcctt ctctgtctgc aatggacctc ttagcctacg 1320
agaggcaact ggctctagcc aagatgcac ctcaggctca acattctctg aggcaagcag 1380
gtcttggagt caatgttgct ggaggaactg cagctatgta tgatgggtggc tatcagaatg 1440
tagctgcggc ccatcagcag ctcatgtact atcagtaata aaccctcttc actggctctg 1500
agataccttt ttctgtttct ttctttttct tcttcttaat ttataactt tcttgctttt 1560
tctagacctt ccttggttcaa gagtctttat gtatgtgtct ctttcattta aagccgttgg 1620
ttttatttat gtatgcagag ctttatgtct agtttgtaac ctataggtct tacttggtt 1680
gtaagccaag caataagaca acatcaaata aaaggggatt tggttttctg gggttaatgt 1740
tgtttgtgg tctgtaatga taggtttgaa acaaagtaat ttgtctttta taaaagtttt 1800
atagtttcat ttc

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1498751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

Met Gln Asn Gln Arg Leu Ile Lys Gln Gln Gln Gln Gln Gln Gln Gln
1 5 10 15
Gln His Gln Gln Ala Met Ile Gln Gln Ala Met Met Gln Gln His Pro
20 25 30
Ser Leu Tyr His Pro Gly Val Met Ala Pro Pro Gln Met Glu Pro Leu
35 40 45
Pro Ser Gly Asn Leu Pro Pro Gly Phe Asp Pro Thr Thr Cys Arg Ser
50 55 60
Val Tyr Ala Gly Asn Ile His Thr Gln Val Thr Glu Ile Leu Leu Gln
65 70 75 80
Glu Ile Phe Ala Ser Thr Gly Pro Ile Glu Ser Cys Lys Leu Ile Arg
85 90 95
Lys Asp Lys Ser Ser Tyr Gly Phe Val His Tyr Phe Asp Arg Arg Cys
100 105 110
Ala Ser Met Ala Ile Met Thr Leu Asn Gly Arg His Ile Phe Gly Gln
115 120 125
Pro Met Lys Val Asn Trp Ala Tyr Ala Thr Gly Gln Arg Glu Asp Thr
130 135 140
Ser Ser His Phe Asn Ile Phe Val Gly Asp Leu Ser Pro Glu Val Thr
145 150 155 160
Asp Ala Ala Leu Phe Asp Ser Phe Ser Ala Phe Asn Ser Cys Ser Asp
165 170 175
Ala Arg Val Met Trp Asp Gln Lys Thr Gly Arg Ser Arg Gly Phe Gly